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NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

Abstract:

The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

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(21) International Application Number: PCT/US99/09346 (22) International Filing Date: 30 April 1999 (30.04.99) (30) Priority Data: <table border="0"> <tr><td>60/083,758</td><td>1 May 1998 (01.05.98)</td><td>US</td></tr> <tr><td>60/094,869</td><td>31 July 1998 (31.07.98)</td><td>US</td></tr> <tr><td>60/098,994</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr> <tr><td>60/099,062</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr> <tr><td>60/103,749</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/103,794</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/103,796</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/121,528</td><td>25 February 1999 (25.02.99)</td><td>US</td></tr> </table>		60/083,758	1 May 1998 (01.05.98)	US	60/094,869	31 July 1998 (31.07.98)	US	60/098,994	2 September 1998 (02.09.98)	US	60/099,062	2 September 1998 (02.09.98)	US	60/103,749	9 October 1998 (09.10.98)	US	60/103,794	9 October 1998 (09.10.98)	US	60/103,796	9 October 1998 (09.10.98)	US	60/121,528	25 February 1999 (25.02.99)	US	(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagrazia [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPUOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US). (74) Agent: HARBIN, Alisa, A.; Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA 94662-8097 (US). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
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(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD		Published <i>Without international search report and to be republished upon receipt of that report.</i>																									
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NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (eg. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins).

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria* menB nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Bimstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (α -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable market that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP- 0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in eg. WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E. Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/EBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4\%[(G + C)] - 0.6(\% \text{formamide}) - 600/n - 1.5(\% \text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe with 95% to 100% homology to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) AAAGAAATTC	(<i>Eco</i> RI)
	(AAA) AAAGGTACC	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) AAATGCAG	(<i>Pst</i> I)
	(AAA) AAATCTAGA	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I)
AAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH_4OH , and deprotected by 5 hours incubation at 56°C . The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100 μl or 1.0ml of water. The OD_{260} was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10 $\mu\text{mol}/\mu\text{l}$.

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40μM of each oligonucleotide primer, 400-800μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *TaqI* DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H₂O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 µl of NEB T4 DNA ligase (400 units/µl), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 µl *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 µl LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 µl of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 µg/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 µl. 5 µl of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20µl, that included 0.5µl T4 DNA ligase (400 units/µl, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100µl of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800µl LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200µl of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M'') (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to T _m of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTTAAAATCCCCT
- 919.2 (forward) ATCCTTCCGCCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCCC
- 919.10 (reverse) TCGTTCCGGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCAGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

279 gnm4.seq

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1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTGC GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGCGAGCGG CAGGCGCGCT TTGGCACC GGCTTTTGGC GGAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTTCGA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCATTTCGCT TTGGCGGGCT TCGGCAAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCGCT CATTCGCGCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGGGTGT
401 ATTGCGCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

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1  ITRICGLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCS SSKPRIAATAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

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1      atgacgcgga tttgcggctg cttgatttca acggttttga gtgttttcggc
51     aagtttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101    ccggcagcgg cagggcgctg ttggcaccgg ctctcttggc ggcagccatg
151    gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccgggcga
201    gttgaagttg acggtcttgc ccaacttcgc ctgtgcggat tcggcacaaa
251    tctgacctgac ctgttcatct tccaaacca aaatgcgcgc catgtgcctt
301    acgccttgcg gtacggcgga ctgcattcagt tcggcgcgca ggcggacgag
351    tttagccga tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401    atgcgcgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451    tccaaataq

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1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPPT
151 SK*

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          10      20      30      40      50      60
m279.pep  ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA
           :|||:|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g279       MTRICGCLISTVSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA
           10      20      30      40      50      60

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a279.seq
      1  ATGACNCNGA  TTTGCGGCTG  CTTGATTTCa  ACGGTTTnna  GGGCTTCGGC
     51  GAGTTTGTCTG  GCGGCGGGTT  TCATGAGGCT  GCAATGGGAA  GGTACNGACA
    101  CNGGCAGCGG  CAGGGCGCGT  TTGGCCCCGG  CTTCTTTGGC  GGCAAGCATA
    151  GCGCGCTCGA  CGGCGGCGCG  ATTGCCCTGA  ATCAGCACTT  GTCCGGGCGA
    201  GTTGAAGTTG  ACGGCTTCAA  CCATCTCATC  CTGTGCGGAT  TCGGCGCAAA
    251  TTTGTTTTAC  CTGTTTCATC  TCCAAGCCGA  GAATCGCGCG  CATTGCGCCC
    301  ACGCCTTGCG  GTACGGCGGA  CTGCATCAGT  TCGGCGCGCA  NGCGCACGAG
    351  TTTGACCGCG  TCGGCAAAAT  CCAATGCGCC  GGCGGCAACN  AGTGCAGTGT
    401  ATCCGCCGAN  GCTGTGTCCG  GCAACGCGCG  CAGGCGTTTT  GCCGCCCGCT
    451  TCCGAATAG
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a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	ARSTAAALPA	ITTCGELKL	TASTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAPAT	SAVYSPXLCF	ATAAGVLPPA
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
	:					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAOALTCCSSSKPRIAAAIAPTPCGTADCISSARRRTSLTA					
a279	ITTCPGELKLTASTTSSCADSAQICFTCCSSSKPRIAAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAPAATSAVYSPXLCFATAAGVLPPASEX					
	130	140	150			

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m519.seq (partial)
1 ..TCCGTATCG GCGCATGGA GTTGGACAAA ACGTTTGAAG AACGCGACGA
51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTt9GG
101 GTGTGAAGGT TTTGCGTTAT GAGATTAAG ACTTGGTTCG GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCGCAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
```

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCC3CATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTGTG CGAAGCCAAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLSAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggtttcaa
51 atcctttgtc gtcatccccc agcaggaagt ccacgttgct gaaaggtctg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta ttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggt cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgcgga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcggt aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgcg agaaaatcgc ccgcatcaac cgcgccaag
701 gcgaagcgga atccctgctc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcccctt tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag ccgccaagg ttgccgaaat cgggaacctt
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaataa
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51 IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKCLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLYRIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAQVNA SNAEKIARIN RAKGEAESLR LVAEANAQAN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFP EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519
m519.pep
g519
m519.pep

```

Sequence alignment showing identity between m519.pep and g519 (ORF 519.ng) over a 200 aa overlap. The alignment is shown in blocks of 10, 20, 30, 40, 50, 60, 70, 80, and 90 residues.

```
a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG AGCGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ATCTGTGACG
251 STATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGCAAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAG CGTGCTCTCC GCCTCGATG AAGCGCGCGG AGCTTGGGCT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AATTACTGCT TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATTCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCCG AAGCCGAAAT CCAACAATCG GAAGCGGAGG CTCAGGCTGC
651 GGCTAATGCG TCAAAATCCG AGAAAATCGC CGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATT CGCGCGCCCT TCAAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCCG GTTCAACAAAT CTTGCCAAAT
851 AAAGCAATAC GCTGATTATG CCGCCCAATG TTGCCGACAT CGGCACGCTG
901 ATTTCTGCCG GTATGAAATAT TATCGACAGC AGCAAAACAGC CCAAAATAA
```

```
a519.pep
1  MEFFIILLAA VVVFGKSFV VIPQQEVHVV ERLGRFHRL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIVFQV TDPKLASYGS
101 SNYIMAITQL AQTLIRSVIG RMELDKTFEE KDEINSTVVS ALDEAAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRAIAESEK RKIEQINLAS
201 GQREAEIQQS EGEEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTS GGADAVNLKI AEQYVAEFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*
```

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
a519	YFQVTDPKLASYGSSNYIMAITQLAQTTILRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
	GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGOREAE					
a519	GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGOREAE					
	150	160	170	180	190	200
		100	110	120	130	140
						150

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                |||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                |||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51  ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TCGGTTATCA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILVLA VAVFGKFSV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEIILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGCTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TCGTCTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 CTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTGAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLR YEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQA AVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQA AVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCGGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGC GC CTTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEEI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

a519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVVVFGEKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
m519-1	MEFFIILLVAVAVFGKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS					
	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE					
	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
	LVAEANAEEAIRQIAAALQQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAEEAIRQIAAALQQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	310					
	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1  ..MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLIVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1  ..atgggctgag acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaaat gatgatgaaa
151 ttctctgcagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcgta ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactggtca aaatcggcgc acccgaaaaa
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1  ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLEK NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```
m576.pep      10      20      30      40      50      60
MQQASYAMGVDIGRSLQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAEVMMKFLQ
|||||
```


80

```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLO
                10      20      30      40      50

m576.pep      70      80      90      100     110     120
EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGEKQPTKDDIV
|||||
g576          60      70      80      90      100     110
EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGEKQPTKDDIV

m576.pep      130     140     150     160     170     180
TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
|||||
g576          120     130     140     150     160     170
TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE

m576.pep      190     200     210     220
QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
|||||
g576          180     190     200     210
QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51 ACTTTCGCCG TCGGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC  CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC SGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGCGCA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLKENAA KDGVKTTASG
151 LQYKITQGE  GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

m576.pep      10      20      30
MQQASYAMGVDIGRSLKQMKEQGAEIDLKV
|||||
a576          30      40      50      60      70      80
CGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGVDIGRSLKQMKEQGAEIDLKV

m576.pep      40      50      60      70      80      90
FTEAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
|||||
a576          90      100     110     120     130     140
FTEAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA

```

	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPFVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPFVTFPLSQ					
	150	160	170	180	190	200
	160	170	180	190	200	210
m576.pep	VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
	220					
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCAGC
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCCA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGACAAAAT	CGGTCCGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

1	MNTIFKISAL	TLAALALSA	CGKKEAAPAS	ASEPAAASSA	QGDTSIGST
51	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
101	AQEVMMKFLO	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
151	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFFPLSQ
201	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
251	KIGAPENAPA	KQPAQVDIKK	VN*		

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTGCCGCG	CAGGGCGACA	CCTCTTCAAT	CGGCAGCAGC
151	ATGCAGCAGG	CAAGCTATGC	AATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAATGAC	CGAAGAGCAG
301	GCCCAGGAAG	TGATGATGAA	ATTCCTGCAG	GAGCAGCAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401	TCCTGAAGGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGT
451	CTGCAGTACA	AAATCACCAA	ACAGGGTGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGGAAT	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCCA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG

701 CCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASAA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISALTLSAALALSACGKKEAPASASEPAASAAQGDTSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAPASASEPAASAAQGDTSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLOEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
 101 CTGCCGCCG TTCTTCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAG
 151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
 201 GCAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAACAGC CGACCAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
 601 GTGATTCTGG GTTGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGGCG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	ATLVFDVKLVKIGAFENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAFENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGCGGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
 301 TCGGCCAAG CCTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

```

451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCTTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAAACCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAACCTCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGGAAG CCGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1  MKKYLFRAAL YGIAAAILAA COSKSIOTFP OPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGGDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IOGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPOR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCGGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGTAT TACGAACCGG TGCTGAAGGG CGACCGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCGCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGcgcgCTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcG tCGaacttTT TTTTATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAAACCCg tccggcaaat acatCCGCat cgggATacgcc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGT ACCCGCAAAG
1151 CCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGCAGGAAG CCGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPVSI GRYMADKGYL
301 KLGOTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

```

m919/g919

      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      MKKHLRSALYGIAAAILAACQSRSIQTFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKQFFER
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSFQAKRFFER
          70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYIGIPDDFISVPLPAGLRGGKN
          130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      LVRIRQTGKNSGTIDNAGGTHTADLSRFPI TARTTAIKGRFEGRFLPYHTRNQINGGAL
          190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPVSI GRYMADKGYL
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPVSI GRYMADKGYL
          250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGOTSMQGI KSYMQRNPORLAEVLGQNPSYIIFRELAYSNDGPVGALGTPLMGEYAGA
          |||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      KLGOTSMQGI KAYMRQNPORLAEVLGQNPSYIIFRELAYSNDGPVGALGTPLMGEYAGA
          310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          :|||:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g919      IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

```

	430	440
m919.pep	QKTTGYVWQLLPNGMKPEYRPX	
g919	QKTTGYVWQLLPNGMKPEYRPX	
	430	440

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```
a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGCCCG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGGCCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCTTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGCCCCAAG CCTTCAAAAC CCCGTCAT TCCGTTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTCACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCTGTCCT CTGCTGCGG GTTTCGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCGCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCTTCCT CCCCTACAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCGATACT CGGTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGCGCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCGCTGA TGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGATAC GCGCAGGAAG CCGGCGAAGT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAAGC
1301 GTATGAAGCC CGAATACCGC CCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```
a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGGAV YTVVPHLSLP HWAQAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQAQFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGSRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPQR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELACK QKTTGYVWQL LPNGMKPEYR P*
```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

	10	20	30	40	50	60
m919.pep	MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
a919	MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
a919	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER					
	70	80	90	100	110	120

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLA3TVTGYE	PVLKGD	DRRTAQARFPIY	GIPDDFISVPL	PAGLRSGKA	
a919	YFTPWQVAGNGSLA3TVTGYE	PVLKGD	DRRTAQARFPIY	GIPDDFISVPL	PAGLRSGKA	
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGT	HTADLSRFPITARTTAIKGR	FEGRFLPYHTRNQINGGAL			
a919	LVRIRQTGKNSGTIDNTGGT	HTADLSRFPITARTTAIKGR	FEGRFLPYHTRNQINGGAL			
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYAD	KNEHPYVSIGRYMADKGYL			
a919	DGKAPILGYAEDPVELFFMH	IQSGRLKTPSGKYIRIGYAD	KNEHPYVSIGRYMADKGYL			
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLQOTSMQGIKSYMQRNPOR	LAELVGNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA		
a919	KLQOTSMQGIKSYMQRNPOR	LAELVGNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA		
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPV	TRKALNRLIMAQDTGSAIK	GA VRVDYFWGYGDEAGELAGK			
a919	VDRHYITLGAPLFVATAHPV	TRKALNRLIMAQDTGSAIK	GA VRVDYFWGYGDEAGELAGK			
	370	380	390	400	410	420
	430	440				
m919.pep	OKTTGYVWQLLPNGMKPEYRPX					
a919	OKTTGYVWQLLPNGMKPEYRPX					
	430	440				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCGCTGCTG GCGxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCGGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```


1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL Axxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
151 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

1 ATGGAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51 GCGGATGCC GTGCTGGTAC GGATGGACGG CCGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCTGACC GGTGCGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCTCGGGTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACtGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGCA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCCGCGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAgcgctg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAgcgag cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgatcc accgcgcaaA ccgTttggga cgcgctctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttgGc GCGGTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

1 METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL
51 DLQDTGTDEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAFLVPAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKW LGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYISQLADLPLL					
	:					

```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLP LL
           70      80      90      100     110     120
           130     140     150     160     170     180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLP PGA
           130     140     150     160     170     180
           190     200     210     220     230     240
m121.pep  XXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : |||||:||||| |||||:| |||||
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190     200     210     220     230     240
           250     260     270     280     290     300
m121.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVSHAAADARQMYICGGGIRNPV
           250     260     270     280     290     300
           310     320     330     340     350     360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
g121      LMADLAECFGTRVSLHSTAE LNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310     320     330     340     350     360

m121.pep  XAGYYYY
           |||||
g121      GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCGCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCACA CCGGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGSC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAEE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLP LL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLP PDA PAFGFDTGPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

		10	20	30	40	50	60
m121.pep		METQLYIGIMSGTSM	DGADAVLIRMDGGKWLGAEGHAFTPY	PGRLRRQLLDLQDTGADEL			
a121		METQLYIGIMSGTSM	DGADAVLIRMDGGKWLGAEGHAFTPY	PGRLRRKLDDLQDTGADEL			
		10	20	30	40	50	60
		70	80	90	100	110	120
m121.pep		HRSRILSQELSR	LYAQTAELLC	SQLNAPS	DIT	ALGCHGQTVR	HAPEHGYSIQ
a121		HRSRILSQELSR	LYAQTAELLC	SQLNAPS	DIT	ALGCHGQTVR	HAPEHSYSVQ
		70	80	90	100	110	120
		130	140	150	160	170	180
m121.pep		AXXX					
		: :			:		
a121		AERTQIFTVGDF	SRDLAAGGQ	GA	PLVPAFHEALFR	DDRETRAVL	NIGGIANISVLP
		130	140	150	160	170	180
		190	200	210	220	230	240
m121.pep		XXXXXXXXXXXXXXXXXXXX	QXLPYD	KNGAKSAQGNIL	PQLLDRL	LAHPYFAQR	HPKST
		:					
a121		PAFGEDTGP	GNMLMDJAWMQ	AHQWLPYD	KNGAKAAQGNIL	PQLLDRL	LAHPYFAQ
		190	200	210	220	230	240
		250	260	270	280	290	300
m121.pep		GRELF	AINWLETYLDG	GENRYD	VLRTLSR	FTAQTVCD	AVSHAAADARQ
a121		GRELF	ALNWLETYLDG	GENRYD	VLRTLSR	FTAQTVCD	AVSHAAADARQ
		250	260	270	280	290	300
		310	320	330	340	350	360
m121.pep		LMADLAECF	GTRVS	LHSTAD	LNLD	PQWVEAA	FAWLAA
a121		LMADLAECF	GTRVS	LHSTAE	LNLD	PQWVEAA	FAWMAAC
		310	320	330	340	350	360
m121.pep		XAGYYYY					
a121		GAGYYYY					

m121-1.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGTATC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCAGCG	CTTTACCCCC	TACCCCGGCA	GGTTACGCCG	CCAATTGTCT
151	GATTTGCAGG	ACACAGGCGC	AGACGAATCT	CACCGCAGCA	GGATTTTGTCT
201	GCAAGAACTC	AGCCGCCTAT	ATGCGCAAAC	CGCCGCGGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TGCGCGATT
351	GCGCGTGCTG	CGGGAACGGA	GCGCGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCGCGC	GGACAAGGCG	CGCCACTCGT	CCCGCCTTT
451	CACGAAGCCC	TGTTCCCGCA	CAACAGGGAA	ACACGCGCGG	TACTGAACAT
501	GCGCGGGATT	GCCAACATCA	CGGTACTCCC	CCCCGACGCA	CCCGCCTTCG
551	GCTTCGACAT	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCTTTACGA	CAAAAACGGT	GCAAAGCGCG	CACAAGGCAA
651	CATATTGCCG	CAACTGTCTG	ACAGGCTGCT	CGCCACCCG	TATTTGCGAC
701	AAATCCCACCC	TAAAGACGAC	AGGCGCGAAT	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTAGCGGCGG	CGAATAACGGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACCGCGCAA	CCGTTTGGCA	CGCCGTCTCA	CACGCGCGGG

```

851 CAGATGCCCC TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
  1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
  51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
 101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPF
 151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWTQA
 201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
 351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELCSQNLAPSDITALGCHGQTVRHAPHEGYISQLADLPLL					
	: : : : :					
g121	HRSRILSQELSRLYAQTAAELCSQNLAPCDITALGCHGQTVRHAPHEGYISQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
	: : : : :					
g121	AELTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	: : : : :					
g121	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICGGGIRNPV					
	: : : : :					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	: : : : :					
g121	LMADLAECFGTRVSLHSTAE LNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
g121	GAGYYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
  1 ATGGAAACAC ACCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

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51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAATG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGGCCGGC GGACAAGGCG CGCCGCTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGTGTA TGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACGTA TAGACGTAT TCGGACGCT
801 TTCCCGATT ACCGCGCAA CCGTTTTCGA CGCGCTCTCA CACGCAGCGG
851 CAGATGCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACGCGCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTG
1001 CATGGATGCG GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGEG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAFWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLDLQDTGADEL				
a121-1	METQLYIGIMSGTSMGDADAVLIRMDGGKW	LGAEGHAFTPYPGRLLRRQLDLQDTGADEL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPEHGYSIQADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLITYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLITYLDGGENRYDVLRTLSRFTAQTVFDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDLPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDLPQWVEAAAFWMAACWNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTGT
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAyTTCCCyG TCGGCAAwGT ATTAAACGGA CTGTTCCGCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGACAAAG ACGTGGCTA TtkTGAATTG CAACAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCTCT TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTcAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCGGCCAAAA ACTTCCAAsg CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```

m128.pep (partial)
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51  NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVTFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVK YFPVGXVLNG LFAQXKKLYG IGFTKTVPV
51  WHKDVRYXEL QNGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFS DGTGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHSGF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1   atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTC
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGGCGGATTT CGTATTGAGC GCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACCTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTGGCCGCC
601 GCCCGCGAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCGATTTC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGcctaa ctGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGCG GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCGC CGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCTCACCC TCTTCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgtA GAATGGGACG CGGTCGAAC GCCCAGCCAG
1501 TTTATGGAAT ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCTGCGCGAA AGAACTCTT GACAAAATGC
1601 TcgCGCCAA AACTTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGAGG CTATTACAGC TACGCATGGG CCGAAGTcct
1851 cAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAACG CTTCTGGCAA GAAatccttg ccgctcggcg ctCCCGCAGC
1951 gcgCGGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTCGCG CAaagcggT TCGACAACGC gCcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1   MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTTGWA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLPSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY PDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KPDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNFIHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGT LQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHBTGH GLHHLLTOVD ELGVSGINGV EWD AVELPSQ
501 FMENFVWEYN VLAQMSAHER TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECR LKNW QQVLDSVRKE VAVIOPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRS

```

651 AAESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQICTEDIKPAVQTAIAEARGQIAAVKAQTHGTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPAQTAIAEAREQIAAIKAQTHGTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLSNVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep				YAGEKLREAKYAFSETEVKKYFPVGKVLG		
m128				YASEKLREAKYAFSETXVKYFPVGXVLNG		
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQRGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDCRLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330


```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTAC CGACACGCCC GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCAAGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAAATCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCCGCGAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCGC
1101 CCAAAACAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGCGGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA SAGCGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC SCCCCTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCACGA
1401 AACCGGACAC GGCCTCCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAC TCCAGTCAG
1501 TTTATGGAAT ATTTGTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGCCCAA AAATTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAGAA GTCCGCCGTCG
1751 TCCGACCGCC CGAATAACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAAACG CTTTGGGAG GAAATCTTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIFHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLPLTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKE VAVVREPEYN RFANSFGHIF
 501 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
 551 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHTGWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQTHTGWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIGVGVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIGVGVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep	-----					
a128	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQKKLYGIGFTEKTVPVVHKDVRXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRXFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRKKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDSVRKEVAVVREPEYNRFANSFGHIF					
	550	560	570	580	590	600

m128-1.seq

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

m128-1.pap.

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

```

101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEI SLATKMADTP EQVLNLFHDI
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAFPVG
451 GREARLSHDE ILILFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1 ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51 AATCAAAACC GAAGACATCA AACCAGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TGGCGGATTT CGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCCT
501 CCAAACCGTC CTAGACGCGA CCGACGCGTT CGGCATTATC TTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GEACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901 CCGCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AAACCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGCTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1 MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAOTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPOP WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAFPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10

20

30

40

50

60

100

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA_KAQHTGWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNREKTIKNSPEFA
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNREKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHVLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHVLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPDLSYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQPDLDGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTGGGC	GAAGAACCCC	GTTTGTATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTCG	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTGGTG	TCGCACCTCA	ACTCCGTCAC	CGACACGCCC	GAACGCGCG
251	CGGCCTACAA	TGAATTAATG	CCCGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAACCTCCC
351	CGAGTTCGAC	ACCCTCTCCC	ACGCGCAAAA	AACCAAACTC	AACCACGATC
401	TGCGCGATTT	CGTCCTCAGC	GGCGCGGAAC	TGCCGCGCGA	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTTCGG	CCAAATTCTC

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 TCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTACCCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTT3AG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAC TCCCGAGTCAG
1501 TTTATGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCG AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAAGTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGACAGAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTGA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVY YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDDMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN REANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAERG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGTGWANTVEPLTGIT					
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAA IKAQHTGTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a128-1.pep	ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
m128-1	ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMAOTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMAOTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVVHKDVRVFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

m206 . pep . .

g206.seq

g206.pep

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLLSALLSCGTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	:					
g206	MFSPDKTLFLCLGALLSCGTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRRTARDMAAASRKIPDSRXKAGD					
	:					
g206	LGLIGTPYKWGGSSTATGFDCSGMIQLVYKNALNVKLPRRTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	: :					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTE					

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA .AAACTCTCC ACACGTTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE+
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTCTCTG AAAAAGAGAC AGAGGCAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGCGCGCG CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGATCCG AATATGCTTG CCGGAAATAT GGAATCAAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTCAGATCC CATCCCCGCG TCAAACCTTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGGAA GGGTTGATTG GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAAT CAGAATTGTA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCGAG
1201 TTTGCCGCAA AAGTCGATTG CGGCAGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGCAT GATTTCGATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCG ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTGCGCGCA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSPKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTFNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAA
151 DGMQGGDDPSA GGQNAAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRRS
301 ARSRRLPAE MPLIPVNQAD TLIVDGEAVS LTCHSGNIFA PEGNYRYLTY
351 GAELPLGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQFK AADIDNGFEK TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

```

g287.seq
1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcggtggcg gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggcgcgcccc gttgttctg aaaatgcccg ggaagggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggagggt gcgccgaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttccggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgcgcg aaaaataaac
501 gttgaccac tgtaaggcg attcttgtaa tggtagaaat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaacgat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaataatc atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggc
751 gagattccgc tgattccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaagcgaaa tgcttggtg
951 cagggccgtg tacaacggcg aagtgtgca tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaaattc aaagccgcca tcgatggaaa cggcttaag gggacttga
1151 cggaaaatgg cggcggggat gtttccgga ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

```

g287.pep
1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

51 LPKEKKDEEA AGGAPQADTQ DATAGEGSDQ MAAVSAENTG NGGAATTDNP
101 KNEDAGAQN MPQNAAESAN QTGNQNPAGS SDSAPASNPA PANGGSDFGFR
151 TNVGNVVID GPSQNTLTH CKGDSGNDN LLDEEAPS KS EFELKSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPPT R SARSRRLPA
251 EIPLIPVQNA DTLIVDGEAV SLTGHSNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEFA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTKQF KAAIDGNGFK GTWTENGSGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

7/g287 ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

```

      10      20      30      40      49
m287.pep MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA
      10      20      30      40      50      60

      50      60      70      80      90      100      109
m287.pep KEDAPQAGSQGQAGPASAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
      |||  :|  |  ::|||  |||||  |||||  |||||  |||||  |||||  |||||
g287      AGGAPQADTQD--ATAGEGSDMAAVSAENTGNGGAATTNPKNEDAGAQNDMPQNA--
      70      80      90      100      110

      110      120      130      140      150      160      169
m287.pep DSSTPNHTPDFNMLAGNMENQATDAGESSQFANQPDMANAADGMQGGDPSAGGQNAAGTA
g287      -----

      170      180      190      200      210      220      229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRVDLANGVLIDGPSQNTLTHCKGDS
      ::|||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      -ESANQTGNQNPAGSSDSAPASNPAANGGSDFGRTNVGNVVIDGPSQNTLTHCKGDS
      120      130      140      150      160      170

      230      240      250      260      270      280      289
m287.pep CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKNDKFGVLVADSVQMKGINQYIIFYKP
      |:|  :|  |||  |||||  |||||  |||||  |||||  |||||  |||||
g287      CNGDNLDEEAPSKSEFEKLSDDEEKIKRYKKDEQRENFVGLVADRVRKKDGNTKYIIFYTD
      180      190      200      210      220      230

      290      300      310      320      330      340      349
m287.pep KPTSFARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT
      ||  :  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      KPPT-----RSARSRRSLPAEIPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT
      240      250      260      270      280      290

      350      360      370      380      390      400      409
m287.pep YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTGRFAAKVDFGS
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHFMENGRPYPSGGRFAAKVDFGS
      300      310      320      330      340      350

      410      420      430      440      450      460      469
m287.pep KSVDDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      KSVDDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYR
      360      370      380      390      400      410

      470      480      489
m287.pep PTDAEKGFGFVFAGKKEODX

```

a287, seq

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

1	MFKRSVIAMA	CIVALSACGG	GGGGSPDVKS	ADTLSPKPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDNP
101	ENKDEGPOND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAN	GMQGDPPSAG	ENAGNTADVA	ANQAENNQVG	GQSNPASSTN
201	PNATNGSGDSF	GRINVANGIK	LDSGSENQTL	THCKDKVCDR	FLDEEAEPFK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGNTNG	VIIYKDKSAS
301	SSSARFYRSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSGNIFAP
351	EGNYRRLTSA	AEKLSGGSYA	LSVQGEAPGD	EMLAGTAVYN	GEVLHFHFKM
401	GRPSPSGGRF	AAKLVDFGSKS	VDGIIDSGDK	LHMGTKQFKA	VIDNGNPFKGT
451	WTENGGGDSV	GRFYGPAGEE	VAGKYSYRPT	DAEKGGEFVF	AGKKEOD*

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

[illegible]


```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATCTTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAGG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTGCA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGACATTGTC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPREYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA	AVKMDLQALHGR				
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA	AVKMDLQALHGR				

110

	10	20	30	40	50	60
	70	80	90	100	110	120
g406 . pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406 . pep	LTTSLSTLNAPALSRTQSDGSGSRSSGLNIGGMGYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSGLNIGGMGYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406 . pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406 . pep	IKPKTNAFEAAYKENYALWMGPYKVS KGIKPT EGLMVD FSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAYKENYALWMGPYKVS KGIKPT EGLMVD FSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406 . pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACTGACAG GTATTCCATC GCATGCGCGA GGTAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACCTC
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406 . pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARA AVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVS PANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA

```

251	AYKENYALWM	GPYKVS	KG	IK	PTEGLM	VDFS	DIQPYG	NHMG	NSAPS	VEADN
301	SHEGYGYSDE	AVRRHR	QGQP	*						
m406/a406	ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap									
		10	20	30	40	50	60			
m406.pep		MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAAYKMDLQALHGR								
a406		MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAAYKMDLQALHGR								
		10	20	30	40	50	60			
		70	80	90	100	110	120			
m406.pep		KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG								
a406		KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG								
		70	80	90	100	110	120			
		130	140	150	160	170	180			
m406.pep		LTTSLSTLNAPALSRTQSDGSGSKSSLGGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF								
a406		LTTSLSTLNAPALSRTQSDGSGSKSSLGGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF								
		130	140	150	160	170	180			
		190	200	210	220	230	240			
m406.pep		FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL								
a406		FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL								
		190	200	210	220	230	240			
		250	260	270	280	290	300			
m406.pep		IKPKTNAFEAAAYKENYALWMGPYKVS								
a406		IKPKTNAFEAAAYKENYALWMGPYKVS								
		250	260	270	280	290	300			
		310	320							
m406.pep		SHEGYGYSDEVVRQHRQGQPX								
a406		SHEGYGYSDEAVRRHRQGQPX								
		310	320							

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used *Neisseria* strains

Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 22491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z2491 <SEQ ID 3116>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z001_225 <SEQ ID 3117>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z002_225 <SEQ ID 3118>
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z003_225 <SEQ ID 3119>
 MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQPVLPINRAFARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z004_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z005_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGSAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z006_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z007_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z008_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGSAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z009_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z010_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z011_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLNEQPVL PVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z012_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPINRAPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z023_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z024_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z025_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z026_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSISTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z027_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z028_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z029_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PINRAPARRAG
NADELIGSAMGLNEQPVL PVNRVPARRAGNADELIGNAMGLNEQPVL PVNRAPARRAGNA
DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHI FKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFERTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDSRFLN*

Z032_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFERTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z033_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVL PVNRAPARRAG
NADELIGSAMGLNEQPVL PVNRAPARRAGNADELIGSAMGLLGIAIYRYGGTSVSTGFDCS
GFMQHI FKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFERTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z096_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLFINRAPARRAG
 NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGSAMGLNEQVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMCHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFERTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Reference
Group B		
gnmzq01	NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02	BZ198	Seiler <i>et al.</i> , 1996
gnmzq03	NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04	1000	Seiler <i>et al.</i> , 1996
gnmzq05	1000	Seiler <i>et al.</i> , 1996
gnmzq07	BZ169	Seiler <i>et al.</i> , 1996
gnmzq08	528	Seiler <i>et al.</i> , 1996
gnmzq09	NGP165	Seiler <i>et al.</i> , 1996
gnmzq10	BZ133	Seiler <i>et al.</i> , 1996
gnmzq11	NGE31	Seiler <i>et al.</i> , 1996
gnmzq13	NGE28	Seiler <i>et al.</i> , 1996
gnmzq14	NGH38	Seiler <i>et al.</i> , 1996
gnmzq15	SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16	NGH15	Seiler <i>et al.</i> , 1996
gnmzq17	NGH36	Seiler <i>et al.</i> , 1996
gnmzq18	BZ232	Seiler <i>et al.</i> , 1996
gnmzq19	BZ83	Seiler <i>et al.</i> , 1996
gnmzq21	MC58	Virji <i>et al.</i> , 1992
Group A		
gnmzq22	205900	Our collection

gnmzq23	F6124	Our collection
z2491	Z2491	Maiden <i>et al.</i> , 1998

Group C

gnmzq24	90/18311	Our collection
gnmzq25	93/4286	Our collection

Others

gnmzq26	A22	(group W) Maiden <i>et al.</i> , 1998
gnmzq27	E26	(group X) Maiden <i>et al.</i> , 1998
gnmzq28	860800	(group Y) Maiden <i>et al.</i> , 1998
gnmzq29	E32	(group Z) Maiden <i>et al.</i> , 1998
gnmzq31	<i>N. lactamica</i>	Our collection

Gonococcus

gnmzq32	Ng F62	Maiden <i>et al.</i> , 1998
gnmzq33	Ng SN4	Our collection

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLVITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGA'VNQIANSLT
DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLVITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSA'VNQIANNLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLVITVTEYGTS
YQILDVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSA'VNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AEP LSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSARARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>
 MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS
 YQILDSVTTVSARARLVDSRNGKVLWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>
 MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

Z2491 <SEQ ID 3178>
 MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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Group B		
287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992
Group A		
z2491	Z2491	Maiden <i>et al.</i> , 1998
Gonococcus		
fa1090	FA1090	Dempsey <i>et al.</i> 1991

References:

- Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FAR
FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGRRPSPSRGRFAAKVDFGSKSV DGI I
DSGDGLHMGTKQKFAAIDGNGFKGTWTENG GGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
GFGVFAGKKEQD*

287_2 <SEQ ID 3180>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS
NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ
TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGDS CSGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FAR
FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP
GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGRRPSPSRGRFAAKVDFGSKSV DGI I
DSGDGLHMGTKQKFAAIDGNGFKGTWTENG GGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
GFGVFAGKKEQD*

287_21. <SEQ ID 3181>
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPAPVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNGGAAVADNPKNEDEVAQNDMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
AAGSSDPFASNPAPANGGSGNFRVLDLGVLIIDGPSQNTLTHCKGDS CSGNNFLDEEV
QLKSEFEKLSADAKISNYKKDGKNDKDFVGLVADSVQMKGINQYIIIFYKPKPTS FARFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDGIIDSGD
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATTNPNKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQDDPSAGENAGNTADQA
ANQAENNQVGGSQNPASSTNPATNGGSDFGFRINVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVKNGTNYVVIYKDKSAS
SSSARFRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYG
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGFGVFAKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
AGGAPQADTQDATAGEGSDMAAVSAENTGNGGAATTNPNKDEGAGQNDMPQNAAESAN
QTGNNQFAGSSDSAPASNAPANGGSDFGRTNVGNSVVIDGPSQNTLTHCKGDSGNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKGDTNKYIIFYTDKPTR
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGS
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKSVDGIIDSG
DDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFGV
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSOG
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESSQPANQPDMAAADGMQDDPSAGGQAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGSDFGFRVLDLGVLDGPSQNTLTHCKGDSGSGNNFLDEEV
QLKSEFEKLSADADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFARFRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVDGIIDSGD
DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIC
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTQGGAGAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA AEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEIILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSIVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAEAIRQIAAALQTGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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number**Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22 (group W)	R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26 (group X)	R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800 (group Y)	R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32 (group Z)	R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.

Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

Z2491 <SEQ ID 3208>

MKKYLFRALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM01 <SEQ ID 3209>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM02 <SEQ ID 3210>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM03 <SEQ ID 3211>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQQNQRRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
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QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>

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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
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VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>

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LVRIQGTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQOTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
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QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>

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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
LVRIQGTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
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KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>

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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>

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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYGIIPDDFISVPLPAGLRSGKA
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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQOTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
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ZM17 <SEQ ID 3225>

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LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

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LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

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LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

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DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

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LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPORLAEVLGQNPYSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYEPEVLKGDORRTAQARFPIYIGIPDDFISVPLPAGLRSGKA
LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLQQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

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YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLQQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

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YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAILAACQSKSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDORRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLQQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATTHPIRTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYVFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRL-MAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA
 LVRIQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSGGDPVGALGTPLMGYYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRL-MAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
 LVRIQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKSYMQRNPKLAEVLGQNPSYI FFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRL-MAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
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 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA
 LVRIQTGKNSGTIDNTGGTHADLSRFEITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRL-MAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGTCTTGCCAC	XhoI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	XhoI
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCC	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	XhoI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	XhoI
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	XhoI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	XhoI
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAATCT	XhoI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	XhoI
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	Eco RI
	Reverse	AAACTGCAG-TCAGCGGGCGGGACAATGCCCAT	Pst I
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCCG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	XhoI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	NdeI
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	NdeI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTCTACGCCGTACTGCC	NdeI
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	NdeI
041	Forward	CGCGGATCCCATATG-TTCGTGCGGAACCGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	NdeI
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	XhoI
			Kpn I
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTTCGCCGC	Pst I
043a	Forward	AAAAAAGGTACC-GCAAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-	Pst I
		TTAATCCTGCAACACGAATTCGCCCGTCCG	
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	XhoI
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	Eco RI
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	Pst I
047	Forward	CGCGGATCCCATATG-GTCATCATACAGGCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	XhoI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Eco RI
	Reverse	AAACTGCAG-TCAAGATTTCGACGGGGATGATGCC	Pst I
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Eco RI
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	Pst I
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	Eco RI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTTCACCTTCCT	Sal I
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCCAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAAATTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCCGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTGAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAAAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGGCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
			XhoI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Pst I
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Eco RI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Pst I
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	XhoI
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCGGCATTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	XhoI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAAACGCGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	XhoI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Pst I
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Xba I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Pst I
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTGGAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Xba I
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGAACACGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Xba I
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	BamHI-

	Reverse	CCCGCTCGAG-AAACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC-	XhoI
		ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC-	Eco RI
		ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG-	Pst I
		TTACGCCGACGAAATACTCAGACTTTTCGG	
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTTGCCCCGCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTTCGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTTGCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
			BamHI-
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	NdeI
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	NdeI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGTTCTAAGTTCCTGATATG	NheI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	NdeI
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	NdeI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	NdeI
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	NdeI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	NdeI
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	NdeI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	NdeI
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	NdeI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	XhoI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Eco RI
			Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCTTTCAGTATTATTGAA	XhoI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Pst I
277	Forward	AAAAAAGAATTC-ATGCCCGCTTTGAGGACAAGCTCGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Eco RI
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Pst I
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	XhoI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Pst I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Pst I
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	XhoI
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAAGT	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTCCGAAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	EcoRI- NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGGC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATTT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGCGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTCGCCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTTACCGATTTCCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCAFTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTCGGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTTCACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAAGTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTGCGGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCAAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCTG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCTGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGCGTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTGCGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	Eco RI
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Pst I
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Eco RI
645	Forward	AAAAAAGAATTC-GTGAACAGAGCAACACGTAAATCG	Pst I
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Eco RI
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Pst I
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Eco RI
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Eco RI
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Eco RI
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAAACCATCGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Kpn I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Pst I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Eco RI
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Pst I
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Eco RI
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Pst I
	Reverse	AAAAAACTGCAG-CTACGATTTTCGGCGATTTCCACATCGT	Eco RI
657	Forward	AAAAAAGAATTC-GCAGAAATTTGCCGACCGCCATTTGTGCGC	Pst I
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	BamHI- NdeI XhoI
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	Eco RI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	Pst I
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	BamHI- NdeI XhoI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCGCCGTCGGGC	Eco RI
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	Pst I
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	BamHI- NdeI XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	Eco RI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	Pst I
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTGCCGACGATTC	Eco RI
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Pst I
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGGAAACGCGTCGGAAGTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI-
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	NdeI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	XhoI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	BamHI-
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTGGATACTTC	BamHI-
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	NdeI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	XhoI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Eco RI
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	Pst I
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	BamHI-
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	NheI
	Reverse	AAAAAACTGCAG-TTAGTTTGGCCGATAATATGGCGGGTGCG	XhoI
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	Eco RI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	Pst I
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	NheI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	XhoI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	BamHI-
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	NdeI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	XhoI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	BamHI-
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI-
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	NdeI
			XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	NdeI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	XhoI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	BamHI-
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI-
	Reverse	GCCCAAGCTT-TTTGTCGGTTTGGGTATC	NdeI
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	HindIII
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	BamHI-
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	NheI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	EcoRI-
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	NdeI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	XhoI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	BamHI-
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	XhoI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGAGAAATT	BamHI-
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI-
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	NdeI
743	Forward	CGCGGATCCCATATG-GACGGTGTTGTGCCTGTT	XhoI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	BamHI-
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTCCGCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTCGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTGCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTTCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward	CCGGAATTCTACATATG-TTGCACCTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCTGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTTT	XhoI
910	Forward	AAAGAATTC-GCATTTCGGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTTCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCGCCTTACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTT	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAAACCGCCAATCCGCCGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTGCGGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	Eco RI
	Reverse	CCCGCTCGAG-TTAGAACCGCATTGTC	BamHI-
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	NdeI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	XhoI
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-GGGTCGTTTGTGCGTC	NdeI
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC-	XhoI
		TTGACTAACAGGGGGGGAGCGAAATTAAAAAC	Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

g001.seq

```

1 ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
51 CCGCAGGGCT TGC GCCCGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101 AACGCGATAC TTAAACGGC TCGGGTACGC ATACTTTACC GGTTCGGCG
151 ATTTGCCGA GGTCTTGGC CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGGTCGGTTT GAACTCGGC GCGCGGCGT TCGTCTTGT
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CCGGATTGC CCGCTTCAT CCGCAGGTG GGACAATACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

g001.pep

```

1 MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDITNG SGHTLPVWA
51 ILPRSLRSKS TIITFSARFF GSVNSAARR SSCPSKIGA VPFISVLMV
101 PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

m001.seq

```

1 ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
51 CCGCAGGGCT ss.GCTTGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGTTCGGCG
151 ATTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGT
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CCGGATTGC CCCTCCGCAT CCGCAGGTG GGACAAGACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

m001.pep

```

1 MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDITNG SGHTVPVWA
51 ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSKIGA VPFISVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

a001.seq

```

1 ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
51 CCGCAAGGCT TGGGCTTGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGGTACGC ATACTGTGCC GGTTCGGCG
151 ATTTGCCGA GGTCTTACG CAGCAAATCG ACAATCATCA CGTTTCGGC
201 GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGT
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGAGAAAC ACAGCGTCCA
351 CCGGATTGC CCTTGTGCAT CCGCAGGTG GGACAAACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

a001.pep

```

1 MLPOGKAARR MSANEVCGKA WAWXVLVICQ TLPKRDITNG SGHTVPVWA
51 ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSKIGA VPFISVLMV
101 PSEPILRKSS GEKHSVHAD C PASGRWDKT A*

```

m001/a001 96.2% identity over a 131 aa overlap

	10	20	30	40	50	60
m001.pep	MLPOGKAARRMSANEVCGXLXAWXVLVICQTLPKRDITNGSGHTVPVWAILPRSLRSKS					
a001.pep	MLPOGKAARRMSANEVCGKAWAWXVLVICQTLPKRDITNGSGHTVPVWAILPRSLRSKS					

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	10	20	30	40	50	60
m001.pep	70	80	90	100	110	120
	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	70	80	90	100	110	120
	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
m001.pep	130					
	PSASGRWDKTAX					
a001.pep	130					
	PCASGRWDKTAX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRKS					
g001	MLPQGKAARRVSAANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRKS					
m001.pep	70	80	90	100	110	120
	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	70	80	90	100	110	120
	TIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
m001.pep	130					
	PSASGRWDKTAX					
g001	130					
	PASGRWDNTAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTCGCGCTG TTTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCGETG CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTCGT CGGCTTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTAATCAGG TAGTCCTGAT GGTATTCCTC GGCCTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGGCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTgttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCAAG CCGTcgatgc gttggaAATa
601 ggCTTCCAAG ccccaaaagc agccgccggc gaagtaaagtg gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFa DVDVAVAVGV FNQVVLNVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGGD GFFGGVGVVH AAAVLRAGVV TLFVEAGRIN DAEIILQDVV

```

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVIDALEIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51 CTTGsTATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCCGCTC GAAGCCTTTG CCTTGCCTGG CCGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CAGCKTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGk CCGCGATGAC GGCTTTTTTCG kCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CCGTGTCTTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTGCGCAT CGTAGGTCAC TTTGACGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTT CGTGTGCCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFEG VTRFFIRCRV EAFALRGGLG
51 FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGXGDD GFFXGVGVVH AAALVLTGVV ALFVEAGRIN DAEELQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVIDALEI
201 GFQAPEAAXG EVNGARVHDF *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTGCGCTG TTTTGGGTAA
51 CTTGGTATTG CTCTTCGGTC AGGGTGCCTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCCGCTC GAAGCCTTTG CCTTGCCTGG CCGTCTTGGT
151 TTTGCCCGGC AGCGGTTCTG CCGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CCGCGATGAC GGCTTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTAC CCGTGTCTTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTGCGCAT CGTAGGTCAC TTTGACGTT TCGGCGTGGC
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTT CGTGTGCCG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGCG GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFEG VTRFFIRCRV EAFALRCGLG
51 FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFGGGVVH AAALVLTGVV ALFVEAGRIN DAEELQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVIDALEI
201 GFQAPEAAG EVDGARVHDF *

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXL	LFGQGAFFEGVTRFFIRCRV	EAFALRGGLGFARQRFVSXA			
a003	MVVFVAEGIFGRAVLGNLVL	LFGQGAFFEGVTRFFIRCRV	EAFALRCGLGFARQRFVGFA			
	10	20	30	40	50	60

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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALIEIGFQAPEAAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALIEIGFQAPEAAAGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVFVFAEGIFGRAVLGNLXLLFGQGAFFEGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVFVFAEGVFGRVVLGHLVLLFGQGAFFEGVTRFFIRCRVEAFALRCGFGFARQRFVGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNQQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALIEIGFQAPEAAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALIEIGFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51  GCGCCCATGC CAACAagtg gccaAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcgcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtcg accttgaTTT TTGAACGATA
201 CTTCCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTCGgga ctggttaaACA CCACGCCAAT
301 GGTgctgcgg cGCAAACCGC TGCCGATATt cgGgtagcgg ccccgcggtta
351 ttgcccggca atcttacctt ggtcggcggc ttcatGCAGC AGGGGcagtt
401 ggttggaacg gtcgcccga ataaAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgcgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTTCGG ACGGCgACCT ACGGCTGCCA

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551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGETTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCGCG CCAAACCGAA AATTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004.pep

```

1 MVERHIQHLR NGHLMRCP CQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAAQTAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMPP MIPKPKIST
251 FTPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTGAT
51 GTGCCCAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCTG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCGATATT CGGCTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTtag CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATTCCGCCCA AACCGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004.pep

```

1 MVERHIQHLR NGHLMCPs QQVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHA
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAM KICGILVCMV
151 SGSATGTPRA SFSILIFSKP ILSTFGRRP AASIYSATNT PFSPPSCSQWT
201 STLPSASSL SVLASRCSFN SSPNTAFASS ETTGSEMPPM IPPKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTGCGG AACGCTCATC TTCATTGAT
51 GTGCCCAGC CAACAGGTGC GCCAAATGTT CGGCGGCCCG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCTG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCGATATT CGGCTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCTC GAGTTTGCC TCGGTTTtag CATCCAAATG
651 CAGTTTCAAT TCTTACCAGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCCGATG ATGCCACCCA AACCGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

a004.pep

```

1  MVERHIQHLR NGHLHLMCPs QQVRQMFGGR TYDFCADEAA GGFFGIQAHM
51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAQAATAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT FFSPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*

```

m004/a004 94.9% identity over a 257 aa overlap

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLHLMCPsQQVRQMFGGRAYDFRADKAAGGFFGIQAHMAFVHQAHAHA					
a004	MVERHIQHLRNGHLHLMCPsQQVRQMFGGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	120
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI					
a004	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAQAATAADIRVAAALSPAI					
	70	80	90	100	110	120
m004.pep	130	140	150	160	170	180
	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILIFSKPILSTFGRRPT					
a004	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILMFSKPILSTFGRRPT					
	130	140	150	160	170	180
m004.pep	190	200	210	220	230	240
	AASIYSATNTFFSPSCSQWTSTLPSASSLSVLASRCFNSPNTAFASSETTGSEMPPM					
a004	AASIYSATNTFFSPSCSQWTSTLPSASSLASVLASKCFNSPNTAFASSETTGSEMPPM					
	190	200	210	220	230	240
m004.pep	250					
	IPPKPKISTFTPKRCNAX					
a004	MPPKPKISTFTPKRCNAX					
	250					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

m004.pep	10	20	30	40	50	60
	MVERHIQHLRNGHLHLMCPsQQVRQMFGGRAYDFRADKAAGGFFGIQAHMAFVHQAHAHA					
g004	MVERHIQHLRNGHLHLMRPCQVQSQMFGRAYDFRADKAAGGFFGIQAHMAFVYQHHAHA					
	10	20	30	40	50	60
m004.pep	70	80	90	100	110	119
	ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA					
g004	TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHANGAAQAATAADIRVAAPRYCPA					
	70	80	90	100	110	120
m004.pep	120	130	140	150	160	179
	ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFILIFSKPILSTFGRRP					

g005.seq

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

g005.pap

```

1  MGDMDNIDMF  PEQEEIQSMW  KEILLNYGIF  LLELLTVFGA  IALIVLAIVQ
51  SKKQSESGSV  VLTDFSENYK  KQRQSFETFF  LSEETKFEQE  KKEKKKEKAE
101  AKAEEKRLKE  GGEKSAETQK  SRLFVLDFFD  DLYAHAVESL  RHEITAVLLI
151  AKPEDVELLR  LESPGAVVHG  YGLAASQLRD  LRERNIPLTV  ADVKVAASGG
201  YMMACVADKI  VSAPFAVIGS  VGVVAEVPNI  HRLLLKXHD  VDVMTAGFEK
251  RTVTFMGENT  EKGKQKFRQE  LEETHQLFKQ  FVSENRPGLD  IEKIATGEHW
301  FRQALALNL  IDEISTSDML  LLKAFENKQV  IEVKYQEKR  LQRIQLQAE
351  ASVEKFLAKL  VNRRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 21>:

m005.seq

1	ATGGACAATA	TTGACATGTT	CATGCCTGAA	CAAGAGGAAA	TCCAATCAAT
51	CTGGAGAAAG	ATTTTACTGA	ATTACCGGTAT	TTTCTCTGCT	GAACTGCTTA
101	CGGTGTTCGG	CGCAATTGCG	CTGATTCTGT	TGGCTATCGT	ACAGAGTTAG
151	AAACAGTTCG	AWAGCGGCAG	TGTCGTACTG	ACGGATTTTT	CGGAAAATTA
201	TAAAAAACCA	CGGCAATCGT	TTGAAGCAAT	CTTTTAAAG	GGGGAAGAGG
251	CACAACATCA	GGAAAAAGAG	GAAAAAGAAA	AGTTAAAAAG	CGGAAGCABA

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGTTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCCG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGCGGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGTGAG GAAACGCATC AGTTGTTCAG GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHKEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
351 VEKLEAKLVN RRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGTTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTGTGT TGGATTTTGA CGGCGATTTG TATGCACACG
401 CCGTAGAATC CTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGGTTCA
501 CGGTACCGT TTGCGGCTT CGCAGCTTAG GCGTTTGC GCACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTTG CGATTGTCCG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGCGGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGTGAG GAAACGCATC AGTTGTTCAG GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGCGGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTTTGCCAA ACTTGTC AAC CGGCGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHKEKE EKKKEKAEAK
101 AEKXRLKEGG EKSSSETQKSR LFVLDFDGL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
 351 VEKLFALNVN RRADVM'

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	10	20	30	40	50	60
	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVOSKKQXSXSGSVL					
a005	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVOSKKQSESXSGSVL					
	10	20	30	40	50	60
m005.pep	70	80	90	100	110	120
	TDFSENYKKQSQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKRLKEGGEKSAETXKSR					
a005	TDFSENYKKQSQSFEAFFLSGEEAKHQEKEKKKEKAEAKAEKRLKEGGEKSSETQKSR					
	70	80	90	100	110	120
m005.pep	130	140	150	160	170	180
	LFVLXX					
a005	LFVLDFDGDLYAHAVESLRHEITAVLLIAKPEDEVLLRLES?GGVVHGYGLAASQLRRLR					
	130	140	150	160	170	180
m005.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSGVVAEVPNIHRLKKHDIDVD					
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSGVVAEVPNIHRLKKHDIDVD					
	190	200	210	220	230	240
m005.pep	250	260	270	280	290	300
	VMTAGEFKRTVTFMGENTKKGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG					
a005	VMTAGEFKRTVTFMGENTKKGKQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG					
	250	260	270	280	290	300
m005.pep	310	320	330	340	350	360
	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFALNVN					
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFALNVN					
	310	320	330	340	350	360
m005.pep	RRADVMX					
a005	RRADVMX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	10	20	30	40	50
	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVOSKKQXSXSGSV				
g005	MGMDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVOSKKQSESXSGSV				
	10	20	30	40	50
m005.pep	60	70	80	90	100
	VLTDFSENYKKQSQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKRLKEGGEKSAETXK				
g005	VLTDFSENYKKQSQSFETFFLSEETKHQEKKEKKKEKAEAKAEKRLKEGGEKSAETQK				
	70	80	90	100	110
					120

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
		:				
g005	SRLFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEGKGKQFRQELEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEGKGKQFRQELEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLLLKAFENQVIEVKYQEKQSLIQRIGLOAEASVEKLFaki.					
g005	FGRQALALNLIDEISTSDDLLLKAFENQVIEVKYQEKRSIQRIGLOAEASVEKLFaki					
	310	320	330	340	350	360
	360					
m005.pep	VNRRADV MX					
g005	VNRRADV MX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

```

1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 CCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCG
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAAC TT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

```

1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAPVMTLK
101 GYGSAGHIYS VGTYLWMPAM SLDDVPRLVE QYNLKDIGO RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

```

1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTCG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTTCGCGCCT
201 CCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CGGCGATGGG TATTTGTTC GGCTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT

```

```

351 GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep

```

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSLNKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq

```

1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
51 TCGGTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGATTTCCG CCTGAAGAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGAAGTC TTGCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGTCGGCA
251 CGGCGATGGG TATTTGTTC GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
451 GCCGGAACCT GA

```

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep

```

1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMTLK
101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSLNKDIGQ RIEWSKRNIK
151 AGT*

```

m006/a006 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVSavgilALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					
a006	MLLVLEFWVGVSavgilALFLWLLPRFAAISENLYFRLKNSLERDNHFIRKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	SLDDVPRLVEQYSLNKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLNKDIGQRIEWSKRNIKAGTX					
	130	140	150			
m006.pep	SLDDVPRLVEQYSLNKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLNKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVSavgilALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					


```

g006      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| |||||
          MLLVLEFWFGVSAGVILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDERQLYRH
              10         20         30         40         50         60

              70         80         90        100        110        120
m006.pep  YGLLARLRVLISNREAFGYLCVGTTAMGILFGFAFVMMLTKGYSSAGHVYSVGTYLWMFAM
          |||:: ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| ||||| : ||||| |||||
g006      YGLVSRRLRVLIENREAFGYLCVGAAMGILFGFAFVMMLTKGYSSAGHIYSVGTYLWMFAM
              70         80         90        100        110        120

              130        140        150
m006.pep  SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g118      SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGT
              130        140        150

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 31>:

g006-1.seq

```
1 ATGTGAAAAA TGTGAAAAA CATAGCCAAA ACCCACCACA AGCGATTGAT
51 TGGCACAATT TCCCGGTCG GACTGCGAAA CCTTTTGATG CTGGGGTATC
101 CGGTGTTTGG CGGTGCGGCG ATTAATGCCG TGATTGCGGG GAGGGTGTGG
151 CAGGCGTTGC TGTACGCTTT GGTGTATTT TTGATGTGC TGTCGGTGG
201 GGCACGGCGG ATTGCCGATA CGCGCAGCTT TAGCGGATT TATACCGAAA
251 TCGCCGTGCC GGTGTGTGTT GAACAACGGC AGCGGCAAGT CCGCATTCAC
301 CGGGTAACTC CACGGGTGCG CCTGTGCGCT GAATTTGTCA GCTTTTTTGA
351 AGAACACCTG CCGATTGCCG CGACATCCGT CGTATCCATA TTCGGCGCGT
401 GCATCATGCT GCTGTGTGCTG GAATTTTGGG TCGGCGTGTG GCGGTGGGCG
451 ATACTTGCCT TGTTTTTATG GCTTTTGCCA CGTTTGGCCG CCATCAGCGA
501 AAACCTGTAT TTCCGCCTGA ACAACAGCTT GGAACGCGAC AACCACTTTA
551 TCCGAAAAGG CGACGAGCGG CAGCTGTACC GCCATTACGG ACTGGTTTCG
601 CGCCTGCGTG TGCTGATTTT CACCCGCGAA GCCTTGGGCT ATCTCTCGCT
651 CGCGCGCGCG ATGGGTATTT TGTTGGCTT TGCTTTTGTG ATGATGACGC
701 TCAAAGGCTA CGGCAGCGCG GGGCATATTT ATTGCGTCGG CACTATCTCG
751 TGGATGTTTG CCATGAGTTT GGACGATGTG CCGCGATTGG TCGAACATAA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTGC GAACGGAACA
851 TCAAAGCCGG AACTTGA
```

This corresponds to the amino acid sequence <SEQ ID 32; ORF 006-1.ng>:

g006-1. pep

1	MWKMLKHIAK	THRKRLICTF	SPVGLENLIM	LGYPVFGGWA	INAVIAGRVRW
51	<u>QALLYALVVF</u>	<u>LMWLVGAA</u>	IAOTRTFTRI	YTEIAVPVVL	EQRQQRQVPH
101	QATVARVALSR	EFVSEFEEHL	PIATSSVSI	FGACIMLLVL	EFQVWGVSAGV
151	<u>ILALFVLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDER	QLYRHYGLVS
201	RLRVLSLNDRE	AFGYLCVGAA	MGILFGFAFV	MMTLKGYGSA	GHIYSVGTYL
251	WMFAMSLDDV	PRLVEOYSNL	KDIGORIEVS	ERNIKAGT*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 33>:

```
m006-1.seq
1  ATGTGAAAAA  TGTTGAAACA  CATAGCCCAA  ACCCACCGBA  AGCGATTGAT
51  TGGCACAATT  TCCCTGGTCG  GACTGGAAAA  CCTTTTGATG  CTGGTGTGATC
101 CGGTGATTGG  CGGCCGGGCG  ATCAATGCCG  TGATTGCCGG  GAGGTTGTGG
151 CAGGCGTTGC  TGTACGCTTT  GGTGTGCTT  TTGATGTGCC  TGCTCGGTGC
201 GGTGCGGCG  ATTGCCGATA  CGCGCACGTT  TACGCGAATT  TATACCGAAA
251 TCCGCTGTCC  GGTCGTGTTG  GAACACGGC  AGCGACAAGT  CCGCATTCG
301 GCGGTAACGT  CGCGGGTTGC  CCTGTGCGGT  GAGTTTGTC  GCTTTTTTGA
351 AGAACACCTG  CCGATTGCGC  GCACATCCGT  CGTATCCATA  TTCGGCGCGT
401 GCATCATGCT  GCTGTGCTG  GAATTTTGG  TCGGCGTCTC  GCGGTGGCG
451 ATACTTGGT  TGTTTTTATG  GCTTTTGCCA  CGTTTTGCG  CATACGCGA
501 AAACCTGTAT  TTCCCGCTGA  ACAACAGCTT  GGAACGCGAC  AACTCAITTA
551 TCCGAAAAG  CGACGGCGG  CAGCTGTACC  GCCATTACGG  AATGCTTGGC
601 CGCCTGCGTG  TGCTGATTTC  CAACCGCGAA  GCCTTCGGCT  ATCTCTGCGT
```

m006-1.pep

	1	MWKMLKHIAQ	THRKRLLIGTF	SLVGLLENLIM	LVPVFVGGRRA	INAVIAGEVM
51		<u>QALLYLVLVL</u>	LMWLGVGARR	IADTRTFTSI	YTEIAPFVVL	EQRQRQVSAS
101		ATVARVALSR	EEVSEFEHEL	PIAATSSTFSI	FGACIMLVLL	EFWVGVSAGS
151		<u>ILALFLWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDRR	QLYRHYGLLA
201		RLRVLSNRE	AFGLVCVSTA	MGILFGFAFW	MMTLKGYSSEA	GHVSYSGTYL
251		WMFAMSLDDV	PRLYEQSYNL	KDIGORIEWS	ERNIKAGT*	

1/q006-1

		10	20	30	40	50	60
m006-1.pep	MWKMLK	HIAQTHRKRLIGTFSLVGL	ENLLMLLVYPVF	GGRAINAVIAGEVWQALLYALVV			
		:	:	:	:	:	:
g006-1	MWKMLK	HIAKTHRKRLIGTFSPVGLENLLMLGYPVF	GGWAINAVIAGR	VWQALLYALVV	F		
		10	20	30	40	50	60
		70	80	90	100	110	120
m006-1.pep	LMWL	VGA	VRR	IADTRTFTTRIYTEIAVPV	VLEQRQRQVP	HS	AVTARVALSREFVSFFEEHL
		:	:	:	:	:	:
g006-1	LMWL	VGA	AARRIADTRTFTTRIYTEIAVPV	VLEQRQRQVP	HS	AVTARVALSREFVSFFEEHL	
		70	80	90	100	110	120
		130	140	150	160	170	180
m006-1.pep	PIAATS	VSVSIFGACIMLLVLEFWVGVS	AVGILALFLWLLPRFAAIS	ENLYFR	LNN	S	LERD
		:	:	:	:	:	:
g006-1	PIAATS	VSVSIFGACIMLLVLEFWVGVS	AVGILALFLWLLPRFAAIS	ENLYFR	LNN	S	LERD
		130	140	150	160	170	180
		190	200	210	220	230	240
m006-1.pep	NHFIRK	GDRRQLYRHYGILLARLRVLISNREAF	GYLCVGTAMGILFGFAFM	MTLKGYS	SA		
		:	:	:	:	:	:
g006-1	NHFIRK	GDERQLYRHYGIVLSRLVLISNREAF	GYLCVGAAMGILFGFAFM	MTLKGYS	SA		
		190	200	210	220	230	240
		250	260	270	280	289	
m006-1.pep	GHVYS	VGTYLWMFAMS	LDVPRIVEQYSNLKD	IGQRIEWSERNIKACTX			
	:	:	:	:	:	:	:
g006-1	GHIYS	VGTYLWMFAMS	LDVPRIVEQYSNLKD	IGQRIEWSERNIKACTX			
		250	260	270	280		

a006-1.seq (partial)

1	AGCCAAAACC	ACCGAAGCG	ATTGATTGGC	ACATTCTTTC	TGGTCGGACT
51	GGAAAAACCT	TTGATGCTGG	TGTATCCGGT	GTTTGGCGGC	TGGGCGATTA
101	ATGCGCGTAG	TGCGGGGACG	CGGTGGCAGG	CGTTGCTGTA	CCGCTTTGGTT
151	GTGCTTTTGA	TGTGGCTTGT	TGTCGCGCG	CGCGGCAATTG	CGCATACCGC
201	CACGCTTACG	CGGATTTATA	CGAAATCCG	CGTCCCGGTT	GTGTTGGAAC
251	AGCGGCAGCG	GCAAGTCCCG	CATTGCGCG	TAACTGCGCG	GGTTGCCCTG
301	TCGCGTGAGT	TTGTGACGTT	TTTGAAGAA	CACCTGCCGA	TGTCCGCGAC
351	ATTCGCTCGTA	TCCATATTCG	GCGCGTGCAT	CATGCTGCTG	GTGCTGGAAT
401	TTTGGGTCGG	CGTGTCCGGC	TGCGGCATAC	TTGCGTTGTT	TTTATGGCTT
451	TTGCGCAGTT	TTGCCGCCAT	CAGCGAAAC	CTGATTTTCC	GCCTAGAAGAA
501	CAGCTTGGAA	CGCGACAACC	ACTTTATCCG	AAAAGGCGAC	GAGCGCGACG
551	TGGACCGCCA	TTACGGAGAT	CTTGC CGCGC	TGCGTGTGCT	GATTTCCAAC
601	CGCGAAGCTT	TCGGCTATCT	CTGCGTCGGC	ACGGCGATGG	GTATTTTGTT
651	CGGCTTTGCT	TTTGTGATGA	TGAGCTCAA	AGCTACAGC	AGCGCGGGGG

701 ATGTCTATTC GGTCCGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGVS VLGILALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN
 201 REAFGYLCVG TAMGILFGFA FVMMTLKGY SAGHVYSVGT YLWMFAISLD
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENL LMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLIGTFSLVGLENL LMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
m006-1	LMLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKERNIKAGTX				
m006-1	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGcgC
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCctgctg cacagca-gg tcaaaggcAt cgacgggaca ttcaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPLFRSD CIMNKPHVLL HSMVKIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRHLYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

m007.seq

1	ATGAACACAA	CCCgACTGCC	GACCGCCCTC	GTCTTGGGCT	GCTTCTGCGC
51	CGCCGCTTCT	GCCGCCGACA	ACAGCATCAT	GACAAAAGGG	CAAAAAGTGT
101	ACGAATCCAA	CTCGCTGCCT	TGCCACGGCA	AAAAGGGCGA	AGGCCGCGGA
151	ACCATGTTTC	CGCCGCTCTA	CCGCTCCGAC	TTCATCATGA	AAAAACCGCA
201	GGTGCTGCTG	CACAGCATGG	TCAAAGGCAT	CAACGGTACA	ATCAAAGTC.
251	AACGGCAAAA	CCTACAACGG	ATTATATGCC	GCAACCGCGA	TCAGCGATGC
301	GGACATTGCC	GCCGTCCGCA	CTTATATCAT	GCAACCTTTT	GA

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.pgp

1 MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GHCRRHHLYH ERI *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

a007.seq

1	ATGAACACAA	CCC G ACTGCC	GACCGCCCTC	GTCTTGGGCT	GCTCTGCGC
51	CGCCGCTTCT	GCCGCCGACA	ACAGCATCAT	GACAAAAGGG	CAAAAAGTGT
101	ACGAATCCAA	CTGCGTGCCT	TGCCACGGCA	AAAAGGGCGA	AGGCCGCGGA
151	ACCATGTTTC	CGCCGCTCTA	CGCGTCCGAC	TTTCATCA	AAAAACCGCA
201	GGTGCTGCTG	CACAGCATGG	TCAAAGGCAT	CAACGGTACA	ATCAAAGTC
251	AACGCCAAAA	CCTACAACGG	ATTTCATGCC	GCCAATGCCA	TCAGCGATGC
301	GGACATTGCC	GCGCTCGCA	CTTATATCAT	GACGCGCTTT	GA

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pgp

1 MNTTRLPTAL VLGCLCAAS AADNSIMTKG QKVEYSNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARHCQRC
101 GHCRRRRLHYL ERL*

m007/a007 97.3% identity over a 113 aa overlap

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFCAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
	: : : : : : : : : :					
a007	MNTTRLPTALVLGCLCAASAADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD					
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLYHERLX					
	: : : : : : : : :					
a007	FIMKKPQVLLHSMVKGINGTIKVXRQNLQRIHARCHQRCGHCRRRHLYHERLX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

```

              10          20          30          40          50          60
m007.pep    MNTRLPTALVLGCFCAAASADNSIMTKGQKVYESNCVACHGKKGEGRGTMFPPLYRSD
              |||||::|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g007         MNTRLPTAFILCLCAAASADNSIMTKGQKVYESNCIACHGKKGEGRGTAFFPLFRSD
              10          20          30          40          50          60

              70          80          90          100         110
m007.pep    FIMKKPQVLLHSMVKINGTIKVXRQNLQRIHARNRHQRCGHCRRRHLYHERLX
              ||:|:|:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

```

g007 CIMNKPHVLLHSMVKGIDGTFKVERQNLRIYARNRHQRCGHCRRLHYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)
 1 ATGAACACAA CCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
 101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGTTTC CTCGCTTTT CCGGTCGGAC TATATTATGA ACAAAACGCA
 201 CGTCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
 251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
 301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
 351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAAC.

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)
 1 MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD YIMNKPHVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
 101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq
 1 ATGAACACAA CCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
 101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
 151 ACCATGTTTC CGCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
 201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
 251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
 301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
 351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT
 401 AA

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep
 1 MNTTRLPTAL VLGCFCAAAS AADNSIMTKG QKYESNCVA CHGKKGEGRG
 51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
 101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	ADNSIMTKGQKYESNCVACHGKKGEGRG	TMFPPLYRSD			
g007-1	MNTTRLPTAFILCLCAAAS	ADNSIMTKGQKYESNCIACHGKKGEGRG	TAFPPLFRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISD	ADIAAVATYIMNAFDNGGGSV			
g007-1	YIMNKPHVLLHSMVKGINGT	IKVNGKTYNGFMPATAISD	ADIAAVATYIMNAFDNGGGSV			
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
g007-1	TEKDVQAKGKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)
 1 ATGAACACAA CCGACTGCC GACCGCCTTC GTCTTGGGCT GCCTCTGCGC
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
 101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAAC3GA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAG ACGTAAAACA GGCAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGCLCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTI	KVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
a007-1	FIMKKPQVLLHSMVKGINGTI	KVNGKTYNGFMPATAISDADIAAVATYIM	NAFDNGGGSV			
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCACACAA CAAATAcgCG gCGcattaga cgcgctctcg tcccatcctg
101 acatccgctg tgaACaggtt tcctcaactgt aTatgaccgc acctgtcggt
151 tacgAcaatC agcccgATTT CATCaatgcc gTCTgcaccg TTCCACCAC
201 CtTGGACGGC ATTGccctGC TTGCCgaACT CAAccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCAGCAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTtTG GGAAAATACG GAAAGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLDD
101 IIDFDGISSD DPRLTLPHRP AHERSFVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTGGA CAGCTGTGCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT TGTCAATGCC GTCTGCACCG TTTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAC CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTTGGAC
301 ATTATCGACT TTGACGGCAT CTCAGCGAC GACCCCGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFGRRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

```

m008/g008
      10      20      30      40      50      60
m008.pep MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYNQPDFVNA
g008     MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYNQPDFINA

```

183

	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008						
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008						
	AHERSFVIRPLAEILPDFILGKYGVVLELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

```

1  ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGTTGTGCG cGTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARNQSVMAV
51  QLPLVAFSDK  VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

```

1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGTTGTGCG CGTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPPVAFSDK  VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009						
	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009						
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAVAFER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

```

      10      20      30      40      50      60
m009.pep MPRAAVAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK
          |||||
a009      MPRAAVAFERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK
          10      20      30      40      50      60

      70      80
m009.pep VVVAFAQVQAEIQVFADGGKTWQKPX
          |||||
a009      VVVAFAQVLQAEIQVFADGGKTWQKPX
          70      80
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGGTTTC CTGTTGCGAA GTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGACGCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTGC TAAAGTGTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCG TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGAacgc
801 cgacggcgaA cgcTTATGG AAcgctatgc GCcgACCGta aAgaCTTGG
851 CTTCCTCGCga cgtGGTTTCA CgcgcGatgG CGatggaAat ctatgaaggt
901 cgcggtctgTG GtaaaAAacaA agaCCacgtC TTACTGAAAA TCGACcAtAt
951 cggTGCAGAA AAAATATATG AAAAATGCC GGGCATCCGC GAGATTTCCA
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc cgttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTcG aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTc cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSWLWG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAODLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCGTGCCA
401 ATACGCAATT CTTTGTGGAA TGGACGGCAC AAGATTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACC GCCATG GAAATGGAAA CCGCGCAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGC CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCAGCCG ACCGCGGTG CCGGTGCGG CGTGTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPT SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSWLDGQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMEFWQFQP TGAVAGAVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTTGGA AGCGGTAAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCGG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGGAG GCGGTATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCETA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCCC GGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCACT ATATGATGGG CGGTATCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAATA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGACAGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCAGCGCG TGGCGACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTGTTCCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVFP PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSOWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGGKNDHV LLKIDHIGAE KIMEKLGIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVPV QGDEYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKESDWWP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVERTDEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPPERDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV
                                |||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDDHMYDTVKGSOWLGQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||
a010      QEDRWDDHMYDTVKGSOWLGQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDDVGV
                                |||
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDDVGV
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |||
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

m010.pep				10	20	30	
				XQLSKSGLNCAVL	SKVFPTR	SHTVAAQGGISASXGNV	
g010	MGFPVRKFD	DAVIVGGGGAGL	RALQLSKSGLNCAVL	SKVFPTR	SHTVAAQGGISASLGNV		
	10	20	30	40	50	60	
m010.pep	40	50	60	70	80	90	
	QEDRW	DWHMYD	TVKGS	DWLGDD	DAIEFMCRAA	PEAVIELEHMGMPFDR	VESGKIYQRPFG
g010	QEDRW	DWHMYD	TVKGS	DWLGDD	DAIEFMCRAA	PEAVIELEHMGMPFDR	VESGKIYQRPFG
	70	80	90	100	110	120	
m010.pep	100	110	120	130	140	150	
	GHTAE	HGKRAVER	XCAVADR	IGHAM	LHTLYQQN	VRANTQFFVEWTAQDLIR	DENG
g010	GHTAE	HGKRAVER	ACAVADR	TGHAM	LHTLYQQN	VRANTQFFVEWTAQDLIR	DENG
	130	140	150	160	170	180	
m010.pep	160	170	180	190	200	210	
	TAMEM	TGEVYIF	HAKAV	MFATG	GGGRIYAS	STNAYMNTGDGLGICARAGI	PLEDM
g010	TAMEM	TGEVYIF	HAKAV	MFATG	GGGRIYAS	STNAYMNTGDGLGICARAGI	PLEDM
	190	200	210	220	230	240	
m010.pep	220	230					
	FQPTG	VAGAGV	LITE				
g010	FHPTG	VAGAGV	LITEG	VRGEGG	ILLNADGER	FMERYAPT	VKDLASROVVS
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTC CTGTTTCGCAA GTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGTTCCGA CTGGCTGGCC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCGGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGTAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGGTTTCA CGCGCGATGG CGATGGAAAT CTATGAAGGT
901 CCGGCTGTG GTAAAAACAA AGACCACGTC TTACTGAAAA TCGACCATAT
951 CCGTGCAAG AAATATATGG AAAAATGCCC GGCATCCGC GAGATTTCCA
1001 TTCAGTTTGC CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGCGCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHF LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVFVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKSGLNCVLSKVF PTRSHTVAAQGGISASLGNV 60
 M PVR+FDVAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
 Sbjct: 1 MKLPVREFDAVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLG DQDAIEFMCR AAPEAVIELEHMGMFPDRVESGKIYQRPFG 120
 ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
 Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILEHMG LPPSRLLDDGRIYQRPFG 120

Query: 121 GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENG DVVG V 180
 G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL+++++G VVG
 Sbjct: 121 GQSKNFGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVRNQDCAVVG C 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
 TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+C+ RAG+P++DME WQ
 Sbjct: 181 TALCIETGEVVYFKARATVLATGGAGRIYQSTTNAHINTGDGVM AIRAGVPVQDMMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
 FHPTG+AGAGVL+TEG RGE G L LN GERFMERYAP KDLA RDVV+R++ +EI EG
 Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLA GRDVVARSIMIEIREG 300

Query: 301 RGC 303
 RGC
 Sbjct: 301 RGC 303

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
 H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
 Sbjct: 310 HAKLKL DHLGKEVLESRLPGILELSRTFAHVPVKEPIPIPTCHYMMGGIPTKV TQAL 369

Query: 369 VPQGEYEVFVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
 +V V GL+A GE AC SVHGANRLG NSLLDLVVF
 Sbjct: 370 TVNEKGEDVVVPG LFAVGELACVSVHGANRLGCNSLLDLVVF 411

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGCAA GTTGTATGCC GTGATTGTGC GCGGTGGTGG
51  TGCAGGTTTTC CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCGGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```

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451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 ECTACCGGCG GCGGCGGTGCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGATATTC TGTGGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCCG GGGCATCCGC GAGATTCCA
1001 TTCAGTTCG CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTCGTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAG ACCTTGATGC ATTGCGTCGC GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCGGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CTTGTCTCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDMHY DTVKGSDWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVBRANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLSARDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPFVVP
351 TTHYMMGGIP TNYHGEVVVP QGEDYEVVK GLYAAGECAC ASVHCANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAAH SDDHEERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

	10	20	30	40	50	60
m010-1.pep	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVF PTRSHTVAAQGGISASLGNV					
g010-1	MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVF PTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
m010-1.pep	QEDRWDMHYDTVKGSDWLG DQDAIEFMCR AAPEAVIELE HMGMPPFDRVESGKIYQRPFG					
g010-1	QEDRWDMHYDTVKGSDWLG DQDAIEFMCR AAPEAVIELE HMGMPPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
m010-1.pep	GHTAEHGKRAVERACAVADR TGHAMLHTLYQQNVBRANTQF FVEWTAQDLI RDENGDVVG					
g010-1	GHTAEHGKRAVERACAVADR TGHAMLHTLYQQNVBRANTQF FVEWTAQDLI RDENGDVVG					
	130	140	150	160	170	180
m010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGI PLEDMEFWQ					
g010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGI PLEDMEFWQ					
	190	200	210	220	230	240

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
m010-1.pep	310	320	330	340	350	360
	RGCGKXNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
g010-1	310	320	330	340	350	360
	RGCGKXNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVVPVKGLYAAGECACASVHGANRLGTSLLDLVVFKAAGDSMTK					
g010-1	370	380	390	400	410	
	TNYHGEVVVPQGEDYEVVPVKGLYAAGECACASVHGANRLGTSLLDLVVFRTPRX					
m010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTGC GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTCCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGGC
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATCGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGTTTGGG GTATTGTGTC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGCGCAG GCGGTATTCT TGTGAATGC
801 CGACGCGCAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTA CTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCGG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCGTATATG
1151 CGGCAAGTGA GTGCGCCTGT GCTTCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGA CAATCAAACCT
1351 GATGGTGAAA ACSTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA ECACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF FTRSHTVAAQ
51  GGISASLGNV QEDRDWDHMY DTVKGSDWLG DQDAIEFMCR AAPEAVIELE
101  HMGMFPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPVPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERODE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 567 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFDIVGCGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
a010-1	MGFPVRKFDIVGCGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV					
	10	20	30	40	50	60
a010-1.pep	70	80	90	100	110	120
	QEDRWDMHYDTVKGSDWLGEQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
m010-1	QEDRWDMHYDTVKGSDWLGEQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
a010-1.pep	130	140	150	160	170	180
	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
m010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV					
	130	140	150	160	170	180
a010-1.pep	190	200	210	220	230	240
	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
m010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
a010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
m010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
a010-1.pep	310	320	330	340	350	360
	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPVPVPTTHYMMGGIP					
m010-1	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPVPVPTTHYMMGGIP					
	310	320	330	340	350	360
a010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGDEYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
m010-1	TNYHGEVVVPQGDEYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVF GKAAGDSMIK					
	370	380	390	400	410	420
a010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRELQRSVQLHAGVFRTEILS					
m010-1	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRELQRSVQLHAGVFRTEILS					
	430	440	450	460	470	480
a010-1.pep	490	500	510	520	530	540
	KGVREVMIAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
m010-1	KGVREVMIAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
	490	500	510	520	530	540
a010-1.pep	550	560	570	580		
	SDDHPERDDENWMKHTLYHSDANTLSYKPVHTKPLSVEYIKPAKRVYX					

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGCGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT
501 GGGCGAAGTC AACAAAATCT TGAAAaccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GCGCGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSA	VCFAFQTASK	PAVSIRHPSE	DIMSLKIRLT	EDMKTAMRAK	DQVSLGTIRL
g011	MRTHRKTCSA	VCFAFQTASK	PAVSIRHPSE	DIMSLKTRLT	EDMKTAMRAK	DQVSLGTIRL
	10	20	30	40	50	60
m011.pep	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDSAKIYT	EAGRQDLADK	ENAEIEVLHR
g011	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDGAKIYT	EAGRQDLADK	ENAEIDVLHR

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	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKLRLAGKA					
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGEVNLKLTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1  ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTTAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAAACAAT TTTATCCGcc acacacgcca tcatatagcc
301 gcCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAATCC AACACAAAAA GCGGGATT TCGGTTTCG
551 GCAGATTTCT CCCCGCCCTC CTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTC CTGATGTTT GTCTCTTCCT
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1  MLARRYFFNI QPGAVETDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRHFRHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLDIDG GQRNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LREGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGAAT
101 TTCTGTTTGC CCTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
351 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
401 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
451 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn
501 nnnnnnnnnnnn nnnnnnnnnnnn AACACAAAAA GGCGTGATTT nTGC GTTTCG
551 GCAGATTTCT CCCCACCTC CTCAAACGT TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTG GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDRKRSGSN FIRHTRHHIT
1C1 AARXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXQHKKA*F XREGRFLPTL LQTFFLCFGF
2C1 RLFLFLFLFF LMLCLFPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
  1 ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
 51 TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGAT ATTTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGCGGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTTCT CCCACCTTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
  1 MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
 51 KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
a012	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYERHHHT	RTDNRKRSNGNFIRHTRHHIT	AARXXXXXXXXXXXXXXXXXX			
a012	70	80	90	100	110	120
	NIMFFQQAVDIRYFRYNTH	RTDNRKRSNGNFIRHTRHHIT	TARRHLIDGDGQRNIAFAQT			
m012.pep	130	140	150	160	170	180
	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXXXXXXXXX	XXXXXXXXXXXXQHKKAXF		
a012	130	140	150	160	170	180
	PKLRSRQTVTQVNHAARTF	QSKQNLIFRLGNQKHRRNL	MTQGFYGVCIQIAVKIQH	KKAGF		
m012.pep	190	200	210	219		
	XRFGRLPTLLQTLFLCF	GRFLFLFLFLFLMLCLF	PAX			
a012	190	200	210			
	LRFGRLPTLLQTLFLCF	GRFLFLFLFLFLMLCLF	PAX			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLPEFLFALFR	IFTHKSNRALKFARRHHIHI			
g012	10	20	30	40	50	60
	MLARRYFFNIQPGAVFTDKL	LEQLMRFLQFLPEFLFALFR	IFTHKSNRALKFARRHHIHI			

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	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVIDIRYFRHHHTRTDNRRKSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
	: : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVIDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012.pep	130	140	150	160	170	180
	XXQHKKAXF					
	:	:	:	:	:	
g012	130	140	150	160	170	180
	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
m012.pep	190	200	210	219		
	XRFGRLPTLLQTFFLCFGRFLFLFLFLMLCLFPAX					
	: : : :					
g012	190	200	210			
	LRFGRLPALQLTLFCFGRLFLFLFFFLMFLFLAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCCTCGC
51  TGACAACTG  CTGAACAAC  TGATGCGTTT  CCTCCAGTTC  CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCGTCATCA  CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCCGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTAT  CGACGCGGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAAC  TCATCTCAG  GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATCTACG  GCGTGTGCAT
501 ACAATCGCC  GTCAAATCC  AACACAAAA  GGCGGATT  TTGCGTTTCG
551 GCAGATTCT  CCCCACCCTC CTTCAAACGC TTTTCTCTG  CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT  CCTCTTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR FTHKSNRAL
51  KFARRHHIHI NIMFFQQAVID IRYFRHHHTR TDNRKSGSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT  XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKRRNLMTQ  GFYGVCIQIA VKIQHKKAGF LRFGRLPTL  LQTLFCFGF
201 RLFLFLFLFF LMFLFLFA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : :					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVIDIRYFRHHHTRTDNRRKSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	: : : :					
g012	70	80	90	100	110	120
	NIMFFQQAVIDIRHFRHHHTRTDDRKRSGNNFIRHTRHHIAAACRDLIDGDGQRNIAFAQT					
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : :					
g012	PKLRSRQTVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	: : : : :					
g012	LRFGRLPALQLTLFLCFGRFLFLFLFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 CGCGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCAG
401 CCGCCCGGAC TTTCGAATCT AAGCAGAACC TCATCTTCAG GCTTGCCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAATCC AACACAAAAA GGCGGGATT TTGCGTTTCG
551 GAAGATTTCT CCCCACCTTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	: : : : :					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSNGNFIRHTRHHITARRHLIDGDGQRNIAFAQT					
	: : : : :					
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
	: : : : :					
m012-1	XKLRSRQTVT VNHAARTFQSEQNLIIFRLGNQKHRRLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	: : : : :					
m012-1	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataataca
51  gtCcagaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCCTTCT
101 TGCCGTGGCA GGCGATGCag tTgGATTcGT ACACCTTTTG CCCTTTtGtc

```

197

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgtt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng>:

g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHKMKAV GSRVVFIGVS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGCGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCTG ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTTC TGGTGTTC TTTATGTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS FMFETLLLLI RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGCGTTTTT ICATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCTG ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTTC TGGTGTTC TTAATGTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS LMFETLLLLI RSG*KIFLPN
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQRQPKTRAVGSRVVFIGVSFMFETLLILRSGXKIFLENQX					
a013	AQRQPKTRAVGSRVVFIGVSLMFETLLILRSGXKIFLENRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFPCPFVMMLLSAAEAA					
	:: :: ::					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNAVPRPSPFLPWQAMQLDSYTFPCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIVGSF-MFETLLILR-SGXKIFLPNQX					
	: :					
g013	AQRQHKMKAVGSRVVFIVGSPNVLKPCFLILPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

```

g015.seq
1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTITGGTA TTCAACATCC GTTTTTCCT ACTTTGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAATCCT GCTCTGTTC GCCTACATCG
251 CACTGGGCAT GGTAAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAACCAAAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

```

g015.pep
1  MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFW KALPHLNDTM
51  LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

```

m015.seq (partial)
1  ..AAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51  CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAACCAAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

```

m015.pep (partial)
1  ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

```

a015.seq
1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTITGGTA TTCAACATCC GTGTTTTCNT ACTTTGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAACCAAAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

```

a015.pep

```

```

1  MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
101 TVYLLAMCCL TCIVYLAKTK VLPF*

```

m015/a015 96.7% identity over a 91 aa overlap

```

                                10      20      30
m015.pep                      KIRKALAGFWKALPHLNDTMLLFTGLWLMKITH
                                | | | | | | | | | | | | | | | | | |
a015      LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTMLLFTGLWLMKITH
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m015.pep      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFTVYLLAMCCVACIVYLAKTKVLP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a015      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFTVYLLAMCCLTCIVYLAKTKVLP
                                70      80      90      100     110     120

m015.pep      FX
               ||
a015          FX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

```

                                10      20      30
m015.pep                      KIRKALAGFWKALPHLNDTMLLFTGLWLMKITH
                                | | | | | | | | | | | | | | | | | |
g015      LIVKYSHQIFVTITILVFNIRFLLWKNPEKPLVGFWKALPHLNDTMLLFTGLWLMKITH
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m015.pep      FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFTVYLLAMCCVACIVYLAKTKVLP
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g015      FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTKFTVYLLAMCCVACIVYLAKTKVLP
                                70      80      90      100     110     120

m015.pep      FX
               ||
g015          FX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

```

g018.seq
1  atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
101 tctttgTCGA TATTGATGTT TTCCAACCG ATATTgTCAA CGTTCGGACG
151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

```

g018.pep
1  MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
51 ATYGQHFIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF

```


200

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1  ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1  MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCQHIFG NKYAFAILL PMDFYIACI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1  ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1  MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCQHIFG NKYAFAILL PMDFYIACV EFDLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG					
	10	20	30	40	50	60
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCQHIFG					
	10	20	30	40	50	60
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIACIEFDLGFSIQMQFQFFAEHGVRLVX					
	70	80	90	100		
a018	NKYAFAILLPMDFYIACVEFDLGFSIQMQFQFFTEHGFRLVX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

```
m018/g018
10 20 30 40 50 60
m018.pep MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCQHIFG
g018 MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIDVFQTDIVNVRTATYGCQHIFG
10 20 30 40 50 60
```

201

	70	80	90	100
m018.pep	NKYAFFAILLEPMDFYIAVCIEFDLGFSIQMQFFFAEHGVRVLX			
g018	NKYAFFAILLEPMDFYIAVCVEFDLGFSIQMQFFSEHGFRVLX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1  ..ctgctggcgg ccctgggtgct tgccgcgtgt tcttcgACAA ACacactGCC
51  AGCCGGCAAG ACCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC cgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGTACC CGTCCGCACT GGATGCAGTG AAACAGAAAC ACGATGCCGC
201 AGCCGCGCC TATTTGAAA Acgcaggaga cagCGcgatg gcGGAAtg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1  ..LLAALVLAAC SSTNTLPAGK TPADNIETAD LSASVPTRPA EPEGKTLADY
51  GGYPSALDAV KQNDAAAAA YLENAGDSAM AENVRKEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTCTTCTGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGCGGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCGCG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCGA ACAGTGGACG CTGTTTGAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGCGC CGTGGCGGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGGCCTT TGGACTATTA
801 CGGCAAGGTT GCCGACC3CC GCCAAGTAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCGGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCAGCG AGCCGCGCGC CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGGTGCGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAAACGG
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG CGGTTTGCC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCAAGGT TTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTG
1351 CGCTATATTT CGCCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCGGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENACDSA MAENVRNEWL
101 KSLGARROWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGVL
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQN SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

a019.seq

```

1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCTGGT
51  GCTTGCCGCG TGTTCCTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNGCCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGCG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCCG AACTGGTCAA AAATACGGCG
451 AAAGTGCCTT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCGGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAGG GCACGCAAA' CGCGAATGCG CGCCGCCCTG CTGTCCGAAA
701 TGGAAGCGCG TTTAAGCCTC GAACAACGCA GTTTCGCGTG EGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCTT TGGAATATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCANNNTNGC NNNCGNNGTT NGNANGANN' GGCNNCCGNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCAGCG AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAC
1001 TNTACAAACA GCGCGCAGCA NCGGGCANGA ATTTTATGCT NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCTC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGTGTGCT GTCCGAAAC AGCCGAACCG CCGCGGATGC GAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGCGGCT TCATGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGT CGACCAAGGT TTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACCTCA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGSTA ATCGGCCACG CGAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCGC
1551 ACAACTTTAC ACCGCGGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTTG CAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCG AGCGCGCGCA TGGCAGGCGG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGCGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCT ACTACGCTC CCTCTTCGGC
1801 GCGCCGACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

a019.pep

```

1  MYPPSLKHS LLLVXLVLA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGVL
251 GHYQSQNLNV PAALDYXGKV ADRRQLTDDQ IEWYARAAXX XXXXXXXXXX
301 XXXXXXXXXX XXXXXXXXX SRAATGNTQX AXKLYQAAA XGNFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNLYTL

```

451 RYISXXXTDV IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV
 501 MPATAREIAG KIGMDAAQLY TADGNIRMGY WYMADTKRRL QNNEVLATAG
 551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
 601 APHIPLKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	10	20	30	40	50	60
	MYPPSLKHSLPLLVXVLAACSXTNTLSADKTPADNIETADLSASVPTXPAPPEKTXAD					
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
a019	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLXAXEYAKLE					
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLEQAAASGLLDGNDAWRRVRG					
a019	130	140	150	160	170	180
	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLEQAAASGLLDGNDAWRRVRG					
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
m019.pep	250	260	270	280	290	300
	EQRSAWGLVGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	250	260	270	280	290	300
	EQRSAWGLVGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAAXXRXRXRXAXX					
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYQAAATGRNFYAVLAGEELGRKIDT					
a019	310	320	330	340	350	360
	XXXXXXXXXXXXXXXXXARSRAATGNTQXAKLYQAAAXGNFYAVLXGEELGRKIDT					
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFA TRGFDEDKLL					
a019	370	380	390	400	410	420
	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSTAGDAKMRRXAQAEWRFA TRGFDEDKLL					
m019.pep	430	440	450	460	470	480
	TAAQTA FDHGFYDMAVNSAERTDRKLN YTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	430	440	450	460	470	480
	TAAQTA FDHGFYDMAVNSAERTDRKLN YTLRYISXXXTDVIRHAQNVNVDPAWVYGLIRQ					
m019.pep	490	500	510	520		
	ESRFVIGA QSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	490	500	510	520	530	540
	ESRFVIGA QSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGY WYMADTKRRL					
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTPLEGAVYAETIPFSETRDYVKKVMA NAAYYASLFG					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49	
g019.pep		LLAALVLAACSSSTNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD					
m019		MYLPSMKHSLPLLAALVLAACSSSTNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50	60
	50	60	70	80	89		
g019.pep	YGGYPSALDAVKQNNDAAYLENAGDSAMAENVRKEWL						
	: : : : : : : :						
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE						
	70	80	90	100	110	120	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCC TTCGG CGTGCGTTT TTTTGCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVLFAL PKEYPAWQAF
51  FSQAWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCC TTCGG CGTGCGTTT TTTTGCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVLFSL PKEYSAWQAF
51  FSQTWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

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205

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCTTTCGG CGTGCGTTTG TTTTGCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGCTGCT TGGTGATTTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVL7AL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL7ALPKEYSAWQAF	FSQTWVKVFT			
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYT	VALLVVL7ALPKEYSAWQAF	FSQTWVKVFT			
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL	VGCLVYSIKVIWGX			
a023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL	VGCLVYSIKVIWGX			
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL7ALPKEYPAWQAF	FSQAWVKVFT			
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYT	VALLVVL7ALPKEYSAWQAF	FSQTWVKVFT			
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL	VGCLVYSIKVIWGX			
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRL	FLQVATIVWL	VGCLVYSIKVIWGX			
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq
 1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TGCCCGCTCT
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact gcgcgggttT ATTGCCTTCC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTC
 351 caaAcgCtac CATATCTCTC AAGACGATT TCCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCGCGCAA ACCCTGTGA AACCGCCGC gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGCA CGCGTTCGGT
 651 CGCGGCATT GTTTGGCAGC GTCCGACCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1   MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51  TPNNAAPAAAN DAPYVPFVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAAO TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEQQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1   ..GTGCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTC
51  GCCGTCTGCA CCTGCCGTTT CGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGATC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGAG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGATC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCTGTGAAA CCGCGCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCTTCCGG CACGCGTTCG GTCGCGGGCA
701 TTGTTTGGCA GGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACACAAGG GTGTCGATAT TGCCGGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAGTGG TTTATGCCGG TTCAGGTTT AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1   ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51  NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNLSIGQIV KVKPAGYAAP KTAAVESRPA VPAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSFALTAYG
301 HNQKLLVGEG QQVKRQQQVA LMGNTDASRT QLHFEVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1   ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51  GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCAAT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```

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```
151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGCTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCTTT CTTACGCANC CGTCGACATC
301 AACCGCGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401 CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCGTGTGA AACCCGCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCGCAAT
851 CTCCTGCCGC TTCGCTTCC GGCACGCGTT CCGTCGCGCG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTGGCC GATTTCGGCG GCAACAACAA
951 GGGTGTTCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGG GCGGCGGCTG
1001 ACGGCAAAGT GGTTTATGCA GGTTCCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCTTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTCGAGGTG
1201 CGGCAAAACG GCAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

```
a025.pep
1  MLTPTTL*VA CTALAAQLGG CPTQHPSPVI AGNSGMQTVP SAPVYNPYGA
31  TPNAAAPAA DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATHTIVRG DTVYKISKCY HISQDDFRAW NGMTDNTLSI GQIVKVKPAG
131 YAAPKAAAVK SRPAVPAAQ PLVQSAPVDI NAATHTIVRG DTVYNISKRY
201 HISQDDFRAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
231 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQGVVVA DFGGNNKGVD IAGNAGOPVL AAADGKVVYA GSGLRGYGNL
331 VIIQHNSFL TAYGHNQKLL VEGEQQVKRG QQVALMGNTE ASRTQLHFEV
401 RQNGKPVNPN SYIAF*

m025/a025 97.4% identity over a 351 aa overlap

                                10      20      30
m025.pep                                VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||:|||:|||:|||:|||:|||:|||
a025      GMQTVPSAPVYNPYGATPNAAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
                                40      50      60      70      80      90

                                40      50      60      70      80      90
m025.pep      YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
                || |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      YAXVDINAATHTIVRGDTVYKISKCYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
                100      110      120      130      140      150

                                100      110      120      130      140      150
m025.pep      KAAAVKSRPAVPAAQPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      KAAAVKSRPAVPAAQPLVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
                160      170      180      190      200      210

                                160      170      180      190      200      210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTAAVESRPVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
                || |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAVQTPVKPAAQPPVQSAPQPAAPAAEN
                220      230      240      250      260      270

                                220      230      240      250      260      270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGVVADFGGNNKGVDIAGNAGQPVLAAD
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```


Homology with a predicted ORF from *N. gonorrhoeae*

m025/q025

```

m025.pep                                10      20      30
                                VPPVQSAPVYTTPPAYVPPSAPAVSGTYVPS
                                |||||:||||:|||||
g025    GMQTVSSAPVYNPYGATFYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
              40      50      60      70      80      90

              40      50      60      70      80      90
m025.pep    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
              |||||:||||:|||||
g025    YAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMTDNTLSIGQIVKVKPAGYAAP
              100     110     120     130     140     150

              100     110     120     130     140     150
m025.pep    KAAAVKSRPAVPAQAAPPVQSAPVDINAATHTIVRGDTVYNISKRYHISQDDFRAWNGMT
              |
g025    K-----

              160     170     180     190     200     210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              |||||:||||:|||||
g025    -----TAAVESRPAPVAAQTPVKPAAQPPVQSAPQPAAPAAEN
              160     170     180     190

              220     230     240     250     260
m025.pep    KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
              |||||:||||:|||||
g025    KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
              200     210     220     230     240     250

              270     280     290     300     310     320
m025.pep    ADGKVYVYAGSGLRGYNLVI IQHNSSFLTAYGHNQKLLVGEGQQVQKRGQQVALMGNTDAS
              |||||:||||:|||||
g025    ADGKVYVYAGSGLRGYNLVI IQHNSSFLTAYGHNQKLLVGEGQQVQKRGQQVALMGNTDAS
              260     270     280     290     300     310

              330     340     350
m025.pep    RTQLHFEVRQNGKPVNPNSYIAFX

```

g025 |||||
 RTQLHFEVRQNGKPVNPNYSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTC CTTTTCGCC AGCCAAATAT CATGCGTATC TTTCGGTTCG
 101 GGCTTGTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG
 401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCTGCGGCC AGCCAAGCCA AACCTCCAT CACACGCAA ACCTGTTCCG
 501 TcgcACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC
 601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt
 651 cccaatcaac gtcatagetg tctcccggtg taaaatgttc ttcacttcag
 701 aatccccccc ttcttccag cccgaaacct tcatgtgtta nacctgtggg
 751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcg gaaaacttgt tgtccccgtc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSLRFRFGN HFRRHSDFN LFRQPNIMRI FRFGLVGHGN LQQRHHRNR
 51 RSLNQQRQHH HGKRHIKQOV RIGNAHHRH HRQRNRYGSS QAQPTDIRLF
 101 TQAVIEFPQT AEHCQTRDQ HQERRNRQGF RRPVQHAGGR NQQTEDHDEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQKP
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFMCXTLG
 251 CPNGFSNLPM TLLVAPFARF LLPGKLVVEV LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTC TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCCGCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAACGTG
 201 CGGACAAAGT GGTGAAACC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRNRQGFRRP
 51 VQHVGRNRNQ QRHSQTCGQS GRNHAQKQOC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA
 51 CTGCCGCGCG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGACAAAG TGGTCGAAAC CACGCTCAGA AACACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCR TRDQHQERRN RQGFRFPVQH VSRNRQQQRH
 51 SQTCCQSGRN HAQKQCATR Q

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031 . pep	RLKHGVLH	FYSAIRLFTQAVIEFPQTA	EHCRRTRDCHQERRNRQGFRR	VPQHVGRNRQ		
a031		IRLFTQAVIEFPQTA	EHCRRTRDCHQERRNRQGFRR	VPQHVGRNRQ		
		10	20	30	40	

	70	80
m031 . pep	QRHSQTCGQSGRNHAQKQCCATRQ	
a031	QRHSQTCGQSGRNHAQKQCCATRQ	
	50	60

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031 . pep		RLKHGVLH	FYSAIRLFTQAVIEFPQTA	EH
g031	NQQRQHHHGKRHIKQVVRIGNAHQRHHRQNRNYGSSQAQPTDIRLFTQAVIEFPQTA	EH		
	60	70	80	90

	40	50	60	70	80
m031 . pep	CRRTRDQHQERRNRQGFRRFVQHVGRNRNQQRHS-QTCGQSGRNHAQKQCCATRQ				
g031	CQRTRDQHQERRNRQGFRRFVQHVGRNRNQTEHDEQSLRQPSQTVHHTQNVFRRTVALV				
	120	130	140	150	160

g031	TDNDAGKVNROKAAAAYGIGKRKHQPARHNRQVQTFRTHLQFPINVIASVRVKMFFTS
	180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032 . seq

```

1  ATGCGGCGAA  ACGTGCTGCG  CGTCGCCGTA  TTGCGCCGCC  CACGATTTCGA
51  GCGGTTTTTG  GATTGCGCGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGGCA  GATAGTTTTT
151 CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201 CTTTGGCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301 GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCCACGGGCA
351 AATCCAACAT  CCGGTTTCAGC  CATTCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTGCG  CGGCATCAG
451 CCCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501 GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551 GccgTAAAT  CGCGCCGCGA  CAAGTCCTGC  GGCACGCcgc  ctgcatCTTC
601 AGACGGCATT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATacgcccC  AAACccgTCC  AAAACCATAA  CCGTCCACA
751 CAAATATCAA  AAAACCAGTG  A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032 . pep

```

1  MRRNVEAVAV  LRRPRFEAF  L  DLALAQARAV  PAGKQGFVR  CRLTQRQIVF
51  QGFHAFAGQR  NLTLAPFAG  N  VYPRFVQIY  IICIQAVYLA  HAQTAHVHOL

```

```

101 EQRVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PPRRLARQR PTVQTALRQP PQRRRKIAPR QVLRHAACIF
201 RRHLCQQCKQ FFQIAPVCRN RVLRLALAHF VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
  1 ATGCGGCGAA ACGTGCmTGC mGTGCGCGTT kTGCGCCGCC CATTGCGCCA
  51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AACGTGTACC CACGcyTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTACG CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGCGG GTCGGGTCGG CGTGCAATCAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCTCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
  1 MRRNVXAVAV XRRPLRQTFI DLALAQARAV PAGKQGFVR CRLTQRQIVF
  51 QGFHAFADQR HLPLXAFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQPNAIL PPRRKLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
  1 ATGCGGCGAA ACGTGCCTGC CGTGCCTGTT TTGCGCCGCC CATTGCGCCA
  51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTACAGCG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGGT AACGTGTACC CACGCCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTACG CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGCGG GTCGGGTCGG TATGCAGCAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGCTTGC
501 GCGCCAGCGT CCGCGCATTC AAACCGCGCT GCGACAGCGG CCGCAACGCC
551 GCCGTAAAT CGCGCTGCGA CAAGCCCTGC GGCACGCCGC CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCGGTT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CGCGCACGAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCGC AAACCCGTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
  1 MRRNVPAAVAV LRRPLRQTFI DLALAQARAV PAGKQGFVR CRLTQRQIVF
  51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHQF
101 EQRVIAHRQR VAAVHGQIQH PVQPFRLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PPRRLARQR PRIQTALRQP PQRRRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAHF VFQISVKMRK KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

          10      20      30      40      50      60
m032.pep MRRNVXAVAVXRRPLRQTFI DLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFADQR
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
a032     MRRNVPAAVAVLRRPLRQTFI DLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFAGQR
          10      20      30      40      50      60

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAAHAQTAAVHQFEQGVVAHRQRVAAVHGQIQH					
a032	NLPLLASFAGNVYPRLVQIYIICIQAVYLAAHAQTAAVHQFEQRVIAHRQRVAAVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPERRKLASQRPFQTA					
a032	PVQPFLLRQGFYALGLLRRFDVGGRVGMQQTAFDQPGAILPERRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVRLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng)

from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLALAAQARAVPAGKQGFVAVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAAHAQTAAVHQFEQGVVAHRQRVAAVHGQIQH					
g032	NLTLLAPFAGNVYPRFVQIYIICIQAVYLAAHAQTAAVHQLERQVVAHRQRVAAVHGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPERRKLASQRPFQTA					
g032	PVQPFLLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPERRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQCKQFFQIAPVCRNRVRLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 GCTCGTGCAC GATATGCACG GACTGTTGAG TACCGTCAAA GCGCAAAcgg
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGagtTTGC CCAAAAAGTC
301 GAACAcaaa TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAATCTG GTGGACGTAT TGAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tcaAATACCA CGCGTCGcC aACCTGCcta
551 AAGAAGGCGG GGCGCAAATg ccGTCTGAAA AAGAACCCAA GCCCGCCgCc
601 aaaccgACCT ATACCAAGT ATTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCATGCGC GAGGGCAGCG

```

```

701 GACTGGTGGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGC GAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGTG CCGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGTCTGC TTTGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGCG ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TTcatTGCCT TCGGCAGTAT GGTGCGCCAC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACg
1301 accGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGTCTTGG AAGTGTGGC GAAACACGCC ATCTGCAAC CGTTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAAACTTT
1451 TGGACGATTG GGGTTTGTAGT GCCGAAGCGG TGGAAACGCC GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGC AAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLLKDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPPTYQVFGK WLCDRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAELKNA TVADMRFVKP IDEBLIVRLA RSHDRIVTLE ENAEOGGAGG
451 AVLEVLAKHG ICKPVLLIGV ADTVTEHGDP KKLLDDLGLS AEAVERVRRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1 ATGGCGCGCG CAGACAAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGCGGAC GCGCGGATGA CGCGCGGCA GCGCTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTt GATTGCTtG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAAA GCCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCTTTG TTTGAAAACT TCGGCTTCCG CTACACCGGC CCGGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGCGGCG
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT C3ATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTGCGGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA C3CGCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGGT TTTGTTTGCC
901 GTCGACCGCG CCGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTCG GCTGCGTGCC GAACATGATT GTCGCGCGCG
1001 CGAGCGATGA AAACGAATGC CGCTGTGTC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGCG ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

```

```

1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAG3CGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAAACGGC TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1 MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 LAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRRESEKTA FIAFGSMVAP
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLGLGV ADTVTGHGDP KKLLDDLGLS AEAEVRRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1 ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GGC GCGATGA CGGCGGGTCA GCGGTTTGAA GCCTTGAAC
101 GCGCGGCGCA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTGCGATTT CCCCCAACGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCGCGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACATAAAA TCAAAACCCCT TGCCGAAGAA GCCGAACACG CCAACAGTC
351 ACTGTCTTTT TTTGAAAAC TCGGCTTCCG CTATACCGCG CCCGTGGACG
401 GACACAACGT CGAAAATCTG CTCGATGTAT TGGAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCGAAATG CCGTCTGAAA AAGAACCCTA GCCCGCGCG
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCCGG
751 ATCGCCGAGC AGCAGCCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCAC CTTTTTACAA CGCGCTACG
851 ACCAAGTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGGC
901 GTCGACCGCG CCGGCATCGT CCGCGCGGAC GGCCCGACCC ATGCCGTTT
951 GTAGGATTTA AGCTTTTTCG GCTGCATTCC GAATATGATT GTCGCGCGCG
1001 CGAGCGATGA AAATGAATGC CGCCTGCTGC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGCTCCG CTATCCGCGC GGCACGGSTA CCGGCGTGCC
1101 GGTTCAGAC GGCATGGAAT CCGTGGAAT CCGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCT
1201 GCATTGGCGG TCGCCGGAAT ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CSTCAAACCG ATAGACGAAG AGTTGATTCT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGCGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTT GGGCTTGAGT GCCGAAGCGG TGGAAACGGC TGTGCGCGCG
1501 TGGCTGTCCG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1 MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

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301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAP
 401 ALAVAGKLN TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAHKG ICKPVLLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPNVGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPNVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAHQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAHQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGKTAFFIAFGSMVAPALAVAELNATVADMRFVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGKTAFFIAFGSMVAPALAVAGKLNATVADMRFVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAHKGICKPVLLLGVDVTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAGVLEVLAHKGICKPVLLLGVDVTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIIGDGAMTAGQAFEALNCAXDMDVLLVVLNDNEMSISPNVGAL	60
g033	MAAADKLLGSDRRSVAIIIGDGAMTAGQAFEALNCAGDMDVLLVVLNDNEMSISPNVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKKTLAEEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKKTLAEEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPKQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRSLVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNLFPVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMPVVAIYSTFLQRAYDQLVHDIALQNLFPVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMEITVEIGKGIIRREGEKTAFIAPGSMVAPALAVAELNATVADMRFVKP	420
g033	GTGTGAPVSDGMEITVEIGKGIIRREGEKTAFIAPGSMVATALAVAELNATVADMRFVKP	420
m033 . pep	IDDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
g033	IDDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVRENLPDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

```

1  ATGAGCCGTT TATGGTTTTT TGCCGTAAAA AACATTATAA TCCGCCTTAT
51  TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGACCA CGCCGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAA TACGcgggCG
251 CGCCGTTTTT GCGCCACCTG ATTCTGGCGG CAGTCGAAGA ATTTCCGCAC
301 ATCCCGCTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTgtgCCA
351 ACGTCCATC CAACTGGGCT TCTCTCCGT GATGATGGAC GGCTCTTTGC
401 TCGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACC
451 CGTACCGTCG TCAACTTCTC CCACGCCCTG GCGGTGTCCG TCGAAGCGCA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGAAGCAGGC GAAGAAGACG
551 GAGTGGGCGC GGCAGGCAAA CTCTCACAGC ACCAAATGCT CACCAGCGTT
601 GAAGATGCCG TGCCTTTCGT TAAAGATACC GCGTGTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCACAG

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701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAT CAAACCTGTT TCGTTGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQSI QLGFSVMMD GSLLEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKVI NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGCG GTTCAACGTC
151 AACAACTCG wACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAAA TATCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGGCGG CTGTGCAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAATTCTC CCACGCTTGC GCGGTATCCG TTGAAGCGCA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGTTGACG CATTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLEQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCORSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIAVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCGC ACCAAGTCAA
201 CGCGCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGGCGG CTGTGCAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGTCCATC CAACTGGGCT TTTCTCTCCG GATGATGGAC GSCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

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218

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451 CGTACCGTGG TTAATTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TCGTTTCGT TAAAGATACC GCGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCCACAG
701 GCGACGTGTT GCGTATCSAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTTCCGC AAGAAATGGCT
801 GAAAGTCATC AACGAATACG GCGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTC3AA GGCATCAAAC ACGGCGTGC TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

a034.pep

```

1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51  NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPKYL SKTIEAMKQI CLDRYLAFCG
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

	10	20	30	40	50	60
m034.pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM					
a034	MSRLWFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM					
	10	20	30	40	50	60
m034.pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI					
a034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
	70	80	90	100	110	120
m034.pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI					
a034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI					
	70	80	90	100	110	120
m034.pep	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLNLETGDAG					
a034	QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLNLETGEAG					
	130	140	150	160	170	180
m034.pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
a034	EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
	190	200	210	220	230	240
m034.pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
a034	EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSYGAYKFTRPPTGDVLRID					
	190	200	210	220	230	240
m034.pep	RIKEIHQALPNTHIVMH					
a034	RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVKRVN					
	250	260	270	280	290	300

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMMDGSLMEDGKTPSSYEYNVNATRTVNVNFSHACGVSVGEIGVLGNLETGDAG	180
g034	QLGFSSVMMDGSLLEDGKTPSSYEYNVNATRTVNVNFSHACGVSVGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPEWLKVINEYGGNIGETYGVPVEEIVEGIIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

1	ATGCTGAAGC	CGTGTGTTGGT	ATACAGTGCC	TGTGCGGCGG	cgttgcCTGC
51	GCGGACTTCG	AGCAGCAGGC	GTTGCGTGCC	TTCGGGCAGA	TGTGCGTACC
101	AATATTCGAG	CAGGGCGGAC	GCAACGCCCC	GTCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAAGTC	GGATTCGTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCTGCCGT	CTTTTCCGCG	AAGGAAAACC	TGTTGCGGACG
251	GCGAAACAAG	CGCGGACTCA	AATTGGCGTT	GCGTCCACGC	GGACGGGTTG
301	CAGACGGTAT	CGAGCGCGGC	CAGTGCGGCG	CAGTCGGACG	GTGAGGCTGG
351	GCGGATGTTT	ATGTTGCTGC	CTTCCGTTCC	GCCTGTTCTT	TGGCAGTCAG
401	GGCGATTTTG	TTGCGGACGT	AGAGCAGTTC	GGCGTGTGCC	GCGCCAGTTG
451	CGGATAGGCC	GCCGCCGAGG	GCGAGCGCGA	GAAATCGGC	GCGGTCGCGC
501	ATATCGGGTT	TGCCTGAGAA	GGGCGGACGG	TTTTCAGTG	CGAACGCACT
551	GCCGATGCCG	TCTGAAAAGA	CGTACCCCTC	GGGAGGGGCA	ATGTCTGCCG
601	CCCTACCGAC	TTGATAATCG	CTCAAACGGC	GGCGGTTTCA	CGTGTGCAAC
651	CACGCATAAA	ACACTTCGCC	CATACGCGCG	TCCGACGCGG	CGAGTATGCA
701	GCTTTGCGGC	GGCGGCAGCG	AGGCGGCGGC	ATCGAGCGTG	GGGATGCCGA
751	TTAAAGGCGT	GTCGAACGGC	GTTGCCAAAC	CTTGCGCCAC	GCCGATGCCG
801	ATACGCAGTC	CGGTAA			

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

1	MLKPCLVYSA	CAAALPARTS	SSRRCVPSGR	CAYQYSSRAD	ATPRRRHSGA
51	VAIRCSSDSS	GRFCQTIKAA	ILPSFSARKT	CSDGETSADS	NWRCVHADGL
101	QTVSSAASAA	QSDGEAGRMF	MFVPSVPPVL	WQSGRFCCGR	RAVRRVPRQL
151	RDSRRRRGRAR	ENRRRSAYRV	CLRRADGFPV	RTHCRCLRK	RTPRGGQCLP
201	PYRLDNRSNG	GGACRTTHK	TLRPYARPQR	RVCSEAAAAA	RRRHRAWGCR
251	LKACRTALPN	LAPRRCRYAV	R*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCAAGTC	GGATTCGTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCG .CGT	CTTTTCCGCG	AAGGAAAACC	TGTTGCGGACG
251	GCGAAACCCAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTTG
301	CAGACGGCAT	CGAGTGC3GC	CAGCTCCTCA	CAATCGGCAC	AAACGGCAGC

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTG3CT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTTCGCC CACACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGCGCAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAAC3GC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

m036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNREWLPMR ESRQSAYPV CLRTAELLE RTRCLRLKR RIFPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

a036.seq

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGCTG
51 ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTCGCG AAGGAAAACC TGTTCGAGC
251 CGGAAACAGG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCG GCCTGTTCTT TGGCAGTCAA
401 GCGGATTTTG TTGCGGACGT AGAGCAGCTC GCGGTGTGCC GCAGCGACGG
451 CCGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGCG GCGGTCGCGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCGGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CATGCATAAA AACTTTCGCC CACACGAGCG TCCGAGCGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGCG GTTGCCAAAC CTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

a036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRFFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSAKRTCSDETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPPSFSARKTCSDETSADSNWRCVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
a036	TGAPSVPPVLWQSGRRFCCGRRRAARVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	130	140	150	160	170	180
m036.pep	RTRCLCRLKRRIPPAAGCLFPARPDNRSNGGSSAYRTMHKTLRPYERPKRQGCSEFAAAAA					
a036	RTHCRCLKRRILPAAGCLPPDRPDNRSNGGGSACRTMHKTLRPYVRPQRQGCSEFAAAAA					
	190	200	210	220	230	240
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRRRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNYSSRADAIPWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSARKTCSGGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCSGGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA					
g036	MEVPSVPVLWQSGRFCCGRRRAVRVPRLRDSRRRGRARENRRRSAYRVCLRRADGFVP					
	130	140	150	160	170	180
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPKRQGCSEFAAAAA					
g036	RTHCRCLKRRTPRGQCLPPYRLDNRSNGGGSACRTTHKTLRPYARPPRRVCSFAAAAA					
	190	200	210	220	230	240
m036.pep	RRRHRARVRRRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRAGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCTGTC GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTCCTGC AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCGGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

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```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTGGCTT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTCGCC CATAAGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

m036-1.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMP ESRQRSAYPV CLRTAELLPA RTRCLRLKR RIPPAAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

	10	20	30	40	50	60
m036-1.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGR	CVNQYSSRAD	AIPWRRHSGA	VAIRCSSDSS		
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGR	CAYQYSSRADATPRRRHSGA	VAIRCSSDSS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m036-1.pep	GRFCQTIKAAIPPSFSARKTCS	DGETSADSNWRCVHADGL	QTASSAASSSQSAQTARRMF			
g036	GRFCQTIKAAILPSFSARKTCS	DGETSADSNWRCVHADGL	QTVSSAASAAQSDGEAGRMF			
	70	80	90	100	110	120
	130	140	150	160	170	180
m036-1.pep	TGALSVRPVLWQSGRFCCGR	RANRRVRHGRQDNRPWLP	MRESRRQRSAYPVCLRTAELLPA			
g036	MFVPSVPPVLWQSGRFCCGR	RAVRVPRLRDSRRRGRARENR	RRRSAYRVCLRRADGFPV			
	130	140	150	160	170	180
	190	200	210	220	229	
m036-1.pep	RTRCLRLKRRIPPAAGCLPP	PARPDNRSNGGSSAYRTMHK	TLRPYERP*			
g036	RTHCRRLKRRTPRGQCLPP	YRLDNRSNGGSACRTHK	TLRPYARPQRRVCSFAAAAA			
	190	200	210	220	230	240
g036	RRRHRAWGCRLKACR	TALPNLAPRRCRYAVRX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

g038.seq

```

1 ATGACTGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
51 TTTGAAATTC GCGCAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCTACAAAG GCATTATTTT GCGGGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGCGTGTGTG GTCGGCGCGC CGCTTAAAGG
351 GCGCGTGTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAATTTGT CCGCCGTTCA
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTG TATCCTGTTG CAAAACAACC CCGAATTGCG ACAGTTCCTC
601 GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GKLSAVQVEE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGGCGCGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCcGC CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAa AAACAATACG GkCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GGCGAATTTA CCACCAAGGC CGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGCGCGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGGCGCGC CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCcGC CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAa AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDVISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

              10      20      30      40      50      60
m038.pep      MTDFRQDFLKFSLSAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```


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```

|||||
a038      MTDFRQDFLKFSLAQNVLFKGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
           10      20      30      40      50      60
           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           70      80      90      100     110     120
           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
           130     140     150     160     170     180
           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

           10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLFKGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
|||||
g038      MTDFRQDFLKFSLAQNVLFKGEFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
           10      20      30      40      50      60
           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
|||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
           70      80      90      100     110     120
           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQEVEKQYGLPVAPI
|||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQEVEKQYGLPVAPI
           130     140     150     160     170     180
           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
|||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcytCgC ccaagGCTTC GTCGTctgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaagct gtttcgggat gTcaaaCTCG

```

```

251 TCcaccgcAT cggcagcgac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccc atatacctcaa cggcggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

```

g039.pep
  1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
 51 KNAKCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGE NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

```

m039.seq
  1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CGnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCC GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCCCCGATAT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCCGCG CCGCCCGGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTCGCCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

```

m039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPAA PARQDGFNWT
151 IATLFAIIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

```

a039.seq
  1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCCATAT TCAACGATT. TGCCCGAAGC TGTTTCGGAT GTCAAACCTG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTCC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

```

a039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
 51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEI	PCPPVSAPTAKPVSGSKKPN	SMSPPXXXXXXXXXXXXXXXX			
a039	MPSEPPYASDGIKPDTHEEI	PCPPVSAPTAKPVSGSKKPN	SMSPKASSSAKNAKECLKPK			

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	10	20	30	40	50	60
	70	80	90	100	110	120
m039.pep	XXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD					
a039	: :					
	70	80	90	100	110	
	130	140	150	160	170	
m039.pep	PPATAATPAAAPQVTVPAPAPARQDGFNWTIATLFAIVLIMQLSYLVILX					
a039						
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPDTHEEIPCPVVSAPTAKPVSGSKKPNMSPPXXXXXXXXXXXXXXXXXX					
g039	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m039.pep	XXXXXXXXXXXXXXXXXXPEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD					
g039	: :					
	70	80	90	100	110	
	130	140	150	160	170	
m039.pep	PPATAAT-PAAAPQVTVPAPAPARQDGFNWTIATLFAIVLIMQLSYLVILX					
g039						
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC  CCGACAGCTT  TGTCGCCAC  TTCCGCGAAG  CCGCCCCCTA
51  CATCCGCCAA  ATGCGCGGCA  CGACACTGGT  CGCCGGCATA  GAcggCCGCC
101  TGCTCGAAGG  CGGCACCTTA  AATAAGCTCG  CCGCCGACAT  C3GGCTGTTG
151  TCGCAACTGG  GCATCCGACT  CGTCCTCATC  CACGGCGCGT  ACCACTTCCT
201  CGAcgCCTC  GCCGCCGCGC  AAGgcccGAC  GCCGCATTAT  TGCCGgggtt
251  tGCGCGTTAC  CGACGaAACc  tGctcgGAC  AGGCGCAGCA  GtttGCCGGC
301  AccgTCCGCA  GCCGTTTTGA  agcCGCATTG  tgccgagcCG  tttcaggatt
351  cgcgCGCGCG  CCTCCGTCC  CGCTCGTAtc  gggcaacttc  ctgacCGCCC
401  GTCcgatggg  cgtgattgac  ggaACCGata  tggaatacgc  gggggttatc
451  cgcaaaaccg  ACACCGCCGC  CCTCCGTTC  CAACTCGACG  CGGGCAATAT
501  CGTCTGGATG  CCGCCGCTCG  GGCATTCTTA  CGGCGGCAAA  ACCTTCAATC
551  TGATATGGT  GCAGGCCGcC  GCTTCCGTCG  CCGTCTCGCT  TCAGGCCGAA
601  AAACCTGTTT  ACCTGACCCT  TTCAGACGGC  ATTTCCCGCC  CCGACGGCAC
651  GCTCGCCGAA  ACCCTCTCGG  CACAGGAAGC  GCAATCGCTG  GCGGAACACG
701  CCGCCAGCGA  AACCCGACGA  CTGATTTCGT  CCGCGGTGCG  CGCGCTCGAA
751  GCGGCGGTGC  ATCGCGTCCA  AATCCTCAAC  GGGGCGCCG  ACGGCAGCCT
801  GCTGCAAGAA  CTCTTCACCC  GCAACGGCAT  CGGCACGTCC  ATTGCCAAAG
851  AAGCCTTCGT  CTCCATCCGG  CAGGCGCACA  GCGGCGACAT  CCCGCACATC
901  GCCGCCCTCA  TCCGCCCGCT  GGAAGAACAG  GCGTCCTTAT  TGCACCGCAG
951  CCGCGAATAC  CTCGAAACC  ACATTTCGGA  ATTTTCATC  CTCGAACACG

```

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGCGGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101 ctACGCGGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTOGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

```

g040.pep
  1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRILLEGGTL NKLAADIGLL
  51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDDET SLGQAQQFAG
 101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
 151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
 201 KLVYLTSLDG ISRPDGTLAEL TSAQEAQSL AEHAASETRR LISSAVAAL
 251 GGVHRVQILN GAADGSLLEQ LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
 301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFEAD
 351 CSEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
 401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRLRHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

```

m040.seq
  1 ATGAGCGCGC CCGACCTCTT TGTGCGCCAC TTCCGCGAAG CCGTCCCCTA
  51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
 101 TGCTCGAAGG TGATACCTTA AACAAGCTCG CCGCCGACAT CCGGCTGTTG
 151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
 201 CGACCGCCAC GCCGCGGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
 251 TCGCGCTTAC CGACGAAACC TCGCTCGAAC AGGCGCAgCA GTTTGCCGGC
 301 ACCGTCCGCA GCCGTTTTGA AGCCGCATFG TCGGCGAGCG TTCCGGGGTT
 351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
 401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAAATACG GGGCGTTATC
 451 CGCAAACCGC ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
 501 CGTCTGGCTG CCGCCGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
 551 TCGATATGCT TCAAACCGCC GCCTCCGCGC CCGTCTCGCT TCAGGCCGAA
 601 AAACCTCGTTT ACCTGACCCT TTCAGACGGC ATTTCGCCCC CCGACGGCAC
 651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
 701 CCGGCGGGCA AACGCGACGG CTGATTTCTG CCGCCGAAC CTTCACCCGC
 751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
 801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
 851 AAGAACAGGG CATCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
 901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
 951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAAGC CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGGC TGTTGCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTTCGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

```

m040.pep
  1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
  51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDDET SLEQAQQFAG
 101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
 151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
 201 KLVYLTSLDG ISRPDGTLAEL TSAQEAQSL AEHAGGQTRR LISSAELFTR
 251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
 301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
 351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
 401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

```

1  ATGATCGTGC CCGACCTCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGSCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCGC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGT
351 CGCGCGCGCG CCTTCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATAACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCGGCTCG GACATTCCCTA CAGCGGCAAG ACCTTCCATC
551 TCGATATGCT TCAAACCGCC GCCTCCGTCG CCGTCTCGCT TCAGGCCGAA
601 AAATCGTTTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGTA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCGCGCGA AACGCGACGG CTGATTTCTG CCGCCGTTGC CGCGCTCGAA
751 GCGCGCGTGC ATCGCGTCCA AATCCTCAAC GGAGCCGCGC ACGGCAGCCT
801 GCTCAAGAA CTCTTCACCC GCAACGGCAT CGGCACGTC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCACAT CCCGCACATT
901 CCGGCCCTCA TCCGCCCGCT GGAAGAACAG GGATCCTGC TGCACCGCAG
951 CCGCGAATAC CTCGAAAACC ACATTTCCGA ATTTTCCATC CTCGAACACG
1001 ACGGCAACCT GTACGGTTGC GCCGCCCTGA AAACCTTTGC CGAAGCCGAT
1051 TGCGGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGG
1101 CTACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGTTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGGAATC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 152; ORF 040.a>:

```

a040.pep
1  MIVPDLFVAH FREAAPYIRQ MRGKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFHLDMLQTA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGT LAV TLSAQEAQSL AEHAGGETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLOE LFRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRIFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNSHIL VRRLHR*

```

m040/a040 91.5% identity in 436 aa overlap

```

m040.pep      10      20      30      40      50      60
MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a040          10      20      30      40      50      60
MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI

m040.pep      70      80      90     100     110     120
HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a040          70      80      90     100     110     120
HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA

m040.pep     130     140     150     160     170     180
PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a040         130     140     150     160     170     180
PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK

m040.pep     190     200     210     220     230     240
TFYLDMLQTAASAAVSLQAEKLVYLTSDGISRPDGT LAETLSAQEAQSLAEHAGGQTRR
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a040         190     200     210     220     230     240
TFHLDMLQTAASVAVSLQAEKLVYLTSDGISRPDGT LAVTLSAQEAQSLAEHAGGETRR

```

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	190	200	210	220	230	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI					
a040	LISSAVAALGGVHRVQILNGAADGSLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI					
	250	260	270	280	290	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
a040	AALIRPLEEQGILLHRSREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS					
	310	320	330	340	350	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
a040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY					
	370	380	390	400	410	420
m040.pep	RSNGRNSHILVRRRLHRX					
a040	RSNGRNSHILVRRRLHRX					
	430					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*.

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAPYIRQMRGTTLVAGIDGRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAQGRTPHYCRGLRVTDDETSLQAQQFAGTVRSRFEALCGSVSGFARA	120
g040	HGAYHFLDRLAAQGRTPHYCRGLRVTDDETSLQAQQFAGTVRSRFEALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAADGSLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSNGRNSHILVRRRLHRX	413
g040	RSNGRNPILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
  1 ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGCCT
 51 GATTACCGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGATT GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC AAACCTGCCT GCGTGTGCT GTTTTGGAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
  1 MSSPKHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYS PDGGGHT NGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATC GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCTT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGGAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYS PDGGGHT NGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
  1 ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCGAGCA ACGGCGGACT
 51 GATTACTGCC GCCGCCTTCG TGC GCGAACC GCAAAGCATA GGCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCTT GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGGAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
  1 ISSPEHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
 51 GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYS PDGGGHT NGTQREAAD ELACVLLFLK
```

151 EFLG*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
a041	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTCRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTCREADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
g041	PQKYEACKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCGACCC CTACGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCG CGCGCACTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCAGCGCGAT
201 GTACCATTTT CATCAGAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGATG GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTCGCAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATT GGAAGCAGGG
451 GAATTGGTAG AGGGCGGTTT TCACTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAAG TGTGGCTGGT GGAACGCGGC

```



```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACTTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGTCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCAATTGGA AGCGTGGAAA GCACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGGTTTGC CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACCTGGTTTA TCTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTGACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGT TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTGG GCGGTGTCGT CCGACGGCGA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGGCA TTCCTGAATT GCCGATTAT CTGGGCAGCG TCGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCAACATC CGCGCGGCG
1451 GAGAATTCGG CCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAAAC
1501 AAAAGCGTTG ATGATTICTT GGCAGTCGTG CGTGATTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCCCTT GTGCCGGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGAT CGTTATCCG TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGGTGTTGC TGTTTTGA
2001 AGAATTTTTG GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRHH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSOGDTA YTLEVDLEAG
151 ELVEGGEHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDGCVVGYL AGHLLTLRKL DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFVV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLAA SDETTPLTLF ALDLNVMELT
401 VMRLQPQQFV SDGIEVRQFW AVSSDGERIP YFHVGNKNAAP DPTLVYAYG
451 GFGIPELPHY LGSVGYWLE EGNAEVLANI RGGGEFGRPW HQAAQGISKH
501 KSVDDLLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDRVHFA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCGGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGCGC CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGCGACA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGGTGCGCAC TTGGTGGAA AGCCCAACCG CGGTTGTGA ACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATTG GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT CCCTGTGTAT CAAATCGCGC AAGACGGCAT
651 GATGGTGAAC GCGTGGC3TT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGAC3GT TTTTACACCA AAACCTATTT GCGGGTCTCA

```

```

751 GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801 CGGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851 GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901 CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GGCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGGCG ACGTGGTTTA CCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAC TGACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCTT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGCGCA TTCCCGAATT GCCGCATTAT CTGGGCGAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGCAACATC CGCGGCGGCG
1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG CGCGATTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGCGCGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCCAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TCGCTCTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGVS H LVEQPNRALL TSLKLGSDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVS WRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DMNRANQSY S GALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKREVV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQF WGGDVVYLA SDFTTPLTLF ALDLNVMELT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNAA P DMPTLVYAYG
451 GFGEIPELPHV LGSIGKYWLE EGNAPVLANI RGGGEFGPRW HQAAOGISKH
501 KSVDDLLAVY RDLSEGRIS PEHIGLOGGS NGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYPDPYRHFENLDSAETQ	NFAAEANAET	RARFLNDKA	RALSDGILAQ	LQDTRQIPFC	
g041-1	MKSYPDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILNQ	MDTRQIPFC	
	10	20	30	40	50	60
m041-1.pep	QEHRARMYHFHQDAEY	PKG VYRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGVS	H
g041-1	QEHRARMYHFHQNAEY	PKG VYRMCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGVS	H
	70	80	90	100	110	120
m041-1.pep	LVEQPNRALLTSLKLGSDTA	YTLEVDLEAGEL	VEGGFHFPAGKNHVS	WRDENS	SVWVCPAW	
g041-1	LVEQPNRALLTLNKSGGDTA	YTLEVDLEAGEL	VEGGFHFPAGKNHVS	WRDENS	SVWVCPAW	
	130	140	150	160	170	180
m041-1.pep	NERQLTQSGYPREVWL	VERGKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
g041-1	NERQLTQSGYPREVWL	VERGKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREVWL	VERGKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	
g041-1	NERQLTQSGYPREVWL	VERGKSFEESLPVY	QIGEDGMMVN	AWRYLDPQGS	PIDLIEASDG	

g041-1	DERQLTESGYPREVWLVERGKSFEEESLPAYQIDKGAMMVNAWRYLDPQGSFIDLIEASDG
	190 200 210 220 230 240
m041-1.pep	FYTKTYLRVSAEAGEAKPLNLPND CDVVGYLAGHLLTLRKDWNRRANQSYPSGALVAVKLN
g041-1	FYTKTYLQVSSEGGAKPLNLPND CDVVGYLAGHLLTLRKDWHRRANQSYPSGALVAVKLN
	250 260 270 280 290 300
m041-1.pep	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADGKWQEVLEPRLP
g041-1	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADSKWQEAELPHLP
	310 320 330 340 350 360
m041-1.pep	SGALEMTDQPWGGDVVYLAASDFTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW
g041-1	SGALEMTDQPWGGDVVYLAASDFTPLTLFALDLNVMELTVMRLQPQQFVSDGIEVRQFW
	370 380 390 400 410 420
m041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSGIKYWLEEGNAFVLANI
g041-1	AVSSDGERIPYFHVGNKNAAPDPTLVYAYGGFGIPELPHYLGSGVGYWLEEGNAFVLANI
	430 440 450 460 470 480
m041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF
g041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGMSSPKHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
m041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPKYEVCKRRRLGELSYPYHNLSDG
g041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPKYACKRRRLGELSYPYHNLSDG
	550 560 570 580 590 600
m041-1.pep	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPCGGGHTGNGTQRESADELA
g041-1	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPCGGGHTGNGTQRESADKLA
	610 620 630 640 650 660
m041-1.pep	CVLLFLKEFLGX
g041-1	CVLLFLKEFLGX
	670

m041-1/P55577

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4na [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAEQNFANAEANAEARFLNDKARLSDGILAQLDTRQIPFCQ 61

K DP + +D + + N T + ++ L LQ T +I

Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSQPEWKILFSVADFELGDDVYLGGVSH 120

R M +F QD + +G++R T +YRSG P+W+ + V + G G

Sbjct: 102 FARDGNIDNFWQDGTWVQGLWRRTTWESYRSGNPQWRITLDVDALSKAEGKTWVFEFGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENSVMVCPAW 180

L N L+ LS G D E D+ GE V+ GF P GK V+W DEN++V W

Sbjct: 162 LPPTSNLCLIRLS DGGKDADVREFDI AKGEFVKEGFVLPEGKQSVTWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSPI 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTS SSGYAYVTKVVKRGQSLDQAVEIFRGQKKDVS AERGVLRDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPND CDVVGYLAGHLLTLRKDNWRANOS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELA FYPNGH---PDTRKVVLPLPTTAVFSGYKQAIYWLKSDWTS AKGTVFHN 337

Query: 292 GALVAVKLN RGE LGAAQL----LFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAI IAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEV ELPRLPSGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDES DQLFVFSEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDS DGINVQQFWTTSADGERIPYFHVGNAAAP---DMPTLVYAYGGFGIPELPHYL GSI 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGIS KHKSVDDLLAVVRDLSE RGISSPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DU AV +DL - ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWHDAGLKTNRQVYDDFQAVAQDLIAKKVTSTPHL 577

Query: 525 GLQGG SNGGLITAAAFVRE PQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVC 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRDLWNNAVVIQVPL LDMVNFTRMSAGASWQA EYGS PDD-PVE 636

Query: 585 KRRLGELS PYHNLS DGI DYPALITTSLSDDR VHFAHAKFYAKLRETS AQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFLRSISPYHNVKAGVAYPEPFFETSTKDDR VGPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1 ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGCGGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 TCGTTCGCAC CTGTTGGAAC AGCCCAACCG CGCGTTGTTA ACACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTAG AAGCGCGTTT TCACTTTCCG GCAGGCAGAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGTAC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 CCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CCGCTATCTG GCCGGACATC TTTTGCTGAC CTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTTCGT CTGAAAGCGT GCGGTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTCA
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAACGTACC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGCGA TTAACGTGCA
1251 GCAGTTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGCTGGAA GAGGGCAATG CCTTGTATT GCGGAACATC CGCGCGCGGC

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG AGCGATTGTG CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCCTGTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRKL DWHRANQSYPS GALVAVKLN
301 RGE LGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGL
351 WQETELPRLP SGALEMTDQP WGGDVVYLAA SDFTTPLTLF ALDLNVMELT
401 VMFRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNAAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGRW HQAAQGISKH
501 KSVDDLLAVV SDSLSEGISS PEHIGLQGG NGLLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
m041-1	MKSYDPYRHFENLDSAETQ	NFAAEANAET	RARFLNNDKA	RALSDGILAQ	LQDTRQIPFC	
	10	20	30	40	50	60
a041-1.pep	QEHRARMYHFHQDAEYPKGV	YRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
m041-1	QEHRARMYHFHQDAEYPKGV	YRVCTAATYR	SGYPEWKILF	SVADFDELLG	DDVYLGGVSH	
	70	80	90	100	110	120
a041-1.pep	LVEQPNRALL	TSKSGGDTA	YTLEVDLEAG	ELVEGGFHFP	AGKNHVSWRD	ENSVWVCPAW
m041-1	LVEQPNRALL	TSKSGGDTA	YTLEVDLEAG	ELVEGGFHFP	AGKNHVSWRD	ENSVWVCPAW
	130	140	150	160	170	180
a041-1.pep	DERQLTESGY	PREVWLVERG	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG
m041-1	DERQLTESGY	PREVWLVERG	KSFEESLPVY	QIAEDGMMVN	AWRYLDPQGS	PIDLIEASDG
	190	200	210	220	230	240
a041-1.pep	FYTKTYLQVS	AEGEAKPLNL	PNDCDVVGYL	AGHLLTLRKL	DWHRANQSYPS	GALVAVKLN
m041-1	FYTKTYLQVS	AEGEAKPLNL	PNDCDVVGYL	AGHLLTLRKL	DWHRANQSYPS	GALVAVKLN
	250	260	270	280	290	300
a041-1.pep	RGE LGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGL	WQETELPRLP
m041-1	RGE LGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGL	WQETELPRLP
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGL	WQETELPRLP
m041-1	RGELGAAQLL	FAPNETQALE	SVETTKRFVV	ASLLENVQGR	LKAWRFTDGL	WQETELPRLP

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQFWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQFWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSERGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELS PYHNLS DG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELS PYHNLS DG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRHPAHALKFYAKLRETS PQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRHPAHALKFYAKLRETS AQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

```

g042.seq
1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTCGAT GATGAAAATC CAGCCGGGGT TTTCTCTTT GATGTATTCTG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACC CGG
501 CCCGCCGTA ATGACAAACT GCGATTGTG GCGGTGCAGG GATTGCGAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTGCGC CCTGTGCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

```

g042.pep
1  MTMICLRFOA FVPHTSALS N TSTAAGPSCP MAAVRSMKI QPGFFSLMYS
51  KETGCPCLSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRFA NSASICAFNS ATRASLPKIR DRVSICFSEL VRILPLSTVK
151 SMVVAFFANC SYASAPGPV MTNCGLWRCR DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGTCCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1 MTMICLRFOA FVPTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAENS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCGGCGCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGTCCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1 MTMICLRFOA FVPTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAENS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAGC
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042	MTMICLRFOAFVPTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANSASICAENS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSSTPRPLPLAASRVWANSASICAENS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					

239

```

|||||
a042      AARASLPKIRAKVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
           130      140      150      160      170      180

           190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
           |||||
a042      ASXSGSNSVPTVAALSNAGCKX
           190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

           10      20      30      40      50      60
m042.pep  MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
           |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
           10      20      30      40      50      60

           70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRFWANSASICAFNS
           70      80      90      100     110     120

           130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
           |:||||| |:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g042      ATRASLPKIRDRVSICFSPVLRLPLSTVRSMVVAFFANC SYASAPGPPVMTNCGLWRCR
           130     140     150     160     170     180

           190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
           | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCGTAACCG ACAGCACCAG CCGCGCTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1  MTMICLRFOA FVERTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCPVKADTLL PVTDSSTPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSP LRLPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	:					
g042	MTMICLRFAQFVPHTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGPRMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGPRMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRFWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANC SYASAGPPVMTSX					
	: :					
g042	ATRASLPKIRDRVSICFSPILVRILPLSTVKSMVVAFFANC SYASAGPPVMTNCGLRWR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA  TTTGCTTGCG  CTTCCAAGCG  TTCGTGCCGC  GTACCAGCGC
51  GTTATCCAAT  ACTTCGACAG  CCGCCGGCCC  TTCCTGCCCG  ATGGCGGCGG
101  TACGGTCGAT  GATGAAAATC  CAATCGGGGT  TTTTCTCTTT  GATGTATTCT
151  AAGGAAACAG  GCTGCCCGTG  CCCCTCGTTG  CGTAAAGATT  CGTCTACAGG
201  CGGTAGGCCG  ATGTCGCCGT  GTATCCAAC  TGCCAACCGC  GACTGCGTGC
251  CGAAGGCGGA  CACCTTGTTG  CCCGTAACCG  ACAGCACCAG  CCCGCGTCCT
301  TTGCCTTTGG  CGGCTTCGCG  CGTTTGGGCG  AACAGCGCGT  CAATCTGCGC
351  CTTCAATTCC  GCCGCGCGCG  CTTCTTGCC  GAAATCCGC  GCCAAGGTCT
401  CCATCTGCTT  TTCGCCGCTG  GTGCGGATAT  TGCCGTTGTC  CACCGTCAGA
451  TCTATGGTGG  TCGCGTTTTT  CGCCAACGTG  TCATACGCTT  CCGCGCCCGG
501  CCCGCCGTA  A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFAQ  FVPRTSALSNTSTAAGPSCP  MAAVRSMMKI  QSGFFSLMYS
51  KETGCPGPSL  RKDSSTGGRP  MSPCIQLANR  DCPKADTLL  PVT DSTSPRP
101  LPLAASRVWA  NSASICAFNS  AARASLPKIR  AKVSICFSP  VRILPLSTVR
151  SMVVAFFANC  SYASAGPPV  MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042-1	MTMICLRFAQFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGREMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGREMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANC SYASAGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPILVRILPLSTVRSMVVAFFANC SYASAGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

241

```

g043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTTCG ATGAGGGGcga gcGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 GTCCGGCGAC GGTTCGCGCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTTCGTTC GCGCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

```

g043.pep
1  MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
51  ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFDGGQRA
101 GEFVQNIIGG FVYAPAAVAV VVAAEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

```

m043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 CCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCagGC
201 ATCCGGCGAC GGTTCGCGCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTTCGTTC GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAAACGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

```

m043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPER FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AAGDFDGGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	: : : : : : : : :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPERFVEPSRVAVAAKVHRGLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFDGGQRTGEFVLQDVGGFVYAPTAVTV					
	: : : : : : : : :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAAAGDFDGGQRAGEFAVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
g043	VVAAEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

```

a043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

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```

151 GCCGGATTCTG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
231 ATCCGGCGAC GGTTCGCGG GTTTGCGCTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCG GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCTG TGTTCAGGA TGTGCGCGG TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
  51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSE	FVEPSRVAVA	AKVHGGLDGA	AGFDEGERVF		
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSE	FVEPSRVAVA	AKVHGGLDGA	AGFDEGERVF		
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDA	AGDFGDGQRTGE	FVLQDVGGFVYAPTAVTV			
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDA	AGDFGDGQRTGE	FVLQDVGGFVYAPTAVTV			
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCC ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGCGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGCCC TTCGATAACG GCGGTCAGCT
 201 CCATGCGGTT GTTGGTGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 CGGCTGCCGT AGCGCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
  51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTCCA TGCCATTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGTCC TTCGATGACG GCAGTCAGTT
 201 CCATGCGGTT GTTGGTGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTCG
 251 TGGTACCCT AGCGCAyTAa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPDXXSVEFF PEVVFDGLF GGGFPAVALP TVYPVFHAIF DVLRVGADDD
  51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
1  GTGCCGTCCG ACCAGCGCGT CGAGTTCTTT CCACAAGTCG TCGTTTTTGA
51  CGGGCTGTTT GCGGCGGTTT TTCCAGCCGT TCGGCTTCCA ACCGTGTATC
101 CAGTTTTCCT TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TCGGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGCATTA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
1  VPSDQRVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
51  GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

```
m044.pep      10      20      30      40      50      60
MPSDXSVEFFPEVVVFDGLFGGGFFAVALPTVYPVFHAI FDVLRVGADDDGAAAFERFQS
:| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
a044          10      20      30      40      50      60
VPSDQRVEFFPQVVVFDGLFGGGFFAVALPTVYPVFHAVF DVLRVGADDDGAAAFERFQS

m044.pep      70      80      90
FDDGSQFHAVVGGLRFAAEKFFVFATVAHX
| | | | | :| | | | | :| | | | | :| | | | |
a044          70      80      90
FDDGGQFHTVVVGGLRFAAEKFFFAVAHAX
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

```
m044.pep      10      20      30      40      50      60
MPSDXSVEFFPEVVVFDGLFGGGFFAVALPTVYPVFHAI FDVLRVGADDDGAAAFERFQS
| | | | | :| | | | | :| | | | | :| | | | | :| | | | | :| | | | |
g044          10      20      30      40      50      60
MLPDQSVEFLPQVVVFDGLFGGGFFAVALPTVYPVFHAVF DVLRVGADDDGAAAFERFQP

m044.pep      70      80      90
FDDGSQFHAVVGGLRFAAEKFFVFATVAHX
| | | | | :| | | | | :| | | | | :| | | | |
g044          70      80      90
FDNGGQLHAVVGGLRFAAEKFFFAVAHAX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
1  ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGCGcc gCGCCTGTAT
51  GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGTTTT CGTTATGCC gaATATGGAA AGGCTGCCgt TTtcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCCG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGagaCGCG AGcagcaagt cggcatcttC
351 CgcgccggcG Cgttataatg tgAAGGGGGA TGCGccgttg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg9 TTACGTCGTT GTTGGTGATG GCGCAAGGT TTTGCGCGAC
```

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501 GG TAGAACCT ACCTGCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CCGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TGCGCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CCGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TGCGCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTI	RTRSSAKRKT	CNAPGQSIRP	ASCSVTSCSG	LMVSVMPNME	
a046	MSAMLRPTSSPPRRACMMTI	RTRSSAKRKT	CNAPGQSIRP	ASCSVTSCSG	LMVSVMPNME	

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	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
g046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKTCNAPGQSIRPASCSTSCSGLMVSVMPNME					
	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

```

1  ATGGTCATCA TACAGGCGcg gcGCGGCGGG CTGCTTGTCG GACGCAGCAT
51  TGCCGACATC GCCCAAGATT TGCCGACGG GCGCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT GTTTGCCGCC GCCGCGGAAA ACATCGGGGC
201 GGTACATACC gaATTGCGCC CCAAGAAAC CAGCACCCGC CGCATCATGA
251 TTGCCGCGCG CGGCAACATc tgctACCGCC TCGCCAAGCA GCTCGAACAC

```

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```

301 GCATAcaacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAc ctcgAcaaCA CCCTCGTCCT GCAAGGTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTatg tCCGCCCTTt TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGGC CGGCGCATCC TGAACGAAC GGAGAAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLDPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLDDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGGCGcG C..syGCCGA sTGCTTGTCG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTCATACCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATAAACGT yAAAATCATC GAATGCCGGC CGCGCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTTCG
401 CAACCGACGA AACCTTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GGCGAaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTTGCCGTC CACCCATCC GGCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAG
751 GGCATCAAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTCG TCCGCGCCGG
801 AACC CGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTT GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLDPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETORN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE IEVVAHGDK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGCGGA CTGCTTGTCG GACGCAGCAT

```

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```

51  TGCCGACATC  GCCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCGTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCGGCC  GCCGCCGAAA  ACATCGGCGC
201 GGTCATACCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGGCGG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTTC  GCAACCGACG
401 AAACCTTGCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGGCGAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGCGGACA  TCGTTGCCGT
651 CCACCCCATC  CGGCGCGGCA  CGGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCGCGC  ATCATCGGCA  GGCGCATCAG  CGGCATCAAA
751 TGGCCCGAAG  GCTGCCACAT  TGCCGCCGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GGCGACCACA
851 TCATCTTTT  CGTCTCGCGC  CGGCGCATCC  TGAACGAACT  GGAAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLPDGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRAEWIAEN  LDNTLVLQGS  ATDETLLDNE  YIDEIDVFCA
151 LTNDDESNI  SALLAKNLGA  KRVIGIVNRS  SYVDLLEGNK  IDIVVSPHLI
201 TIGSLAHIR  RGDIVAVHPI  RRGTAEAIEV  VAHGDKKTS  IIGRRISGIK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRILNELEKL
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

m047.pep      10      20      30      40      50      60
MVIIQARXGXLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
||||| | |||||||
a047           10      20      30      40      50      60
MVIIQARRGGLLVGRSIADIAQDLPDGADCQICAVYRNNRLIVPAPQTVIIEGDEILFAA
||||| | |||||||

m047.pep      70      80      90     100     110     120
AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRAEWI
||||| | : ||| |||||||
a047           70      80      90     100     110
AAENIGAVIPELRPKETSTR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRAEWI
||||| | ||| |||

m047.pep     130     140     150     160     170     180
AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNI SALLAKNLGAKRVIGIV
||||| | |||||||
a047          120     130     140     150     160     170
AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNI SALLAKNLGAKRVIGIV
||||| | |||||||

m047.pep     190     200     210     220     230     240
NRSSYVDLLEGNKIDIVVSPHLITIGSLAHIRRGDIVAVHFIRRGTAEAIEVVAHGDKK
||||| | |||||||
a047          180     190     200     210     220     230
NRSSYVDLLEGNKIDIVVSPHLITIGSLAHIRRGDIVAVHFIRRGTAEAIEVVAHGDKK
||||| | |||||||

m047.pep     250     260     270     280     290     300
TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
||||| | |||||||
a047          240     250     260     270     280     290
TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
||||| | |||||||

m047.pep      310
EKLIQVKMGFFGX
|||||

```


a047 EKLIQVKMGFFGX
 300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNNRLVPAPQTVIIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQPPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
	: :	
g047	AAENIGAVIPELRPKETSTR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	297
m047.pep	EKLIQVKMGFFGX 313	
g047	EKLIQVKMGFFGX 310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

1	ATGCTCGACA AAGGCGA3GA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTc ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101	CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCCG CCAAATGCTC
151	AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201	cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251	GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTC CAAAGTCTTG
301	GCGTTCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351	TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401	CCGCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451	TGA

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

1	MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51	KQTGLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101	AFPELGMEAV YEFVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

1	ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTC GGCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

```
m048.pep
  1  MLNKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTQRLM
 51  EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101  APFELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151  *
```

```
a048.seq
  1  ATGCTCGACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGACGAAATC GTCGGCCAG
101 CAGGTCCGAC ACCGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCCTTTGGG CATGATCGGC AAATCCGAGC GCGCGCGCGG
201 CACCTCGGAA GCCATCGCGG ACACAAAGC CGGTACCTC ATGCGCATCGC
251 GCGGCGCGGC GTATCTCGTG GCAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGCAT GGAAGCCATT TAGGAATTG AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCGG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CGGCCCGGCC CCAATGGCAG GCGAAATCG GCATCATCCC CGTCAAATCT
451 TGA
```

```
a048.pep
  1  MLDKGEELPV DFTNRLIYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLGMIG KSERGAATCE AIDNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *
```

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDF	TNRLIYYVGP	VPDVPVGDE	VVGPA	GFTTATRM	DKFTROMLEQ
a048	MLDKGEELPVDF	TNRLIYYVGP	DPDVGDEIV	GPA	GFTTATRM	DKFTROMLEQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAI	ADNKAVYLM	AVGGAAYL	VAKAIKSS	SKVLAFPE	LGM
a048	KSERGAATCEAI	ADNKAVYLM	AVGGAAYL	VAKAIKSS	SKVLAFPE	LGM
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESI	HATAPRKWQ	AKIGIIP	VESX		
a048	TVAVDSKGESI	HATAPPQWQ	AKIGIIP	VKSX		
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 207>:

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

251

```

1  ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTCTAGCTCC TGTTCGGACA
51  GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCCGCTT
201 CAATCTGTCC GGTTTCAAAT TCGGCACTGT CTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTCTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTTGTGTT CTCCTGCCAT
401 TTTTTAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1  MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRN
51  PVCRRTRFCR IGVFFAFNLS GFKFGTVFFG IKPDSPPRFD VFFRNRLQ
101 SLRVEPVFLK DHRVGFDFL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

m049.pep      10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRNRRLIRAGFCL
|||||
a049           10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRNPVCRRTRFCR
|||||

m049.pep      70      80      90     100     110     120
VGVPFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
:|||||
a049           70      80      90     100     110     120
IGVFFAFNLSGFKFGTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
|||||

m049.pep      130     139
AAIGNGGIVFLLPFFQIRL
|||||
a049           130
AAIGNGGIVFLLPFFQIRL

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

m049/g049

```

m049.pep      10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRF FRIVFPVFRNRRLIRAGFCL
|||||
g049           10      20      30      40      50      60
MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAFVFRNPVCRRTGFCR
|||||

m049.pep      70      80      90     100     110     120
VGVPFAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
:|||||
g049           70      80      90     100     110     120
IGVFFALNLCGFKFGTVFFGIEPDSPPRFDVFFRNRLQGSRLRVEPVFLKDDHRVGFDFL
|||||

m049.pep      130     139
AAIGNGGIVFLLPFFQIRL
|||||
g049           130     140
AAIGNGAVVFFLPFLQIRLX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

```
g050.seq
1  atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGg
51  cagccccGAA AAAGccgtgt TGATGGcaaA AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGgtcc
351 TGTCGAactc acgccGCcg gtgtCGAAGA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

```
g050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

```
m050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGCTATCG GCATCGGCGG
51  C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGCGCG GgAATTGTCC
151 ACCACCGAAG CCTGCGCCT CGAACTCTTT GAAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAATC ACGCCGCCG GCGTCGAAGA TGGCCCGATT TGA
```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

```
m050.pep
1  MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

```
a050.seq
1  ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGCGCG GGAATTGTCC
151 ACCACCGAAG CCTGCGCCT CGAACTCTTT GAAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAATC ACGCCGCCG GCGTCGAAGA CTGGCCC
```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

```
a050.pep
1  MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP
```

m050/a050 97.7% identity over a 129 aa overlap

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					
a050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF					

253

	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAELVMAKESLSMHSIDIQELQEKAAASGAELSTTEALRLLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMHSIDIQELQEKAAASGAELSTTEALRLLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACAAACGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGCGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCTTCCCGG CATCTTGGGC ATCGGCATCG GCGGCACgGC CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GGAGGAAAAA GCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCGTCGAAC TTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCAACCG GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCTG ATTTGAATTG GACGGCTCAG GTCTGTGCGA ACTCACGCCG
901 CCGCGGCTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGGCAA
951 AGCGGTCGAT GTCGATAAGC TGACCAAAAG AGAAGTGCCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTCACC AACCCGCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCGCA CCACAGCCAC CCGCATGGAC
1201 AAATTATACC GCCAATGCT CAAACAAACC GGCTCTTGG GCATGATCGG

```

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```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGTACCT CATGGCAGTC GGCGGCGCGG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATTGGGTA TGGAAAGCCGT
1401 TTACGAATTG GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGGCAATC CATCCACGCC ACCGCCCCGC GCAATGGCA GGCAGAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDANTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGMDVQWDADMSV EKMVNEGVR
101 AYTWEENTLR ASVLADPAGK RONTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELOEK AASGAELSTT EALRLELF EK VNALGIGAQG
251 LGGLTTVLVD KILDYPTTHA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVED*PDLT YSPDNGKRV DKLTKKEVA SWKTGVDLLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDF NRIYYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTROMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVYEF EVKDMPTVA VDSKGESIHA TAPRKWOAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
      Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDASFMLRPAHQKQVAAILHDPASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRAYTWEGNTLRASVLADPAGKRONTKDNTPA 130
      A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAILVGGKQQRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGSENKSL-----AMLNPSDNIVDWVLKTIPTMGAGWCP 185
      I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDYKFLCVARGGGSANKTYLYQETKALLTPG-KLKNFLYKMRITLGTACAP 225

```

```

Query: 186 PXXXXXXXXXXTPKAVLMAKESLSHIDIQELQEKAAASGAELSTTEALRLELFKVNXXX 245
      P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGSAETNLKTVKLASAHY-YDELPTEGNEHGQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXTTVLVDKILDYPTTHAASKPIAMFNCAATRHVEFELDGS-----PVELTPP 301
      D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNGKRVVDKLTK---EVASWKTGVDVLLNGKILTGRDAHKRLVNM 358
      + +VD+++ KE +- + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFNRLIYXXXXXXXXXXXXXXXXXXTTATRMDKFTROMLKQTGLLMIGK 418
      +D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVGG--AAYLVAKAIKSSKVLAPFELGMEAVYEFVVKMPV 477
      R +A + YL ++GG AA L ++IK + +A+PELCMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSI GGPAAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
      + VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGCGA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACGCCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```

```

301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCGGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCATA
401 TGAGCATCGT GCCGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAATC CAAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAGAATT
651 CCAGGAAAGG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCTGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGGCGAGT ATTGCTGTTG AACGGCAAAA TCCTCACC GGCGGATGCC
1051 GCACACARAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCC
1151 GCGATTGAAT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGGTACCTT CATGGCAGTC GCGGCGCGGG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCCGC GCAAATGGCA GGCGAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYYPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M NVQWDADMSV EEMVNEGVR
101 AYTWEGLTLK ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSNKSCLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELF EK VNALGIGAQG
251 LGGLTTVLVD KILDYPTHA A SKPIAMIPNC AATRHVEFEL DGSGPVELTP
301 PRVEDWPLDT YSPDNKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVMDLN KGEELPVDET NRIYYVGPV DPVGDEVVGP AGPTTATEMD
401 KFTROMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLM AV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKMPVTV A VDSRGESIHA TAPRKWQAKI
501 GIIPVES*

```

m050-1/g050-1 98.2% identity in 507 aa overlap

	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFI	QSIDAFQFI	SYYPKDYID	ALYKAWQKEE	NPAAKDAMTQ	ILVNSRMCAE
g050-1	MTVIKQEDFI	QSIDAFQFI	SYYPKDYID	ALYKAWQKEE	NPAAKDAMTQ	ILVNSRMCAE
	70	80	90	100	110	120
m050-1.pep	NNRPICQDTG	IATVFLKVG	MNVQWDADMS	VEEMVNEGVR	RAYTWEGNTL	ASVLADPAGK
g050-1	NNRPICQDTG	IATVFLKVG	MNVQWDADMS	VEEMVNEGVR	RAYTWEGNTL	ASVLADPAGK
	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPA	VIHMSIVPGG	KVEVTCAAKG	GGSENKSKLA	MLNPSDNIVD	WVLKTIPTMG
g050-1	RQNTKDNTPA	VIHMSIVPGG	KVEVTCAAKG	GGSENKSKLA	MLNPSDNIVD	WVLKTIPTMG
	190	200	210	220	230	240
m050-1.pep	AGWCPPGILG	IGIGGTPEKA	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELF EK
g050-1	AGWCPPGILG	IGIGGTPEKA	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELF EK
	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGL	GGLTTVLVD	KILDYPTHA	ASKPIAMIPNC	AATRHVEFEL	DGSGPVELTP
g050-1	VNALGIGAQGL	GGLTTVLVD	KILDYPTHA	ASKPIAMIPNC	AATRHVEFEL	DGSGPVELTP

256

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLTYS	SPDNGKRVDVDKLTKEEVASWKTGDVLLNGKIL	TGRDAAHKRLV	DMLN		
g050-1	PRVEDXPDLTYS	SPDNGKRVDVDKLTKEEVASWKTGDVLLNGKIL	TGRDAAHKRLV	NMLD		
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDFNRLI	YYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQT	DLLGMIGKSE			
g050-1	KGEELPVDFNRLI	YYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQT	DLLGMIGKSE			
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEAIADNK	AVYLMVSGAAYLVAKAIKSSKVLAFPELGMEAIYEF	EVKDMPVTVA			
g050-1	RGAATCEAIADNK	AVYLMVSGAAYLVAKAIKSSKVLAFPELGMEAVYEF	EVKDMPVTVA			
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESIHATAPRK	WQAKIGIIPVESX				
g050-1	VDSKGESIHATAPRK	WQAKIGIIPVESX				
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

1	ATGACCGTCA	TCAAACAGGA	AGACTTTATC	CAAAGCATTT	CGCATGCCCT
51	CCAATTCATC	AGCTACTACC	ATCCCAAAGA	CTACATCGAC	CGCCTTTATA
101	AGGCGTGGCA	GAAGGAAGAA	AACCCCGCCG	CCAAAGACGC	GATGACGCAG
151	ATTTTGGTCA	ACAGCCGCAT	GTGTGCCGAA	AACAACCGCC	CCATCTGCCA
201	AGATACCGGT	ATCGCGACCG	TGTTTTTGAA	AGTCGGTATG	GATGTGCAAT
251	GGGATGCAGA	CATGAGCGTC	GAAGAGATGG	TTAACGAAGG	CGTGCGCCSC
301	GCCTACACTT	GGGAAGGCAA	TACGCTGCGC	GCTTCCGTTC	TCGCCGACCC
351	CGCCGGCAAA	CGCCAAAATA	CCAAAGACAA	CACGCCCGCC	GTCTCCATA
401	TGAGCATCGT	CGCGGGCGAC	AAAGTCGAAG	TAACTGCGC	GGCAAAAGGC
451	GGCGGTTCTG	AAAACAAATC	CAAACTCGCC	ATGCTCAACC	CTTCCGACAA
501	CATCGTCGAT	TGGGTATTGA	AAACCATTC	GACCATGGGC	CGCGGCTGST
551	GTCTCTCCGG	CATCTTGGGC	ATCGGCATCG	GCGGTACGCC	CGAAAAAGCC
601	GTGTGTGATG	GAAAGAATC	CCTGATGAGC	CACATCGACA	TCCAAGAATT
651	GCAGGAAAAA	GCCGCGTCCG	GCGCGGAATT	GTCCAACACC	GAAGCCCTGC
701	GCCTCGAACT	CTTTGAAAAA	GTCACGCGC	TAGGCATCGG	CGCGCAAGGC
751	TTGGGCGGTC	TGACCACCGT	GTTGGACGTG	AAATCTCTCG	ATTACCCGAC
801	CCACGCGGCC	TCCAAACCGA	TTGCCATGAT	TCCGAATGTC	GCCGCCACCC
851	GCCACGTCGA	ATTTGAATTG	GACGGCTCAG	GCCCTGTCTG	ACTCACGCCG
901	CCGCGGTGTC	AAGACTGGCC	CGATTTGACT	TACAGCCCCG	ACAACGGCAA
951	ACGCGTCGAT	GTCGACAAGC	TGACCAAAGA	AGAAGTGCCA	AGCTGGAAAA
1001	CCGCGCAGCT	ATTGCTGTTG	AACGGCAAAA	TCCTCACCGG	CCGCGATGCC
1051	GCGACAAAC	GCCTCGTCGA	TATGCTCGAC	AAAGGCCAAG	AATTGCCCGT
1101	CGATTTTACC	AACCGCCTGA	TTTACTACGT	CGGCCCGGTC	GATCCGGTCG
1151	GCGACGAAAT	CGTCGGCCCA	GCAGGTCGGA	CCACCGCCAC	CCGCATGGAC
1201	AAATTCACCC	GCCAAATGCT	CGAACAAACC	GACCTCTTGG	GCATGATCGG
1251	CAAAATCCGAG	CGCGGCGCGG	CCACCTGCGA	AGCCATCGCC	GACAACAAAG
1301	CCGTGTACCT	CATGGCAGTC	GCGGCGCGGG	CGTATCTCGT	GGCAAAAGCC
1351	ATCAAATCTT	CCAAAGTCTT	GCGGTTCCCC	GAATTGGGCA	TGGAAAGCCAT
1401	TTACGAATTT	GAAGTCAAAG	ACATGCCCGT	AACCGTCGCC	GTAGACAGCA
1451	AAGGCGAATC	CATCCACGCC	ACCGCCCGCG	CCCAATGGCA	GGCGAAAATC
1501	GGCATCATCC	CCGTCAAATC	TTGA		

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

1	MTVIKOEDEFI	OSICDAFOFI	SYHHPKDYID	ALYKAWOKEE	NPAKRDAMTO
51	ILVNSRMCAE	NNRPICQDTG	IATVFLKVGM	DVQWDADMSV	EENVNEGVR
101	AYTWEGNTLR	ASVLADPAGK	RONTKDNTPA	VIHMSIVPGD	KVEVTCNAKG
151	GGSENKSKLA	MLNPSDNIVD	WVLKTIPTMG	AGWCPPGILG	IGIGGTPEKA
201	VLMAKESLMS	HIDIQELQEK	AASGAELSTT	EALRLELFER	VNALGIGAQQ
251	LGGLTTVLVD	KILDYPTTHAA	SKPIAMTPNC	AATRHVEFEL	DGSGPVELTP
301	PRVEDWPDLT	YSPDNGRRVD	VDKLTKEEVA	SWKTGDVLLL	NGKILTRDA
351	AHKRLVDNLD	KGEELPVDFN	NRLIYYVGPV	DPVGDEIVGP	AGPTTATRMD
401	KFTRQMLEQT	DLLCMICKSE	RCAATCEAIA	DNKAVYLMVAV	GGAAYLVAKA
451	IKSSKVLAF	ELGMEAIYEF	EVDMPVTVA	VDSKGESIHA	TAPPQWQAKI
501	GIIPVKS*				

a050-1/m050-1 98.4% identity in 507 aa overlap

```

      10      20      30      40      50      60
a050-1.pep  MTKVIOEDFIQSICDAFOFISYYHPKDYICALYKAWQKEENPAKDAMTQILVNSRMCAE
|||||
m050-1      MTKVIOEDFIQSICDAFOFISYYHPKDYICALYKAWQKEENPAKDAMTQILVNSRMCAE
      10      20      30      40      50      60

      70      80      90     100     110     120
a050-1.pep  NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRASVLADPAGK
|||||
m050-1      NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRASVLADPAGK
      70      80      90     100     110     120

      130     140     150     160     170     180
a050-1.pep  RQNTKDNTPAVIHMSIVPGDKVEVTCAARGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
|||||
m050-1      RQNTKDNTPAVIHMSIVPGDKVEVTCAARGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
      130     140     150     160     170     180

      190     200     210     220     230     240
a050-1.pep  AGWCPPGILGIGGTPEKAVLMAKESLMSHIDIOELOEKAASGAELSTTEALRLELFEK
|||||
m050-1      AGWCPPGILGIGGTPEKAVLMAKESLMSHIDIOELOEKAASGAELSTTEALRLELFEK
      190     200     210     220     230     240

      250     260     270     280     290     300
a050-1.pep  VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
|||||
m050-1      VNALGIGAQGLGGLTTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP
      250     260     270     280     290     300

      310     320     330     340     350     360
a050-1.pep  PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD
|||||
m050-1      PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
      310     320     330     340     350     360

      370     380     390     400     410     420
a050-1.pep  KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
|||||
m050-1      KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
      370     380     390     400     410     420

      430     440     450     460     470     480
a050-1.pep  RGAATCEAIADNKAVYLMVGGAAVLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA
|||||
m050-1      RGVATCEAIADNKAVYLMVGGAAVLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA
      430     440     450     460     470     480

      490     500
a050-1.pep  VDSKGESIHATAPPQWQAKIGIIPVKSX
|||||
m050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAACAGC AGTTTGTTGT TGGCTTTGAC
201 GCGCGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAAACGAT TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

258

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq
 1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
 251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq
 1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
 151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTGCTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
 251 TGCCGAATTT GGTAAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep
 1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPLVTM LLIKPTVVPN
 101 RLRLEITWSP ACKKVKNAA*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLSMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

259

```

g052      MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSKASKSATSPKGLDGVSKNS
           10      20      30      40      50      60

           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLEITWSPACKVKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g052      SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKVNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCTCCGCC TCGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAAFS SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CWWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CGGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGTAATGGT TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAACTT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCGCGGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISAA XGWSNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CCACTTCAA GCGGATGACG ATGCCGCCGC CSTTTTGCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMYSKIRVS DGICGVFPPM PSEXRNQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMILAASF SSGCILPCVV VHGWVVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEKRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
a073	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSGNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQASACFKSSIKSPTYSKPTDRRTNPGRMLAASF				
g073	MCMPIAIRVSDGICRIFPMPSETRNQASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSGNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTT GCGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCGCCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAA ATTACAAAT
351 CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTT ATAGCTGTCA
401 TATTACCG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFILLT MENTKSAKT PTTIQASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLRQ VLINFMIFS TKFLKKVCV LCEGFRDRLP
101 GLNLIFFFV ESENYKPPAY LFQCRKSVF IAVIFTG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAATAA CAAAAAGCGC
  51 GGCGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
 101 CCGCTTCCAA AGCGTTTTTT GCGGTATCGG GCAACGTTGC ATTTGCATGT
 151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
 201 TTTACGGCAG GTGTTAATAA ATTTATGAT ATTTTCCTTC AAAAAAGTGT
 251 TGGCGGTAAT GGATGGAGCG TTTTCAGAC GACCGCCGAA CATCCGAAAA
 301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
 351 CTTCCAAACC TCGGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
 401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
  1 MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
  51 AAKARGAAVT TASFAPYLRL VLNFMIFSF KKCLAVMDGA FRRPPNIRK
 101 SVFQKSEYDK FVLVADFFQT CVNRFFEVVE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

      10      20      30      40      50      60
m075.pep MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
      ||||||||||||||| ||||||||||||||| ||||||||||||||| : ||||||| |||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
      10      20      30      40      50      60

      70      80      90      100     110
m075.pep TASFAPYLRLQVLINFMIFSF----KKCLAVMDGAFRRPPNIRKSVFQKSEYDKFVLVAD
      ||||||||||||||| |||: : :| | : : :| | : : :|
g075      TASFAPYLRLQVLINFMIFSFTKFLKKVCGLCEGFRDRLPGLNLIFFFVESENYKFPAY
      70      80      90      100     110     120

      120     130
m075.pep FFQTCVNRFFEVVEIIGIGDX
      :|| :: | :| :|
g075      LFQCRAKSVFIAVIFTGX
      130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
  1 ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAATAA CAAAAAGCGC
  51 GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
 101 CCGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
 151 GCGGCCAAAG CCAGGGGAGC AGCTGTTACA ACAGCCAGTT TTGCGCCGTA
 201 TTTACGGCAG GTGTTAATAA ATTTATGAT ATTTTCCTTC AAAAAAGTGT
 251 TGGCGGTAAT GGATGGAGCG TTTTCAGAC GACCGCCGAA CATCCGAAAA
 301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
 351 CTTCCAAACC TCGGTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
 401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
  1 MPSYFITLLT MEKTKSAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
  51 AAKARGAAVT TASFAPYLRL VLNFMIFSF KKCLAVMDGA FRRPPNIRK
 101 SVFQKSEYDK FVLVADFFQT CVNRFFEVVE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

```

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQFASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          |||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a075      MPSYFITLLTMEKTKSAAKTPTTIQFASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          10      20      30      40      50      60

      70      80      90     100     110     120
m075.pep  TASFAPYLQVLINFMIFSEKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a075      TASFAPYLQVLINFMIFSEKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT
          70      80      90     100     110     120

      130
m075.pep  CVNRFFEVEIIGIGDX
          ||||| ||||| ||||| |||||
a075      CVNRFFEVEIIGIGDX
          130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

```

g080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAAGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA TACGGTTGAG
301 GTCGTCTCTGA CCGAGCGCAA GCCGGTGCAG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAA TGTCTGTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACgaGA TGAAACGCCT CCgGCTTTT
601 ACcgAAGCGT GGCAGCATCT gttgcGTAAG AATAAAAATC GGTTATCCTA
651 TGTGGATATG Aggtataagg acggatttTC agtcccccat gctCCCGACG
701 GTTTACCCGA AAAAGAAATcc gAAGAAATatt gggaaacagg ttgggacata
751 ttacggcctg gcgtcggaaa cggttcgacg caaatttcaa tcagttataA
801 GGGCAGacga acaatggaac AGcagtaa

```

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

```

g080.pep
1  MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLVPK QVSLKGNLVY
51  SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDIVE
101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPYMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWNVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVPH APDGLPBKES EEYWEQVWDI
251 LRPVGNGGST QISISYKGRR TMEQQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

```

m080.seq
1  ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
51  CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTGGTTTAT
151 TCCGATAAGA AGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
251 CGTGGATTGC GTCGGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
301 GTCGTCTCTGA CCGAGCGCAA GCCGGTGCAG CGTTGGGGCG ACCATGCCTT
351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGCTTGGAC AGACCCGGAA
401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
451 TATGACGAAT TTTCGACTGT TTGGCAAAA CAGGGTTTGG GCATCAAAGA
501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCTGTTTG GACAACGGCA
551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTT

```

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAAATC GGTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK OGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES BE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng)

from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKTLGSLA					
080	MWDNAEAMERL LTRWLLVMMAMLLAASGLVWFYNSNHLPVKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTVEVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKOGLGIKEMTYTARSANNVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENMKRLRLFTEAWQHLLRK NKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATCCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCCCGTCAAG CAGGTGTGCG TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGCG AAAGAATACA TCCATGGGAA
 201 TATTTGAGG ACGGACATCA ATGGCGACA GGAGGCCTAC CGCCGGTATC
 251 CGTGGATTGC GTCGTCATG GTGCGCGGCC GTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCCGG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTGTTTTG GACAACGGCA

264

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
 601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLVPK QVSLKGNLVY
 51 SDKKALGSLA KEYIHGNILR TJINGAQEAY RRYPWIASVM VRRRFEDTVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RGPMPVFRGA ESTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

m080/a080 99.2% identity over a 242 aa overlap

m080.pep	10	20	30	40	50	60
	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTLGSLA					
a080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFDPDTEVVVLTERKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFDPDTEVVVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRENEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

1 ATGAAACCAC TGGACCTAAA TTCATCTGCG CAAGCCCTCA AGCTTCCGAT
 51 GCCGCTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
 101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GCGCGGCGCG CGGTGTGGT
 201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
 301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA
 351 GATGCTGGCT GCGGTATTGC GCGCCGTTT CGGCGATGAT GCCGTTTCGG
 401 CGACGCGAGG CAACTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG
 451 AAATtaaAcy aAAAAACCCG CTATGCCGTG ATTGAAATGG GCATGAACCA
 501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT
 551 TGGtcaACAA CGCCCTGCGC GCCCATGTCT GATGCGGTTt cgacggagt
 601 GGCGATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTCAGA
 651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
 701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCTGA TAGCGGCGAT
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

265

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTGCGCG GGACGGTTTG TGTTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTAGACC ACGATTGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTATG CAGAtggAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

```

g081.pep
1 MKPLDLNFIC QALKLMPSE NKPVSRIVD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNA AALALALAAG
301 LSLNDVAEGL QGFSNIKRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMLBELGED EAAAMHAEVG AYARDQIEA AYFVGDSNVE
401 AAEKFGADGL WFAAKDELIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

```

m081.beq
1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TCGCGCGGAA GATTGTGCTG CAATGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCGCGGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGGCGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCT GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTCAGA
651 CGGCATTGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGCGGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCGGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCG TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCCGCCG
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTGCCG GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTG CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

```

m081.pep
1 MKPLDLNFIC QALKLMPSE SKPVSRIVD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

Homology with a predicted ORF from *N. gonorrhoeae*

m081/g081

	10	20	30	40	50	60
m081.pep	MKPLDLNFI	CQALKL	PMPSESK	PVSRIV	TDSRDI	RAGDVFFALAGERF
	DAHDFVED	VLAA				
g081	MKPLDLNFI	CQALKL	PMPSENK	PVSRIV	TDSRDI	REGDVFFALAGGRF
	DAHDFVGG	VLSA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m081.pep	GAAAVVVS	REDCAAM	DGALKV	DDTLAAL	QTLAKA	WRENVNPFVFGITGSGGKT
	TVKEMLA					
g081	GAAAVVVS	REDCAAL	GGALKV	DDTLAAL	QTLAKA	WRDENVNPFVFGITGSGGKT
	TVKEMLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m081.pep	AVLRRR	FGDDAV	LATAGN	FNNHIG	LPLTLL	KLNEKHRYAVIEMGMNHF
	GELAVLT	XIAKP				
g081	AVLRRR	FGDDAV	SATAGN	FNNHIG	LPLTLL	KLNEKHRYAVIEMGMNHF
	GELAVLT	QIAKP				
	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNN	AMRAIV	GC	CGFDG	VGDI	AKAKSEIYQGLCSDGIALI
	PQEDAN	MAVFK	TATLN	LN		
g081	DAALVNN	ALRAHV	GC	CGFDG	VGDI	AKAKSEIYAGLCSDGMALI
	PQEDAN	MAVFK	TATFN	LN		
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGI	DSGDV	HAENI	VLKPL	SCEFDL	VCGDERAAVVL
	VPVGR	HNVH	AAAAA	LALA	AAG	
g081	TCTFGV	DSGDV	RAENI	VLKPL	SCEFDL	VCGDERTAVVL
	VPVGR	HNVH	AAAAA	LALA	AAG	
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDV	AEGLK	GSNI	KGRNL	NVKS	GKIGATLIDDTY
	NANPDS	MKA	AIDV	LARM	PAPRI	FV
g081	LSLNDV	AEGLQ	GSNI	KGRNL	NVKA	GKIGATLIDDTY
	NANPDS	MKA	AVD	LARM	PAPRI	FV
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMG	ELGEL	GEDEA	AA	MHAEV	GAYARDQ
	GIEA	AYFV	GDNS	VEA	EAEK	FGADGLWFAAKDP
g081	MGDMG	ELGE	- - -	DEA	AA	MHAEV
	GAYARD	Q	GIEA	AYFV	GDNS	VEA
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLR	HDLPE	RATV	LVKGS	RFMQM	EEVVEALEDKX
g081	LIQVLS	HDLPE	RATV	LVKGS	RFMQM	EEVVEALEDKX
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1  ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATGCGGTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGGTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGGT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGCTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGGC CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCTT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTTTGCGCC ACGATTGCCC CGAACGCGCC ACCGTGTTGG
1301 TGAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1  MKPLDLNFC QALKLMPSE SKFVSRIVD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGGFDGV
201 GDIKAKSEI YQGLCSOGMA LIPQEDANMA VEKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNA AAAAA.SLAAG
301 LSLNDVAEGL KGF.SNKGRL NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRI.FV MGD.MGELGED EAAAMHAEVG AYARDQIEA AYFVG.DNSVE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFCQALKLMPSESKFVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFCQALKLMPSESKFVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCVAMDGALKVDDTLTALQMLAKAWRENVNPFVFCITGSGCKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCVAMDGALKVDDTLTALQMLAKAWRENVNPFVFCITGSGCKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE.LAVLTQIAKP					
a081	AVLRRRFGD.NAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE.LAVLTQIAKP					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVCGGFDGVDIAKAKSEIYQGLCSDGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVCGGFDGVDIAKAKSEIYQGLCSDGMALIPQEDANMAVFKTATLNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVVLVPVGRHNVHNAALALAAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVVLVPVGRHNVHNAALALAAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFSNIKGRINVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFSNIKGRINVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFMQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

g082.seq

```

1  aTGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTCACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGGT TCACATTATC GCGCCACGCC
151 TTCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTGTTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTGCTTTCGT TAATATTGGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTAGCCGAT TTGCCTTTT CCGCATACCA
601 CGGCGCGGGG TCGTCGGACT GTCTGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

g082.pep

```

1  MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTA AAPADNTPPT KSCASNRPFA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI PSRPAFSRIP
201 RRGVVGLSVD KGKVIARH IGDIPKIIA VIGQLVGFD TPTAES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

m082.seq

```

1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATTTT CTTCACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGAT TCACATTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

m082.per

1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVM PN TNGFTFSRHA
51 FASVCNAASV SSTFNAPSIA AQSSRETTTA AAPAANTSST KSCASNRS PA
101 NAKNTSPARM SRLSVMTMRD GLSDGIGSL RAWQMKFRSS GFIPTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHXSXSF FLYVSQFFRRI FSRFAPSFRP
201 RRGVGQGSVD KGKVIATFALH IGNIPPKIIA VIGOLVGDFD RPTAES*

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m082/q082

		10	20	30	40	50	60
m082.pep		MXLLKLP	AVANTASSPKRRR	NTAASISFTV	VLPPPEV	MPNTNGFTFSR	HAFASVCNAASV
g082		MWLLKLP	AVAETAASSPKRRR	NTAASISFTV	VLPPPEV	MPNTNGFTLSR	HAFANVCNAASV
		10	20	30	40	50	60
		70	80	90	100	110	120
m082.pep		SST'FNAPS	IAAQSSRETTT	AAAPAANTSS	TKSCASNRS	PANAKNTSP	ARMSRLSVTMRDT
g082		SSTFNAPP	KAAQSSRETTT	AAAPADNTP	PTKSCASNRP	PANAKNTSP	SRSIRLSVTMRDT
		70	80	90	100	110	120
		130	140	150	160	170	180
m082.pep		GLLSDG	IGISLR	AWOMKFRSS	GFI	FTFVNIRA	ADTSVAADFFI
g082		GLFSDG	IGISLR	AWOMKFRSS	GFI	FAFVNIRA	ADTSVAADFFI
		130	140	150	160	170	180
		190	200	210	220	230	240
m082.pep		FLYVSFF	RRI	FSRFAFS	RIPRRGV	VQGSVDK	GKGVIAFALH
g082		FLYVSFF	RRI	FSRFAFS	RIPRRGV	VGLSVDK	GKGVIAFARH
		190	200	210	220	230	240
m082.pep		RPTAESAX					
g082		RPTAESAX					

a082.seq

1 ATGTGGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
51 ACGGCGGCGC AATACCGCAG CCAACATTTT CTTACCCGTC GTCTTGCCGC

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```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTGCAACGC GGTAAACGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTA AACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPABA KTALSPKRRR NTAANISFTV VLPPEPVI PN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA APAANTSST KSCASNRPPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRAFSRIP
201 RRGVVGQSV DKGKVI AFALH IGNIPPKIIA VIGQLVGFDT RPTAESAX*

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLP	AVANTASSPKRRR	NTAASISFTV	VLPPEP	VMPNTNGFT	FSRHAFASVCNAASV
a082	MWLLKLP	AVAKTALSPKRRR	NTAANISFTV	VLPPEP	VIPTNGFT	FSRHAFANICNAVSV
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIA	AQSSRETTAA	APAANTSSTK	KSCASNRSPANAKNT	SPARMSRLSVTMRDT	
a082	SSTFNAPSIA	TQSSRETTAA	APAANTSSTK	KSCASNRPPANAKNT	SPARMSRLSVTMRDT	
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSL	RAWQMKFRSSG	FIFTFVNIRA	ADTSVAADFFI	ACFAVVKHRLFSHSHX	F
a082	GLLSDGIGSL	RAWQMKFRSSG	FIFTFVNIRA	ADTSVAADFFI	ACFAVVKHRLFSHSHSA	F
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFRRI	FSRAFSRIP	RRGVVGQSV	DKGKVI AFALH	IGNIPPKIIA	VIGQLVGFDT
a082	FLYVSFFRRI	FSRAFSRIP	RRGVVGQSV	DKGKVI AFALH	IGNIPPKIIA	VIGQLVGFDT
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcG gccatCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTG TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTCTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTTCG
301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG

```

271

```

401 TTTGGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGAGAAAA TCGccggcga taaAGATTGG CGAGaacctg
551 atgccggcct gttgttgaat ATTTTcgacc tgtattaCga cttggctttc
601 cgcgccggca CAATATGCCG CCAAGCGCGC CCACattttg gaagCagcaa
651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgcccaa gTataa

```

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

```

1 MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLIYVGTI ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MEKIAGDKDW REPDAGLLLN IFDLYYDLAF
201 RAGTICRQAR PHFGSSKKS SV NMAYPPTCAQ V*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

```

1 ATGAAACAAT CCGCCcGAAT AAAA .ATATG AATCAGACAT TACTTTATAC
51 ATTGGGCATT TCGCGGCTTT TAACCTTInn nnnnnnnnnnn nnnnnnnnnnn
101 ILESNPAEAR EFVGNLPGSL GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTTCCTCGC
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGCGCGCT GAATTTGTCG GCAATCTTCC
351 CGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAAATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGCGCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTGGCT.TC
601 CGCGCCGCA CAATATGCCG CCAAGCGCGC CCACATTTC GAAGCAGCAA
651 AAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

```

1 MKQSARIKMN NQTLTYTLGI CALLTFXXXX XXXXXHPEY EYGYRYSAVG
51 ALASVVFLLL LARGFPRVSS VLLIYVGTI ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX
201 RAGTICRQAR PHFGSSKKS SV NMAYPSCCAQ V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKMNQTLTYTLGICALLTF-----YHPEY EYGYRYSAVGALASVVFLLL				
	: : :				
g084	MKQSARIKMNQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGS ILESNPAEAREFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIAGDKDW				
	130	140	150	160	170
	180				

272

	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGCGCGCTTT TAGCCCTTTG TTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
151 GCTTGGCTT CCGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGTCGG CTGGCTGTAT GGTGCGCGT CTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGSGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTGGCTTCC
601 .GCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYTLGICALLTFXXXXXXHYHPEYGYRYSAVGALASVVFLLL					
a084	MKQSARIKXMDQTLKNTLGI CALLAFCFGA AIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSI L ESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSI L ESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI L TLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGAC3CGT TGAAAGATAA

```

273

```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCCGCGAA ATCCGCCGCG
101  ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151  GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201  CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251  CGGAAGTGTT taTCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGGL NLTDCVTLEE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCTG CGCGATGCAC TGTTAGGCAA
51  GGCAAAAGGC GTGTTCTGA TTTGGTTCGA TCGCCGCGAA ATCCGCCGCG
101  ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151  GCGGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTGCT
201  CAGCCCCGCC TCGCGAGCTT TTGATATGTT CAAAGGCTAC GCGCACC GTT
251  CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGGL NMTDCATLGE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGGLNLTDCVTLEEA VQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGC TTGCCGGCAA
51  GGCAAAAGGC GTGTTCTGA TCGGTGTCGA TCGCCGCGAA ATCCGCCGCG
101  ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151  GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201  CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251  CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQA E					

```

g086.seq
1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATT ATTCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTT TATTTGACCA
101 GGCAGCGGGG GTTCGTCTGT GCCGCGCTTA TAGCGAGCGG GTTTTTATGG
151 TTCTTTTGCA GGATAGGAC ATGGCGGCGG CTTGTGCCGT GGAATTTTGC
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAAATT CAAGCCGACC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTACACGG
351 CCGTGAAGAA GTGTTCGCGA GCATGGAAG ATTTGGGTTG CAGTCGATT
401 GCGGGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC CAGGCAACGT
451 CGTGAACATa TAGAAATGTA CGgcCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTTCGGCT
601 GGATTGCCGT GGAATATTT TTTTGTCCCT GTAGGACGCG TCTTTGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTTGGa CCCGTGGAaA GACCCGCAGG GTGCCGGCTa CCAGCTTACC
751 CACTCTCTGa TGGCAATCGG GCGCGGAGAG TGTTTCGGTa TGGGTTTGGG
801 TGCGAGTTTG AGCAAAACGG GCTTCTGCC GGAAGCGCAT ACCGATTTTa
851 TTTTGTGCCaT CATCGCTGAA GAATTCGGGT TCTTCGGGAT GTGCGTGTCTG
901 ATATTCTGTt ACGGCTGGCT GGTTGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CCGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGa CCAAAGGTCT GACGctgCcg tTGATGTCTT ATGGcggTTC
1101 GTCAGCTTTT TTCATGCTGa TCAGCATGAT GCTGCTGTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGGTTACC GGGTGGAGTa AA

```

```

g086.pep
1  MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLN
51  FLCRMRTWRR LVPWIFALSQ LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILI LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAIILPIMLV AFGVLVIMVQ PDPGSAFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPGAGAGQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDPFIIAIEE EFGFFGCMVL
301 IFCYGLVLRV AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGNVIG
351 ALPTKGLTLP LMSYGGSSVF PMLISMALLL RIDYENRQKM RGYRVE*

```

```
m086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TA'TTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATTGG
151 TTTCTTTGCA GGTATGAGGAC ATGGCGGCGG CTTGTCCCGT GGAT'TTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCCGATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGAGc
301 GAGCTGTTCa AGcTGCGGcT CATCCTTATt TTGGCAAGCC TGtTCACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAGg TTTGGGTTGG CAGTcGATTT
401 GGCGGGGGAC GGCCAAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CTGTGAaACAT TAGAAATGTA CGCGCGTWTc CGGGCGATCA TCCTGCCGAT
501 TAGCTCGGTG GCGTTTCGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG
```

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCTCG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTTGGA CCCGTGGAAA GACCCGAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGGGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTGGGAT CGGkrTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCyGCCG Tg.AtGTCCw ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

```

m086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTTRREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIQXQ SFFNIGVNI
351 ALPXKGLTXP XMSXGGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

```

m086/g086
      10      20      30      40      50      60
m086.pep  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
          |||
g086      MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
          |||
      10      20      30      40      50      60
m086.pep  LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTTRREE
          |||
g086      LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTTRREE
          |||
      70      80      90     100     110     120
m086.pep  LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTTRREE
          |||
g086      LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTTRREE
          |||
      70      80      90     100     110     120
m086.pep  VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILPIMLV AFGLVLIMVQ
          |||
g086      VLRSMESLGW QSIWRGTANL IMSATNPQAR RETLEMYGRF RAILPIMLV AFGLVLIMVQ
          |||
      130     140     150     160     170     180
m086.pep  VLRSMESLGW QSIWRGTANL IMSATNPQXR RETLEMYGRX RAILPIMLV AFGLVLIMVQ
          |||
g086      VLRSMESLGW QSIWRGTANL IMSATNPQAR RETLEMYGRF RAILPIMLV AFGLVLIMVQ
          |||
      130     140     150     160     170     180
m086.pep  PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
g086      PDFGSFVVIT VITVGMFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
      190     200     210     220     230     240
m086.pep  PDFGSFVVIT VIAVGMLFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
g086      PDFGSFVVIT VITVGMFLA GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK
          |||
      190     200     210     220     230     240
m086.pep  DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
      250     260     270     280     290     300
m086.pep  DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
      250     260     270     280     290     300
m086.pep  DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
      310     320     330     340     350     360
m086.pep  DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||
g086      DPQGAGYQLT HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
          |||

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```
m086.pep      IFCYGWLVRVAFSICKQSRDLGLTFNAYIASGGIGIWIGXQSFFNIGVNIGALPXXKGLTXP
                ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||||
g086          IFCYGWLVRVAFSICKQSRDLGLTFNAYIASGGIGIWIGIQSFFNIGVNIGALPTKGLTLP
                310       320       330       340       350       360

                370       380       390
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMGRGYRVEX
                || ||||| ||||| ||||| ||||| ||||| ||||| : ||||| |||||
g086          LMSYGGSSVFFMLISMMLLLRIDYENRQKMGRGYRVEX
                370       380       390
```

a086, seq

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

a086.ppt

1	MVVLMTAFSL	LMIIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	AGLIASGLLW
51	FLCRMRTWRR	LVPWTFALSG	LLLVLMVLIAG	REINGATRWI	PLGPLNFQPT
101	ELFKLAVILY	LASLFTREE	VLRSMSLJG	QSIWRGTANL	IMSATNPQAR
151	RETLEMYGRF	RAIILPIMLV	AFGLVLIMVQ	PDFGSEFVIT	VIAVGMFLFA
201	GLPWKYFFVL	VGSVLGGMVL	MITAAPYRVQ	RVVAFDPWK	DPQAGYQLT
251	HSLMALTGRG	WFGMGLGASL	SKRGLFPEAH	TDPIFAITAE	EPGFFGMCVL
301	IFCYGWLVR	AFSIGKQSR	KLFTFNAYIA	SGIGIWIGIQ	SEFNIGVNI
351	ALPTKGLTLP	LMSYQGSSVF	FMLTSMMLL	RIDYENRRKM	RSYRVE*

m086/a086 98.0% identity over a 396 aa overlap

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLMTAFSLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYASLFTTRREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYASLFTTRREE					

277

	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRAILPIMLVAFGLVLIMVQ					
a086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m086.pep	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPXKGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
	370	380	390			
m086.pep	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1   ATGGGCGGTA AAACCTTTAT GCTGATGGCG GGCGGAACGG GCGGACACAT
51  TTTCCCAGCT CTGGCTGTGG CGGATTCATT GCGCGTGCGC GGTCAATCATG
101 TAATTGGCT GGGCAGCAAG GATTTCGATGG AAGAGCGCAT CGTGCCGCAA
151 TACGGCATA CTTGGAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGCGTTTIG TTACCTTTCC CGGCGGTCG GCGGCGAAAC TCTTGGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAC GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CTTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTTGAA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGG TGGGCGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAAAC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTGCGGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAAATG CCTCAAATGG GCGGAAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1   MGGKTFMLMA GGTGGHIFPA LAVADSLVR GHVVIWLGSK DSMEERIVPQ
51  YGIRLETLAI KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVBCVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLYAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQGREG RLKILVVGGS LGADVLNKTV

```

278

201 FQALALLPEE VRPQMYHQSG RNKLGNIQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAELG SLNREKCLKW AENARTLALP HSADDAVEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq

1 ATGGGCGGTA AACCTTTAT GCTGAWkkCG GCGGAACGG GCGGACATAT
 51 TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
 101 TGATTGGCT GGGCAGCAAG GATTGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATA GCTTGGAAAC GCTGGCGATT AAAGCGCTGC GCGCCAACGG
 201 CATCAAACGC AAAGTATGTC TGCCGGTTAC TTTGTATCAA ACCGTCCGCG
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
 301 GCGCGGCTTC TTACCTTCCC CGGCGGTTTG GCGGCGAAGC TATTAGCGT
 351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
 401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCGCGCGCG ATATTAGCAA
 501 CTTGCCCGTG CTGCGCGAAG GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTGTAA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCCCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CGGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGCT GCAGGCGGAG GCGGGATTGC
 851 TGTGCGCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCAGTCCG CACAGTCCG ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep

1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
 51 YGIRLETLAI KGVNGNIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGGL AAKLLXVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKT
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXXX XXXXXXXXXX
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAELG
 301 GLNREKCLKW AENARTLALP HSADDAVEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQYGIRLETLAI					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVGRHHVHVLGSKDSMEERIVPQYGIRLETLAI					
	10 20 30 40 50 60					
	70	80	90	100	110	120
m087.pep	KGVNGNIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
	: :					
g087	KGIRNGNIKRKLMLPFTLYKTVEAQRIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70 80 90 100 110 120					
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130 140 150 160 170 180					

279

	190	200	210	220	229	
m087.pep	RLKILVVGGS LGADVLNKTVP HALALLPDNARPHMYHQSGRGKLGILQA-----					
	: : : : : : : :					
g087	RLKILVVGGS LGADVLNKTVPQALALLPEEV RPQMYHQSGRNKLG N LQADYDALGVKAEC					
	190	200	210	220	230	240
			230	240	250	
m087.pep	-----AGLGALLVPYPH AVDDHQTANARFMVQAE					
	: : : : : : :					
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPH AVDDHOTANARFMVQAE					
	250	260	270	280	290	300
	260	270	280	290	300	310
m087.pep	AGLLLPQTQLTAEKLA EILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	: : : : : : :					
g087	AGLLLPQTQLTAEKLA EILGSLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTCCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
301 GCGGCGTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGGCGT
351 GCCGATTGTG ATTACAGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
401 ACCTGTCGCG CTGGGCGAAG CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCGC ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCACT TTGGGCGCGG ACGTTTGA ACAAACCGTA
601 CCGCAGGCAT TGGCTTTGCT GCCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCCGCC
751 TACCGCGATG CCGATTGGT GATTTGCCGT GCCGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTGTCGCGA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG
1001 CCCGTACGTT GGCACGTCCG CACAGTGCGG ACGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHVIVWLGSK DSMEERIVPQ
51  YDILLETLAI KGVRGNGIKR KLMLPFTLYQ TVREAQQIIR KHRVECVIGF
101 GGFVTFPGLL AAKLLGVPIV IHEONAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQGREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQSG R3KLGS LQAD YDALGVQAE VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLA EILG GLNREKCLKW AENARTLALP HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIVWLGSKDSMEERIVPQYGRILETLAI					
	: : : : : : :					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIVWLGSKDSMEERIVPQYDILLETLAI					
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVNRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVNRNGIKRKLMLPFTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
m087.pep	130	140	150	160	170	180
	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180
m087.pep	190	200	210	220	230	240
	RLKILVVGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAEC					
	190	200	210	220	230	240
m087.pep		250	260	270	280	
	XX-----	XXXXXXXXXAGLGALLVPYPHAVDDHOTANARFMVQAE				
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHOTANARFMVQAE					
	250	260	270	280	290	300
m087.pep	290	300	310	320	330	
	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTATAT GGCTCGCACA TTTCAGCAAC TGGTTAACCG GTCTGAATAT
51  TTTTCAATAC ACCACATTCC GCGCCGTTAT GCGCGCGTTG ACCGCTTGG
101 CGTTTTCCTT GATGTTCCGC CCGTGGACGA TACGCAGGCT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGGC TACCGACGGC CCGCAAACCC ACCTCGTCAA
201 AAACGCGACG CCGACGATGG GCGGTTGCTT GATTCTGACC GCCATTACCG
251 TGTCCACCCT GTTGTGGGGC AACTGGGCGA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAC TGCTTGCCAC CCGTGGGCTC GGTTTTACG ACGACTGGCG
351 CAAAGTCGTT TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC GTTatcgCG GTttggcaTT GTTTTACctt
451 GCcgCAATT CCGCCAACAA TATTTTGATT GTCCGtTttT TCAAACAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTttt gGtggtgTCT TACCTGACCA
551 TCGTCGGCAC ATCCAACGCC GTCAACCTCA CcgaCGGCTT GGACGGCCTT
601 GCCGCcttcc cgttcgctcc cgttgccgcC GGGCTCGCCA ttttcgctTA
651 CGTCAGCGGA CACTACCAAT TTTCCTCAATA CCTCCAGCTT CCCTATGTCTG
701 CCGGCGCGAA CGAAGTCGCT ATATTCTGCA CCGCATGTG CGGCGCGTGC
751 CTCGGATTTT TGTGGTTCAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCGCGCGC CTGGCATTGG GTGCGCGCTC CGGTaccGtt gCCGTcaTcg
851 tCCGCCAAGA ATTTGTcttc gtcattatGG GCGGTCTGTT cgtcgtagaa
901 gccgtgTCCG TTATGCTTca tgteggCTGG TACAAGAAAA Ccaaaaaacg
951 CATCTTcCTg acgGcaccga ttcacacca ttaCCAactt cgaTgCTGga
1001 aagaaaaagca agtcgctgct CGTTtCTGGA TTAtTaccat cgtcgTggtt
1051 tTgatagggtt tGagtaccct caAAattcgc ggaaactatg ccgTCCGAAC
1101 ACCTTCAGA CGGCATTGA ACGCGCAATA A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG FWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLLLT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFVLVS YLTIVGTSNA VNLTGDLGL

```

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201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq

1 ATGTTTAT GGCTCGCACA TTTCAGCAⁿC TGGTTAACCG GTCTGAATⁿn
 51 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 101 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 251 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 301 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 501 nnnnnnnnnn nnnGGCGTGG TCGGCTTTT GGTGTTGTCT TACCTGACCA
 551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT
 601 GCGACCTTCC CCGTCGTCCT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA
 651 TGCCAGCGGC CACTACAAT TTGCCAATA CCGCAATTA CCTTACGTG
 701 CCGCGCAAAA CGAAGTGGTG ATTTCTGTA CCGCCATGTG CGGCGCGTGC
 751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
 801 TGTCGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTTATCG
 851 TCCGCCAAGA GTTTGTCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA
 901 GCCGATCCG TTATGCTTCA GGTGGCTGG TATAAGAAAA CCAAAAAACG
 951 CATCTTCTCG ATGCGGCCCA TCCATCACC CTACGAACAA AAAGGCTGGA
 1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGA TTATTACCAT CGTCTGGTG
 1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC
 1101 ATCTTTCAGA CGGCATTGA ACGCGCAATA A

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
 51 KCGQAVRTDG PQTHLVKNGT PTMGSLILT AITVSTLLWG NWANPYIWL
 101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
 151 AANSANNILI VPFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
 201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep

1 MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
 151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
 201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFCTAMCGAC
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE
 301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV
 351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

			10	20	30
m088.pep			GVVGFLVLSYLTIVGTSNAVNLTGDLGDLA		
g088	IAGLALFYLAANSANNILIVPFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGDLA				
	150 160 170 180 190 200				

a088.seq

This corresponds to the amino acid sequence <SEQ ID 288; ORF 088.a>:

a088.pap

1	MFLWLAHFSN	WLTGLNIFQY	TTFRAVMAAL	TALAFSLMFG	PWTIRRLTAL
51	KCGQAVRTDG	PQTHLVKNKT	PTMGGSLILT	AITVSTLLWG	NWANPYIWL
101	LGVLALTAL	GFYDDWRKVV	LYDPNGVSAK	FKMWQSSVA	IIAGLAFYL
151	AANSANNILI	VPPFKQIALP	LKGVGFLVLS	YLTIVGTNSA	NWLTDLGLDL
201	ATFPVVLVAA	GLAIFAYASG	HSQFAQYLQL	PYVAGANEVV	IFCTAMCGAC
251	LGFLWFNAYP	AQVFNVDVGA	LALGAALGTV	AVIVRQEFVL	VIMGGLFVFE
301	AVSVMLQVWG	YKTKTKKRIFL	MAPIHHHHEQ	KGWKETQVVV	RWIIITIVLV
351	LGLSTLKIR	*TYAV*TPFR	RLNAQ*		

m088/a088 99.5% identity over a 205 aa overlap

```

                150      160      170      180      190      200
m088.pep  XXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFVLVLSYLTIVGTSNAVNLTDLGLDGLA
                |||
a088      IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVLSYLTIVGTSNAVNLTDLGLDGLA

```

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	150	160	170	180	190	200
	210	220	230	240	250	260
m088 . pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088 . pep	QVEMGDVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVEMGDVGALALGAALGTAVIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088 . pep	APIHHHYEQKGWKETQVVVRFWIIITIVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIIITIVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089 . seq
1  ATGCCGCCCA AAATCAGGAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCGGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGCGA GCCATAACGT TGGCGCGGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGCTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089 . pep
1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089 . seq
1  ATGCCGCCCA AAATCACKaw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwa
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089 . pep
1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng)

from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
g089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPNGMSCVTIKSSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

```
a089.seq
1  ATGCCGCTA AAATCACGAA GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCGGTCGCA CCGACGTTTCG TGCCTTTGCT GTCGTCGATG AACACCACGC
101 CATTCTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGAAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGGC AAACCGACGG CTTGCACAA
201 GGCAACGGCA GCCATCACGT TAGTGGCGTT GTGCAAGCCT TGCAGCGGAA
251 TATCTTTCGT GGCAATCAA TCTTCATTGC CTTGTTTCAG GCGACCTGTC
301 TCACGTTCGA ACCAAAATC GGCTTCGTAT TCCAACGAAA ACCATTTCAC
351 CTCGCGCCCG GCGCGCTTCA TCGCACGACA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC ACCGTCGCCA CGGAAAATCT TGGCTTGGT ATGCGCGTAG
```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

```
a089.pep
1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGRP*KV
51  LTCSSNASRG KPTASHKATA AITLVALCKP CSGISCVAIK SSLPCFRRPV
101 SRSNQKSASY SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*
```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRFWKVLTCSSNASRD					
	: : : : :					
a089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPXKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPNGMSCVTIKSSSLPCFRRPVSRNQKSASCSNENHFTSRP					
	: : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSSLPCFRRPVSRNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

```
g090.seq
1  ATGCGCGTAG TCGAGCAAAT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
```

q090 . pep

1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA
51 LQFCLQDGR TDIARN DGIQ P ALDAEIADQA GYRGFAVAAG NRNHLVAAAV
101 HNVROOLDVA XHAXRRFA*

m090.seq

51	ATGCGCATAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAA
51	TGTTACGAC	CGTCGCCGCA	GTCGAGCGCA	GGCTTTCGGT	GTTTTCAGT
101	TGGAAGCTGG	AAAGCTCCAA	CACCCACACG	TCCGCTTTT	TGCCTTCGG
151	TGCCATTCC	GCCTCCAAAA	CCGGCTGTC	GATATTGCC	CGATAACGG
201	TATCCAGCCC	GCACTTGATA	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
251	GTTTTGCCGT	TGCTGCCGGT	AATCGCAATT	ACCTTGTCGT	CCCGCCGGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	.CCGCCGTTT
351	TGCTTGA				

m090.pep

1 MRIVEQVVVA VEMVFGNVQH RRRSRTOAFG VFQLEAGKLQ HPHVRLFAFA
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
101 HNVROQFDVA OHAXRRFA*

Homology with a predicted ORF from *N. gonorrhoeae*

m090/q090

	10	20	30	40	50	60
m090.pep	M R I V E Q V V V A V E M V F G N V Q H R R R S R T Q A F G V F Q L E A G K L Q H P H V R L F A F A L P F R L Q N R R A					
	: : : : : :					
g090	M R V V E Q I V V A V E M V F G N V H H R R R S R A Q A F G V F Q L E A G K L P H P H V R L F A F A L Q F C L Q D G R T					
	10	20	30	40	50	60
<hr/>						
	70	80	90	100	110	119
m090.pep	D I A R N D G I Q P A L D T E I A D Q A R Y R G F A V A A G N R N Y L V V P A V H N V R Q Q F D V A Q H A X R R F A X					
	: : : : : : :					
g090	D I A R N D G I Q P A L D A E I A D Q A G Y R G F A V A A G N R N H L V A A A V H N V R Q Q L D V A X H A X R R F A X					
	70	80	90	100	110	

a090.seq

1	ATGCGCGTAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAA
51	TGTTCAACAC	TGTCGCCGCA	GTCGGGCGCA	GGCTTTCGTT	GTTTTCCAGT
101	TGGAAACTCG	AAAGCTCCAA	CACCCACAGC	TCCGCTTTT	TGCCTTCGCG
151	TCGCAATTCC	GCCTCCAAAA	CCGGCGCGCC	GATATTGCC	CGGATAACGG
201	TATCCAGCCC	ACACTTGATG	CAGAGATAGC	CGACCAAGCT	CGTTACCGTG
251	GTTTTGCGGT	TGCTGCCGGT	AATCGCAATC	ACCTTGTCGC	CGCGGCGGTT
301	CACAATGTCC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	C. CGCGGTTT
351	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

286

a090.pep

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
 51 LQFRLQNRRA DIARDNGIQP TLDAEIAADQA RYRGFAVAAG NRNLVAAAV
 101 HNVRRQQFDVA QHAXRRFA*

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGK	LQHPHVR	LFAFALPFR
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGK	LQHPHVR	LFAFALQFRLQNRRA

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQ	ARYRGFAVA	AGNRNYLV	VFAVHNVR	QQFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIAAD	QARYRGFAV	AGNRNLVAA	AVHNVRQQ	FDVAQHAXRRFAX

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence <ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

m090-1.seq

1 ATGACGGCGT TTGCATTTC GACGGCATCA CAAAGCCTTA AACGCTTCGA
 51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
 101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
 151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
 201 AGCCGTCCAA ATCGCGGGCG ATTGCGGCG CATCGACACC AATCAAGAAC
 251 ACGGCTTTTG CCTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCTTG
 301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG
 351 CAATCGCGGC GGCAGTCGCG CCGACATTTC TGCCTTTGCT GTCGTCGATA
 401 AACACCAACG CGTTTTCTC GCCGATTTT TCCACGCGT GCGGCAGGCC
 451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
 501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGTT GTGCAGACCT
 551 TGCAACGGAA TGTCTTGGT GACAATCAA TCTTCATTGC CTTGTTTCAG
 601 GCGGCTGTG TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
 651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
 701 TCCGCATTCA AAACCTGCAC GCCGTGCGCA CGGAAAATCT TGGCTTTGGT
 751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
 801 TGTTAGCACG CGTCGCGGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT
 851 TGGAAAGCTG AAAGCTCCAA CACCCACACG TCCGCTTTT TGCCTTCGCG
 901 CTGCCATTCC GCCTCCAAA CCGGCGTGCC GATATTGCCC GCGATAACGG
 951 TATCCAGCCC GCATTGTGTA CAGAGATAG CGACAGGCT CGTTACCGTG
 1001 GTTTTGCCGT TGCTGCGGT AATCGCAAT ACCTTGTCGT CCCGCGGTT
 1051 CACAATGTCC GCCAGCAAT CGATGTCGCC CAACACGCGT CCGCCGTTTT
 1101 GCTTGAACGC CTCAATATCC GCCTGCCGCT CGCTGATGCC GGGACTGAGA
 1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
 1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCGGCT
 1251 TCAGTCCGCG ATCATACGCA GCAACCTCCG CGCCGTTTT GCGCAGGTAG
 1301 GCAATCATGG AAATACCGT ACCGCCGAGT CCGGCGACGA GGATTTTTTT
 1351 GTTTTGAAAA GTCATTTTGG TTTGCTCTAA

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEH KARAGGAEQH NIACFGLGIC
 51 RLNGFSQSCA VGHIQAAAVQ IAADLRRIDT NQEHAFCLAY QCIAQGREVL
 101 PFTTAAQNH ERLQGTGNRG GSRADIRAF VVDKHHAVEL ADFHFAVRQA
 151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQRNLR DNQIFIALFQ
 201 AACLAFOPEI SFVFQRKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
 251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
 301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVVPAV
 351 HNVRRQQFDVA QHASAVLLER LNIRLEPLADA GTESQNIETV VQRIEQTARV
 401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDF
 451 VLKSHFGLS*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

```
g091.seq
  1 ATGGAATAC CCGTGCCGCC AAGTCCGCG ACGAGGATT TTTGTTTGA
 51 AAGTCATTT GGTTTGTCC TAAACAAAT CATATTGGC AGGAGACGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCCG ATTAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTGCGAGCT GTTTGGTCT CCGTTTGTGAC
201 AAGCCTTGCC AAGCCATTGT TGAGCGAGCG CAAGGTCTTG GCGCACGCCG
251 CGTCCATCGT AATACATCAA GCCCAAATTG TATTGGGCTT GGGCATCCCC
301 TTGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

```
g091.pep
  1 MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
 51 RLQALVIVAA VLVSVLTSLA KPLLSEKVL AHAASIVIHQ AQIVLGLGIP
101 LF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 305>:

```
m091.seq
  1 ATGGAATAC CCGTACCGCC GAGTCCGCG ACGAGGATT TTTGTTTGA
 51 AAGTCATTT TGGTTGTCC TAAACAAAT CATATTGAGC AGGAGATGTC
101 CGCCCTTGCC CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCCTTCAGG CGTTGGTCAT TGTGCGAGCC GTCTTGGTCT CCGTTTGTGAC
201 AAGCCTTGCC AAACCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGCTT GGGCTACCCC
301 CTGCGC...
```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

```
m091.pep
  1 MEIPVPPSPA TRIFLFEKSF WFVLKQIILS RRCPLPKPL SDGIASCSIT
 51 RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101 LR.
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLFEKSFVFLKQIILSRRCPPLPKPLSDGIASCSITRLQALVIVAA					
	: : : : :					
g091	MEIPVPPSPATRIFLFESHFGFVLKQIILGRRPPLPKPLSDGIASRLITRLQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSIAKPFLCKGAVLAHAASFGIHHQAIVLGLGYPLR					
	: : : :					
g091	VLVSVLTSIAKPFLSERKVLHAASIVIHQAIVLGLGIPLFX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

```
a091.seq
  1 ATGGAATAC CCGTGCCGCC AAGTCCGCG ACGAGGATT TTTGTTTGA
 51 GAAATCATTT TGGTTGTCC TAAACAAAT CATATTGAGC AGGGGATGTC
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC
151 CGCTTTCAGG CGTTGGTCAT TGTGCGAGCT GTCTTGGTAT CCGTTTGTGAC
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGTCTTG GCGCACGCCG
251 CGTCTTTCGG CATAATCAC GCCCAAATTG TTTTGGGC
```


This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

```

a091.pep
  1 MEIPVPPSPA TRIFLFWKSF WFVLKQIILS RGCLILLKPL SDGIASCSIT
 51 RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

m091/a091 93.8% identity over a 96 aa overlap

              10      20      30      40      50      60
m091.pep    MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRFQALVIVAA
              |||||
a091         MEIPVPPSPATRIFLFEKSFWFVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep    VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR
              |||||
a091         VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

```

g092.seq
  1 ATGTTTTTAA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGC GC
 51 AAACGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCGGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTGCT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGCCTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgcccgt
451 ACGCACGCA AAACCACGAC CACCAGCCTG ACCGCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACCT AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTCCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGCAAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATT TGCCTTAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAAA AaggCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgcgcgcgG CGAAGAGCCG GTTGCCGCGC CGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgcgcACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGatttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

```

g092.pep
  1 MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
 51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADV VVAST AVKKNPEVV AALEROIPVI PRALMLAELM RFRDGLAIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTGTGCGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGGCG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATGTCCGCG
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCGC
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGCGACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGTCGGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTC'TGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGGACCC TGC CGCCGCA CGCGCGCGT ATCTGGA AAA ACCTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTGGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCCG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG C3CTCTTGCC
1351 CCGGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC T3TTGAACGT TTTGCAGGAC GCGGACATCG
1451 TGTGGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVNTNIHFVG
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLNVLQD GDIVLNMAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng)

from *N. gonorrhoeae*:

m092/g092

```

m092.pep      10      20      30      40      50      60
MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVNTNIHFVGIGGVMSGIA

```

290

	10	20	30	40	50	60
g092	MFFISIRYIFVRKLCWANGQTFKITPLR	TKNQPERNIMMKNRVSN	IFHVGIGGVGMSGIA			
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGH	TAEHVNGADVVTSTAVKKENPEVV				
g092	EVLHNLGFKVSGSDQARNAATEHLSSLGIQVYPGH	TAEHVNGADVVTASTAVKKENPEVV				
m092.pep	AALEQQIPVIPRALMLAELMRFRDGI	AIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL				
g092	AAALERQIPVIPRALMLAELMRFRDGI	AIAGTHGKTTTSLTASILGAAGLDPTFVIGGKL				
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTP	IMSVVTNIDEDHMDTYGHSVEKLHQAFID				
g092	NAAGTNARLGKGEYIVAEADESDASFLHLTP	IMSVVTNIDEDHMDTYGHSVEKLHQAFID				
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADI	YATDIENVGAQMKFTVHV				
g092	FIHRMPFYGKAFLCVDSEHVRAILPKVSKPYATYGLDDTADI	YATDIENVGAQMKFTVHV				
m092.pep	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEVGASVEAIQKGLLG	FGFEGVGRRFQKYG				
g092	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEVGASVEAIQKGLLG	FGFEGVGRRFQKYG				
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLA	FQPHRYTRTRDLFEDFTK				
g092	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYPEKRLVLA	FQPHRYTRTRDLFEDFTK				
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCEN	VADLPQMLMNVLQD				
g092	VLNTVDALVLTEVYAAGEEPVAAADSRALARAIRVLGKLEPIYCEN	VADLPQMLMNVLQD				
m092.pep	GDIVLNMGAGSINRVPAALLALSQI	X				
g092	GDDVLNMGAGSINRVPSALLELSQI	X				

a092.seq

1	ATGTTTTTTT	TTTCAATCCG	CTATATATTT	GTCAGAAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCGCTT	ACGCATCGAA	AATCCAGGAA
101	AACGCACAT	TATGATGAAA	AACTGAGTGA	CCAACATCCA	TTTGTCCGT
151	ATCGGCGCGC	TCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAATTGTTGG
201	TTTTAAAGTT	TCGGGTTCCG	ATCAGGCGCG	AAATGCCGCT	ACCGAGCAAT
251	TGGGACGCCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT

```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGCGGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCAATCAGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAAA TGAAATTCAC CGTCCATGTT
901 TGAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCGC CTCTTGTTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CCGCGACCCCT TCCGCGCGCA CGCGGCGCGT ATCCGAAAAA ACGTTTGTA
1201 CTGCGCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCGCGCGC TGAAGAGCCG ATTGCGCGCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTGCAGGAC GCGACATCG
1451 TGTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092 . pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVNTNIHFVG
51 IGVGMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKL PNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP TAAADSRALA
451 PAIRVLCKLE PIYCENVADL PEMLLNVLQD GDIVLNMCG SINRVPAALL
501 ELSKI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092 . pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMSGIA					
	10	20	30	40	50	60
m092 . pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092 . pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092 . pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
m092 . pep	AALGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	AALGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
	190	200	210	220	230	240
m092 . pep	AALGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	AALGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
m092.pep	250	260	270	280	290	300
	FIHRMPFYGKAFLCIDSEHVRRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKEFVHV					
a092	FIHRMPFYGKAFLCIDSEHVRRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKEFVHV					
	250	260	270	280	290	300
m092.pep	310	320	330	340	350	360
	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	310	320	330	340	350	360
m092.pep	370	380	390	400	410	420
	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLAQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
m092.pep	430	440	450	460	470	480
	VLNTVDALVLTVEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTVEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	430	440	450	460	470	480
m092.pep	490	500				
	GDIVLNMGAGSINRVPAALLALSKQIX					
a092	GDIVLNMGAGSINRVPAALLELSKQIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  aTGCAGAATt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTtTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATT
251 CCTTACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTACCCGTTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTGATGC CGTCGAAGAA AAATGGGGT
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aAAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAaaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTCGCGG CGCACAGGCA ATCGGTGCGG AAGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

g093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTIGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLRPER QRAARHTHP
201 RNRVLRLSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RRTGNRCGLR
251 ARRFPORYRR OTLSVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCtAA GACGGGGCGG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACGCG GACGACACCA
651 TTTATCAATG TCCTTCGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRI FLPRPER QRAARHTHHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR RAGNRCGR LR
251 ARRF PQRYRR QTL SVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

```

m093/g093
      10      20      30      40      50      60
m093.pep  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKAQGFQTA
          |||
g093      MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS ELKERGFQTA
          |||

      10      20      30      40      50      60
m093.pep  FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLH
          |||
g093      FNILHGTYGX DGAVQGALEL LGIPYTGSGV AASAIGMDKY RCKLIWQAL GLPVPEFAVLH
          |||

      70      80      90      100     110     120
m093.pep  DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR
          |||
g093      DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR
          |||

      130     140     150     160     170     180
m093.pep  RRI FLPRPER QRAARHTHHS RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR
          |||
g093      RRI FLPRPER QRAARHTHHS RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR
          |||

      190     200     210     220     230     240
m093.pep  RAGNRCGR LRARRF PQRYRR QTL SVGNQHP ARYDEP X
          |||
g093      RTGNRCGR LRARRF PQRYRR QTL SVGNQHP ARYDRP X
          |||

      250     260     270
m093.pep
g093

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

```
a093.seq
1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 C3CTGCAAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CSTCCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 T3CCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 T3CTGCCCTG TGTTGAACGG CAAAGGCCTG CCCGCATAC ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 C3CGAACTGG CGGTTCCGCG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G
```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

```
a093.pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKKGRLKS VYEELKHFOX RNHCRTVYRR RRIFLPCVER QRPARHTHP
201 RDRVL*LRSQ VQPQRHLSM SFGRSDRSRR KPDARTGGSR RAGNRCGRLR
251 ARRFPQRYRR QTLVGNQHP ARYDRP*
```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL	MGGFSSEREI	SLDSGTAILN	ALKSKGIDAY	AFDPKETPLS	ELKAQGFQTA
a093	MONFGKVAVL	MGGFSSEREI	SLDSGTAILN	ALKSKGIDAY	AFDPKETPLS	ELKAQGFQTA
	70	80	90	100	110	120
m093.pep	FNILHGTYGD	DGAVQGALEL	LGIPYTGSGV	AASAIGMDKY	RCKLIWQALG	LPVPEFAVLH
a093	FNILHGTYGED	DGAVQGALEL	LGIPYTGSGV	AASAIGMDKY	RCKLIWQALG	LPVPEFAVLH
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE	KLGLPMFVKP	AEGSSVGVV	KVKKGRLKS	VYEELKHLQ	XRNHCRTFYRR
a093	DDTDFDAVEE	KLGLPMFVKP	AEGSSVGVV	KVKKGRLKS	VYEELKHFOX	RNHCRTVYRR
	190	200	210	220	230	240
m093.pep	RRIFLPRPER	QRAARHTH	SRNRLRLS	QVQPRRHLS	MSFGRFDRS	RRKPDARTGGS
a093	RRIFLPCVER	QRPARHTH	PRDRLXL	RSQVQPQRH	LSMSFGRSD	RSRRKPDARTGGS
	250	260	270			
m093.pep	RAGNRCGRLR	ARRFPQRYR	RQTLVGNQ	HPARYDEPX		
a093	RAGNRCGRLR	ARRFPQRYR	RQTLVGNQ	HPARYDRPX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTAccggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC CGCTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251 CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTCCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAAACGAC ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRISSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

          10      20      30      40      50      60
m094.pep  MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVPMAMPSPRKRISSAN
          |||
g094       MYSPLPKRALVPAALSLPPIITKVGSSPAAPRMEAVRLVVVVLPVPMAMPSPRKRISSAS
          10      20      30      40      50      60

          70      80      90     100
m094.pep  IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          |||
g094       IKARGITGICRSNAATTSGFSFLTAVEATTTSAPLTCSAVWPGX
          70      80      90     100
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTCCCGGC AATGGCGATC
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:

a094.pep
 1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
 101 WPG*

m094/a094 100.0% identity over a 103 aa overlap

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLPPI	TKVGSSPAAPRMEAVRLVVV	VLPCVPAMAMPSRK	INSAN		
a094	MYSPLPKRALVPAALSLPPI	TKVGSSPAAPRMEAVRLVVV	VLPCVPAMAMPSRK	INSAN		
	10	20	30	40	50	60

	70	80	90	100
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTT	TSAPLTCSAVWPGX		
a094	IRARGITGICCSNAATTSGFSFLTAVEVTT	TSAPLTCSAVWPGX		
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT
 51 TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGTCA GTGTAGGAAA
 301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTGCCC TTGCCCCAAG
 351 CGGGCGTTGG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 EASDRRLRQR CIRLCPGRW CLRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT
 51 TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
 151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
 301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCCC TTGCCCCAAG
 351 CGGGCGTTAG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK
 101 DASDRRLRQR CIRLCPGRX CLRR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

	10	20	30	40	50	60
m095.pep	MSFHLNMDGEFHLRADVFDV	GGVDVGGIVQTVSSIRFAHF	GQNRADVFAVNTQKGF	AVEG		

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1   ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1   MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1   ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGTGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGAtaat ggtgTCGTCT CGGttgtaCt

```

g096.pcp

1 MAGHTGGQVD FQQIEFAVGI FEEIDAAHAF RTDCLCAANR QFAHQAFFGF
51 GQIFRRTLIN GVVSVVLGFV VVKLGCDDV YAGQPFVQD GAGIFAAADK
101 TFGNDFAPEG VSILRKRFSD GLFL*

m096.seq

m096.pwp

m096/g096 96.0% identity in 124 aa overlap

a096.seq

a096.ppt

1 MAGHTGQGVDFQIEFAVGI FEEIDAHAAR RTDCLRAANR OFAHCAFFGF

299

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDCLRAANRQFAHQAFFGFGQIFRRTLIN				
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVKLGCNDVYAGQPFVQDGAGIFAAADKTF	GNDFAXEGVVSILRKRFSD				
a096	GVVAVVLGFVVIKLRGDDVYAGQAFVQHRAGIFAAADK	PFGNDFAXESVSILRKRFSD				
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

```

1  ATGGATATTT CAAAACAAAC ATTGCTGGAT AGGGTTTTTA ACCTGAAGGC
51  AAACGGTACG ACGGTACGTA CCGAGTTGAT GGCGGGTTTG ACGACCTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAATC CCCTGATTTT GGGCGAGACC
151 GGAATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CATCCGCCAT
201 CGGCTGTTTT GTCATGGGTT TTATCGGCAA CTATCCGATT GCGCTTGCCC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TGCCGTCGT TAAGGGTATG
301 GGCCTGCCTT GGCAGGTGGC GTTGGGTGCG GTGTTTCATT CCGGTCTGAT
351 TTTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTGAAATG TCGATTGCCG CCGGTATCGG TTGTTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGCG TTGGGCGATA TTCATCAGCC CAGCGCACTG TTGGCATTGT
551 TCGGTTTTGT CATGGTGGTC GTATTGGGGT ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTCTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAGTTT CACGGCGTGG TCGGCGAAGT ACCGGGCATT GCGCCGACCT
701 TTATGCAGAT GGATTTTAAA GGTCTGTTTA CCGTCAGCAT GGTGAGCGTG
751 ATTTTCGTCT TCTTCTTGGT CGATTGTGTC GACAGTACCG GAACGCTGGT
801 CGGCGTATCC CACCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCAACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TGGCGTGTCT GATGTTCTCC CCATTGGCGA AAAGTGTGCC GGTATTTGCC
1051 ACCGCGCCCG CACTGCTTTA TGTGGGCACG CAGATGCTCC GCAGTGCAG
1101 GGACATTGAT TGGGACGATA TGAAGAAGC CGCGCCCGCG TTCCTGACCA
1151 TTGCTCTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCCTTCGGC
1201 TTCATCAGCT ATGCCGTGGT CAAACTTTTG TGTGCGCGGA CTGGGGACGT
1251 GCCGCCTATG GTATGGGTTG TTGCCGTATT GTGGGCATTG AAATTCTGGT
1301 ATTTGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

```

1  MDISKQTLTD RVFNLIKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFIGNYPI ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFVMVV VLGYFRVQGA
201 IITITLITIV IASLMGLNEF HGVVGEVPGI APTFMQMDFK GLFTVSMVS
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMPF PLAKSVPVFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG

```

401 FISYAVVKLL CRRTGDVPPM VWVAVLWAL KFWYLG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 341>:

```
m097.seq
1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AAACGGTACK ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCyGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGCCTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAATG TCGATTGCTG CCGGTATCGG TTGTTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGT TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCATTGT
551 TCGGTTTTGC TATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATCTTGAC CATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAATGAATTT CACGGCATCA TCGGCGAAGT ACCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTGAA GGCCTGTTTA CCGTCAGCAT GGTCAGTGTG
751 ATTTTCGCTC TCCTCTTGGT CGATCTATTT GACAGTACCG GAACGCTGGT
801 CGGCATATCC CACCGTGCCG GGCCTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCCACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCTGCCTT GATGTTTTCA CCTTTGGCGA AAAGTGTTCG CGCTTTTGCC
1051 ACCGCGCCCC CCCTGCTTTA TGTCCGCACG CAGATGTCCG GCAGTGCGAG
1101 GGATATTGAT TGGGACGATA TGACGGAAGC CGCACCTGCG TTCCTGACCA
1151 TTGTTTTTCA GCCGTTTACT TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCCGCA CCAAAGACGT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT
1301 ATTTGGGCTG A
```

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

```
m097.pep
1  MDTSKQTLDD GIFLKGANGT TVRTELMAGL TTFLTMCYIV IVNPXILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP IALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFE GLFTVSMVSV
251 IFVFLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAHSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWVAVLWAL KFWYLG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng)

from *N. gonorrhoeae*:

```
m097/g097

      10      20      30      40      50      60
m097.pep MDTSKQTLDDGIFLKGANGTTVRTELMAGLTTFLTMCYIVIVNPXILGETGMDMGAVFVA
|| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      MDISKQTLDDRNFNLKANGTTVRTELMAGLTTFLTMCYIVIVNPLILGETGMDMGAVFVA
      10      20      30      40      50      60

      70      80      90     100     110     120
m097.pep TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
|| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      TCIASAIGCFVMGFIGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
      70      80      90     100     110     120

      130     140     150     160     170     180
```

301

m097.pep	FSFFKVR	EMLVN	ALPMGL	KMSIA	AGIGL	FLALIS	LKAGI	IIVAN	PATLV	GLGDI	HQPSAL					
g097	FSFFKVR	EMLVN	ALPMGL	KMSIA	AGIGL	FLALIS	LKAGI	IIVAN	PATLV	GLGDI	HQPSAL					
		130	140	150	160	170	180									
m097.pep	LALFGF	AMVVV	LGHFR	VQGAI	IITILT	ITVIA	SLMGL	NEFHG	IIGEV	PSIAP	TFMQMD	FEE				
g097	LALFGF	AMVVV	LGHFR	VQGAI	IITILT	ITVIA	SLMGL	NEFHG	IIGEV	PSIAP	TFMQMD	FEK				
		190	200	210	220	230	240									
m097.pep	GLFTVS	MVSVI	FVFFL	VDLFD	STGTL	VGIS	HRAGL	LV	DGKL	PRLKR	ALLAD	STAI	VAGAA			
g097	GLFTVS	MVSVI	FVFFL	VDLFD	STGTL	VGVSH	RAGL	LV	DGKL	PRLKR	ALLAD	STAI	VAGAA			
		250	260	270	280	290	300									
m097.pep	LGTSS	TPYVE	SAAGV	SAGGR	TGLT	AVTV	GVLM	LACL	MFSP	LAKSV	PAFAT	APALLY	VYGT			
g097	LGTSS	TPYVE	SAAGV	SAGGR	TGLT	AVTV	GVLM	LACL	MFSP	LAKSV	PAFAT	APALLY	VYGT			
		310	320	330	340	350	360									
m097.pep	QMLRS	ARDID	WDDM	TEA	APAF	LTI	VFM	PFTY	SIAD	GIA	FGFIS	YAVV	KLLCR	RTK	DV	PPM
g097	QMLRS	ARDID	WDDM	TEA	APAF	LTI	VFM	PFTY	SIAD	GIA	FGFIS	YAVV	KLLCR	RTK	DV	PPM
		370	380	390	400	410	420									
m097.pep	VWIVAV	LWALK	FWYL	LGX												
g097	VWVAV	LWALK	FWYL	LGX												
		430														

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AACCGGTACG ACGGTGCGTA CCGAGTTGAT GCGGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCTGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCCT GGCAGGTGCG GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAATGCTG GTCAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTTCGGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCGTG
751 ATTTTCGTCT TTTTCTAGT CGATCTGTTC GACAGTACCG GAACACTGGT
801 CGGTGTATCG CATCGTCCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTCAACCAC GCCTTATGTG GAAAGTCCGG CGGGCGTATC
951 GGCAGGCGGG CGGACAGGTC TGACGGCGGT TACCGTCCGG GTATTGATGC
1001 TCGCTGCTCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCCGACCG CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCCGCA TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCCGCGCA CCAAGACGCT
1251 TCCGCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```
1  MDTSKQTLLD GIFKLGKANGT TVRTELMAGL TTFLTMCIYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VIMLACLMFS PLAKSVPAFA
351 TAPALLYGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLLDGIFKLGKANGT TVRTELMAGL TTFLTMCIYIV VNPXILGET GMDMGAVFVA					
a097	MDTSKQTLLDGIFKLGKANGT TVRTELMAGL TTFLTMCIYIV VNPXILGET GMDMGAVFVA					
	10	20	30	40	50	60
m097.pep	70	80	90	100	110	120
	TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGM GVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGM GVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
m097.pep	130	140	150	160	170	180
	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGI IVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGI IVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
m097.pep	190	200	210	220	230	240
	LALFGFAMVVVLGHFRVQGAI IIITILTITVIASLMGLNEFHGIIGEVPSI APTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAI IIITILTITVIASLMGLNEFHGIIGEVPSI APTFMQMDFK					
	190	200	210	220	230	240
m097.pep	250	260	270	280	290	300
	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRKRALLDSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGSHRAGLLVDGKLPRKRALLDSTAIVAGAA					
	250	260	270	280	290	300
m097.pep	310	320	330	340	350	360
	LGTSSTTPYVESAGVSAGGRTGLTAVTVGVIMLACLMFSPAKSVPAFATAPALLYGT					
a097	LGTSSTTPYVESAGVSAGGRTGLTAVTVGVIMLACLMFSPAKSVPAFATAPALLYGT					
	310	320	330	340	350	360
m097.pep	370	380	390	400	410	420
	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
	370	380	390	400	410	420
m097.pep	430					
	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng)

from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

a098.seq

```
1  ATGACCGCCG  ATGGTCTCTT  CGTCGCTTTC  AACCTCAATG  CGTTTGCCGT
51 TGTGCGAATA  TTGATACCAG  TACAAGAGGA  TGCTGCCGAG  GCTGGCGATC
```


304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTC
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTAA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GGCGACTTCT TCAAACATCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVR1 LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAQHGYA					
a098	MTADGLFVAFNLNAFAVVRILIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMCRAQAFQNFNHTDRQAAHGFEFGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
a098	GTHYVHRMGMCRAQAFQNFNHTDRQAAHGFEFGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCGGATATTG TCGGCGTGGG
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTGTGCGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGAAACCTA CGCCAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTT GAAATTGTAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGG CCGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CTTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCT CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcG CGCGCTcgac CCGAAAATCC AACAAGAAAT
801 CATCGACCGC GAtttgtacg cCACCGCCGT ATGTCAAGG AACCAGCACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCTT CGCTTCGCCT
901 CCTTTGGTCG TTGCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCGGC GATTTTGGCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCCA TTTTGGCCGG cagTGCcgca ggtgaATATT

```

```

1301 TGGCGAAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FPEGARSLIS IGDRTISNM TPEFGATAAM FAIDAQTI DY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEEPSDQOM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSFPAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIDR DLYATAVLGS NRNFDGRIHP YAKQAFASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEVVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRPPYEW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLP LQKPGTNRHT LQLDGTETD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEALVY EAGGVLQRF A QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CGGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGCG GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCGGTTTATC CTCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCGAAC
451 GCCGATTGCG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCGACGGGCT CGGTATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCGTTGGTGC TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCCA TTTTGGCCGT CAGTGCCGCA GGCAGATATT
1301 TGGCGAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGCGC CAAGGCTCGT
1451 TGCCTCCGCT CGAACCAGAA GGCGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

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1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACJG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGCA CAGGATTTT
1901 TGAAGGGAA CGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLs IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEESPdGQM PDGSVIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFACt
251 TCNGMSGALD PKIQKEIIDR DLYATAVLsG NRNFdGRIHP YAKQAFLASp
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351 PQFRDvYVP MFDTGTAQKA PSPLYDWRPM STYIRR?PYW EGALAGERTL
401 RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501 ETYMNKQPL IIAAGADYQ GSSRDWAAG VRLAGVEAIV AEGFERIHRT
551 NLIGMGVLP LQPKDTPNRHT LQLDGTETD VVGERTPRCD LTLVIHRKNG
601 ETVEVPVtCC LDTAEVLVY BAGGVLRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLs					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLs					
	10	20	30	40	50	60
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEESPdGQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
m099.pep	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFDGRIHPYAKQAFLASp					
g099	GFGIVAFACtTCNGMSGALDPKIQBEIIDRDLYATAVLsGNRNFDGRIHPYAKQAFLASp					
	250	260	270	280	290	300
m099.pep	GFGIVAFACtTCNGMSGALDPKIQKEIIDRDLYATAVLsGNRNFDGRIHPYAKQAFLASp					
g099	GFGIVAFACtTCNGMSGALDPKIQBEIIDRDLYATAVLsGNRNFDGRIHPYAKQAFLASp					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099.pep	PLVVAYALAGSIRFDIENEVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVIYP
g099	PLVVAYALAGSIRFDIENEVLGVADGREIRLKDIWPTDEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099.pep	MFDTGTAQKAPSPLYDWRPMSTYIRPPYWEALAGERTLRGMRPLAILPDNITTDHLS
g099	MSDTGTAQKAPSPLYDWRPMSTYIRPPYWEALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099.pep	QGSFARVEPEGETMRMWEAIETYMNKQPLII IAGADYQGSSRDWAAKGVRLAGVEAIV
g099	QGSLARVEPEGQTMRMWEAIETYMNKQPLII IAGADYQGSSRDWAAKGVRLAGVEAIA
	490 500 510 520 530 540
m099.pep	AEGFERIHRTNLIGMGVLPQFKPDTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMGVLPQFKPGTNRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099.pep	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAEALVYEAGGVLRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

```

1  ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51  GCTGAACGGC AAACGGAAGG CGGGCATTAC GCGCAGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGGT TGTCGCGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCAGCGCGC TTTGCGGACC
451 GCCGATTTGG CCGGCAAAGG CTTGGCTAAA CCTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCCTGTA
551 CCAATACTTC CAATCCGCGC AACGTTGTCT CGCCCGCGCT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GCAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCAGATCTGC
701 TGCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTTGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAGCGG CGCGCTGGAT CCGAAAATCC AGAAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTGTCAGGC AACCGCAACT
851 TTGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCTT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGCGGTTG CAGACGGCAA AGAAATCCGC CTGAAAGACA
1001 TTTGGCCTAC CGATGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAAT TTCGCGACGT TTATATCCCG ATGTTTCGCA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGTCCAATG TCTACCTATA
1151 TCCGCCGCCC ACCTTACTGG GAAGGCGCAC TGGCAGGGGA ACGCACATTA
1201 AGCGGTATGC GTCCGTGGC GATTTTGCCC GACAACATCA CCACCGACCA

```

```

1251 TCTCTCGCCA TCCAATGCGA TTTTGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCTT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTCCG
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```

1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEEPSDQGM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK FWVKSSFAPG SKVAEIIYLKE ADLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVIYP MFDGTGAQKA PSPLYDWRPM STYIRPPYVW EGALAGERTI
401 SGMRLAILP DNITTDHLSN SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNRKQPL IIIAGADYGO GSSRDWAAGK VRLAGVEAIV AEGFERIHRF
551 NLIGMGVLP LQFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEELVLY EAGGVLRFA QDFLEGNA*

```

m099/a099 97.5% identity in 639 aa overlap

m099.pep	10	20	30	40	50	60
	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAGLAKPYEEPSDQMPDGSVIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGLAKPYEEPSDQMPDGAIIAAI					
	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWVKSSFAPGSKVAEIIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRKPWVKSSFAPGSKVAEIIYLKEADLLPEMEKL					
	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNENFDGRIHPYAKQAFILASP					
a099	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNENFDGRIHPYAKQAFILASP					
	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVIYP					

q102.80q

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.ppt

```

1  MSAKTPSLFG  GAMIIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLGGMVLTFF  IWATGGLVAD  AKPSVLFDTQ  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDMD  KILSLFPYMA  IATSFLGVTL
301 GLFDNIADIF  KWNDSMSGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGGWLWMLV  FLFGIANIAA
401 QVLSQMEVLP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GGC GCGATGA  TTATCGCCGG
51  CACGGTCATC  GCGCGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCACGG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGGGAC  GTTTCACCTA  CCGTCGGACA  ACTCGTCTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCCGGC
451 GTCCTTATCG  GCGGCATGGT  ATTGACCTTT  ATTTGGGCGG  CCGCGGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCGCCGCGCG
551 GCACAAACTA  CTGGATTAC  GCGGCCACCG  CCCTGCCCGT  CTGCGCTCGT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCAGC  CTGCTCAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCGCGC
751 AACGAGTTCG  CCCCCTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCTCAT
801 CGAAACCCTG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTC  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGACCC  AAAACCGCG  CGCTGACCTT  CCTGCCGCCC  CTGATTTCCT
1001 GCTGCTCTT  CCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGTGTC  TCTACCGTTC
1101 GCGCAAAATA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GCGCGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTAGGCC  AAATGGAAC  CGTCCCGTA  TTTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTFF  IWAAGGLIAD  AKPSVLFDTQ  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWTGT  LIALVIYVLW  QTAIQGNLPR
251 NEFAPVIAAE  QQSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFLGVTL
301 GLFDYIADIF  KWNDSISGRT  KTAALTFLLP  LISCLLFTTG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAO
401 VLSQMEVLPV  PKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFEGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFEGGAMIIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAATGGLVADAKPSVLFDTQ					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
g102	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTCCGGC	GGCGCATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGTA	TGCTGCCTAA	CCCGACCGCC	ACATCCGCGC
101	TATGGTTTAC	CGGCTCGCTG	GCCGTGTTGC	TGTACACCTG	GTTTTCATGT
151	CTCTCCAGCG	GCGTATGAT	TTTGGAACT	AACACCCACT	ACCCCCACGG
201	CGCGANCTTC	GACACCATGG	TAAAGACCT	GCTCGACGG	AGCTGGAACA
251	TCATCAACGG	CATCGCCCTG	GCCTTCGTTT	TATACCTGCT	TACTTAGCCT
301	TATATCTTCG	TCGGCGCGA	CCTGACGCC	AAAGGCTTAG	CGACGCGGCG
351	AGGCGGCAAT	GTTTCACTCA	CCGTGCAGCA	ACTCGTCTTC	TTCGGCATTC
401	TCGCCTTTTG	CGTATGGCA	TCCGCACGCT	TGGTCGACG	ATTCAACAGC
451	GTCCTCATCG	GCGGCATGTT	ATTAACCTTT	ATTGCGGCAA	CCGCGCGCCT
501	GATTGCGGAT	GCAAACTGC	CCGCTCTCTT	CGACACCAA	GCCCCACCG
551	GCACCAACTA	CTGGATTAT	GTCGCCACCG	CCCTGCCCGT	CTGCCTTGCG
601	TCATTTCGGT	TCCACGGCAA	CGTCTCCAGC	CTGCTCAAT	ACTTTAAAGG
651	CGACGCGCCC	AAAGTGCTCA	AATCATCTG	GACGGGCACA	CTGATTGCGC
701	TGGTAATTTA	CGTCTCTGG	CAACCGCCCA	TCCAANGCAA	CTCGCCGCGC
751	AACGAGTTCG	CCCCCGTGAT	TGCCGCCGAA	GGGCAAGTCT	CCGTCTNTGAT
801	TGAAACCCGT	TCCAAATTCG	CCCAAACCGG	CAATATGGAC	AAAATATTGT
851	CCCTGTTTTC	CTATATGGCG	AGCCGCACT	CGTTTTTAGG	CGTAAAGCTC
901	GGACTCTTCG	ACTACATCGC	CGACATCTTC	AAATGGAACG	AGCAGGCTGC
951	CGGCGGCACC	AAAACGCGCG	CGCTGACCTT	CCTGCCGCGT	NTAATTTCTT
1001	GCCTGCTCTT	CCCCACCGCG	TTTGTATCCG	CCATCGGNTA	CGTCGGGCTC
1051	CGCGCAACCG	TCTGGACAGG	CATCATCCCC	GCGATGCTGC	TNTACCGTTC
1101	GCGCAAAAAA	TTCGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGGCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAAT	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

a102.pep

1	MPTKTPSLFG	GAMIIAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGAXF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSAAGGN	VSLTVGQLVF	FGILAFVCWA	SARLVDRFES
151	VLIGGMVLT	IWATGSLGIAD	AKLPVLEDTQ	APTGTNYWYI	VATALPVCLA
201	SFGFGHNVSS	LLKYFKGDAP	KVAKSIWTGT	LIALYIVYVW	QTAIQXNLPR
251	NEFAPVIAAE	GQVSXKIETL	SKFAQTGNMD	KILSLFSYMA	IATSFLGVTL
301	GLFDYIADIF	KWNDSVSGRT	KTAALTFLPP	XISCLLFPTG	FVTAIGYVGL
351	AVLWVTGIIP	AMLLYRSRKK	FGAGKTYKVY	GGLWLMVWVF	LFGIXNIAAX
401	YLSOMELVPV	FKG*			

m102 / a102 95.9% identity in 413 aa overlap

m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFMSLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFMSLSSGLMILEV					
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFFIWAATGGLIADAKLPVLFDTQ					
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSXIIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRITKAALTFLPPLISCLLFTGFTVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRITKAALTFLPPXISCLLFTGFTVTAIGYVGLAATVWTGIIP					
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIVNIAAQVLSQMEI LVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIXNIAAXVLSQMEI LVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1   Atgtccgcag aaaCATACac acAAAtcggc tGGgtaggct taggGcaaatt
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCcgC CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATt GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAAC TCCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CTGCTTTTG
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGccgtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

[illegible]

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDITVEAIGGSANDSPMFQTKKSLWANREFPPAFALKHASK					
	:	:	:	:	:	:
m105	AFSANVQRXXLMARQFGIDTDITVEAIGGSANDSPMFQTKKSLWANREFPPXFFALKHASK					
	180	190	200	210	220	230

	250	260	270	280	289
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH				
	:	:	:	:	:
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH				
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGA  CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCAC AAAACTGCCC CCATCTCCGC CAAAGCGCGA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTGTG  GAAGCCGAG  GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCTG GCCCGCCACC AACGGCACGC
401 TGCTGATPCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGTTCCGGC GCGAAACTCG TCTTGAAC  GCTCTTGGC  ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCG  GGCAGTTCG  CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
651 CCAAACCAA AAATCCCTGT GGGCAAACCG CGAATTTCCA CCCGCCTTCG
701 CCTCAAACA CGCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC  CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGCT  ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG WIGLGQMGLP MVRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVGNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKKT FFGDVGKGS AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	:	:	:	:	:	:
a105	MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60

	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAG-QFAEA					
	:	:	:	:	:	:
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120

	120	130	140	150	160	170	179
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHGDVGKGSAGKLVLSLLG						
	:	:	:	:	:	:	:
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHGDVGKGSAGKLVLSLLG						
	130	140	150	160	170	180	

	180	190	200	210	220	230
--	-----	-----	-----	-----	-----	-----

```

m105.pep    IFGDV-QRXMLMARQFGIDTDITVEAIGDSAMDSPMFQTKKSLWANREFFXAFALKHASK
            |||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFFPAFALKHASK
            190      200      210      220      230      240

m105.pep    240      250      260      270      280
            DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
            250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1  ATGTCCGCAG AACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGA CGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACC GCAGCTCGTC CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCGGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCCG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCCG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGCGCGCTCG GCAATGGACT CGCCTATGTT
651 TCAACAACAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAAAC CGCTTCCAAA GACCTTAACC TCGCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTGCTG CCAGTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGCGAACA GGACGTTTCC GCGCTTACC
851 TGAATTTGCC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1  MSAETYQIG WVLGQMGLP MVRLLDGGI EVGVNRPD KTAPISAKGA
51  KVGSTAEVL RACPVIFLMV SDYAAVCDIL NGVRDLGAK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSSGVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKKEF HFGDVGKGSG AKLVLSLLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFF PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGA CGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAAGCTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCGGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCCG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGTCGGGC GCGAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCCG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGsGACTCG GCAATGGACT CGCCCATGTT
651 CCAAAACAAA AAATCCCTGT GGGCAAACCG CGAATTCCG CCCGCTTCCG
701 CCCTCAAAAC CGCTTCCAAA GACCTCAACC TCGCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTGCTG CCAGTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGCGAACA GGACGTTTCC GCGCTTACC
851 TGAAACTGCC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1  MSANEYAQIG WVLGQMGLP MVRLLDGGI EVGVNRPD KTAPISAKGA
51  KVGNTAEVL RDYPVIFLMV SDYAAVCDIL NGVRDLGAK IIVNMSTISP

```

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101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
 151 IFSLVGKKTFF HFGDVGKGS AKLVNLSLLG IFGEAYSEXM LMARQFGIDT
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLGMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGN	TAE	L	V		
g105-1	MSAETYYTQIGWVGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVY	G	S	T	A	E
	10	20	30	40	50	60
	70	80	90	100	110	120
m105-1.pep	RDYPVIFLMVSDYA	AVCDILNGVRDGLAGKII	VNMSTISPTENLAVKALVEA	AGGQFAEA		
g105-1	RACPVI	FLMVSDYA	AVCDILNGVRDGLAGKII	VNMSTISPTENLAVKALVEA	AGGQFAEA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS	GAKLVNLSLLG				
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS	GAKLVNLSLLG				
	130	140	150	160	170	180
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
	250	260	270	280	290	
m105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS	GVYLKLAEHX				
g105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS	GVYLKLAEHX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1 ATGTCGCGCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
 51 GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGCGC
 101 TATACAACCG CTCGCCGAC AAAACTGCC CCATCTCCGC CAAAGGCGCA
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
 201 CCTGATGTTT TCCGACTATG CCGCCGTGTG CGACATCTG AACGGAGTCC
 251 GCGACGGATT GCCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCG
 301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGAC GCGGACAGTT
 351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
 401 TGCCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAA
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
 501 AGGTTCGGGC GCGAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
 551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCG CATCGATACC
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
 651 CCAAACCAAA AATCCCTGT GGGCAAACCG CGAATCCCA CCCGCCTTCG
 701 CCCTCAACA CGCCTCCAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
 751 CAGGCAGGCA ACACCTGCC CGCGCTCGAA ACCGTTGCTG CCAGCTACCG
 801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTCC GCGTTTACC
 851 TGAATTTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1 MSANEYTQIG WIGLGMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51 KVYNTAELV RDYPVIFLMV SDYA

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTQIGWIGLGMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGN	TAE	L	V		
	10	20	30	40	50	60

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m105-1	MSANEYAQIGWIGLQMGMLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV
	10 20 30 40 50 60
a105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
m105-1	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
	70 80 90 100 110 120
a105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
	130 140 150 160 170 180
m105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
	130 140 150 160 170 180
a105-1.pep	IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
m105-1	IFGEAYSEXMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
	190 200 210 220 230 240
a105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
	250 260 270 280 290
m105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAHX
	250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

g107.seq

```

1   ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTGtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc caccctcttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

g107.pep

```

1   MVLTFIWATG GLVADAKPSV LFDTOAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAABRQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

m107.seq

```

1   ATGGTATTGA CCTTTATTTG GGCGGCCGGC GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGs CACCGCCCTG CCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTACGTCC
251 TCTGGCAAAC CGCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

m107.pep..

```

1   MVLTFIWAAG GLIADAKPSV LFDTOAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWGTGLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
 151 IAHLMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng)

from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLT	FIWAAGGLIADAKPSV	LFD	TQAPAGTNYWIYAX	TALPVCLASFGFH	GNVSSLLKYF
g107	MVLT	FIWATGGLVADAKPSV	LFD	TQAPVGTGYWIYAAT	ALPVCLASFGFH	GNVSSLLKYF
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPK	VAKSIWGT	LIALVIYVLWQ	TAIQGNLPRNEFAP	VIAAEGQVSV	LIETLSKFAQ
g107	KGDAPK	VAKSIWAGT	LVALVIYVLWQ	TAIQSNLPRNEFAP	VIAAERQLSV	INETLSKFAQ
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDK	ILSLFSYMAIATSF	LGVTLGLFDY	IA-HLMERQHL	LRAAPKPPR	
g107	TGDMDK	ILSLFPYMAIATSF	LGVTLGLFDNI	AGHLQMERQYV	RAAPKPSR	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGG3CA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGCGGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATC3TC AACATCGCCG CACAGGTATT GAGCCAAAT
751 GAACTCGTCC CCGTATT1AA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWATG GLIADAKLPV LFDTQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGGWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG+

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLT	FIWAAGGLIADAKPSV	LFD	TQAPAGTNYWIYAX	TALPVCLASFGFH	GNVSSLLKYF
a107	MVLT	FIWATGGLIADAKLPV	LFD	TQAPTGTNYWIYVAT	ALPVCLASFGFH	GNVSSLLKYF
	10	20	30	40	50	60

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```

              70      80      90      100      110      120
m107.pep      KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              |||||
a107           KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              70      80      90      100      110      120

              130      140      150      160      170
m107.pep      TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHRLRAAPKPPRX
              |||||
a107           TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL
              130      140      150      160      170      180

a107           LEPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIV
              190      200      210      220      230      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AACggCGCAT AAAACGCCGc ccTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCCGC GGCACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGAATTG
301 GACAGGCGCA GCGAATGGCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAACA AGATTGCGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAGCT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CCTgaccgTC AAAacgggTT CcgctgcTT
501 CAAacgcctg tACCGCTaa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALT KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGTG GCAATCTTAC TCGGCGGCTG
201 CGCCGCCGGA GCGGTAACA CATTGCGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CGCTTGCGTC GCCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCTGACC GCCAAAACGG TTTCCGCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLILPV AILLGGCAAG GNTFGSLDGG GTGMGGSIVK MAVGQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng)

from *N. gonorrhoeae*:

m108/g108

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 385>:

```

1   ATGTTGCCGG  GCTTCAACCG  GATATTCAA  CGGTTTGTTC  CAACACTCGG
51  AACCGGCGCAT  AAAACGCCGC  CCTTCGCGTT  ATCCCGAACG  GGGCGGCTAA
101 TCAGATTCTA  TCGCCATAAA  AGCGGGGTT  TCAACCGAAA  AGGAATTGAG
151 ATGAATAAAA  CCTTGTCTAT  TTTGCCGGTG  GCAATCTTAC  TCGCGCGCTG
201 CGCCGCCCGGG  GGCGCCGTACA  CATTCGGGAG  CTTAGACGGC  GCGCAGGTA
251 TGGCGCCGCG  CATCGTCAA  ATGGCGGTAG  AAAGCCAATG  CCGTGCGGAA
301 TTGAACAAC  GCAGCGAATG  GCGTTTGACC  GCGCTGGCGA  TGAGTGCCGA
351 AAAACAGGCG  GAATGGGAAA  ACAAGATTTG  CGCTTGCCTC  GCCCAAGAAG
401 CACCCAACCA  GTGACCGGG  AACCATGTGA  TGAGATGTCT  GGATCCGTCC
451 ACTCGCAATC  AGGCCATTGC  GCGCCTGACC  GCCAAAACGG  TTTCCGCCTG
501 CTTCAACAC  CTGTACCGCT  AA

```

1 MLPGFNRIKF RFVPTLGTAH KTPPFALSRT GLRIRFYRHK RRGFNKRKIE
51 MNKTLSLIPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE
101 LNKRESEWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS
151 TRNQALAAAL AKTVSACFKH LYR*

	10	20	30	40	50	60
m108.pep	MLPGFNRIKRFVPTLGT	AHKTPPFALSRTGRLIRFYRH	KRRGFNRKGIEMNK	TL	SILPV	
a108	MLPGFNRIKRFVPTLGT	AHKTPPFALSRTGRLIRFYRH	KRRGFNRKGIEMNK	TL	SILPV	
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVGSQ	CR	AE	LDKRSEWR	LTALAMSAE	KQA
a108	AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVESQ	CR	AE	LDKRSEWR	LTALAMSAE	KQA
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICACVAQEAPERMTGNDVMQMLAPSTRNQAL	AALTAKTVSACFKHLYRX				
a108	EWENKICACVAQEAPNQLTGNDVMQMLDPSTRNQAL	AALTAKTVSACFKHLYRX				
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

321

g109.seq
 1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC
 51 AGCCGGTATT GATCGTAGGC GTATGCTTAC CGCTTTTGA AGCGGGCATG
 101 GAAATGACGC GCAAAGGCAA AACCACCCAA TCCGCCGCCA TCGTGGTGT
 151 CTCTCCGTC TGGTCAATCC GGTTCCTCGC TGGGCGTTGA CGATGCTGTT
 201 GGATAATTTG GGCTTAATCG GCTGCAAAGA ACGCAGCGCG CAATTAGGTT
 251 TTGTCGGACG AGTATTGATA CCCGCACTAG GTTCTTAAT CTTGTGTGTG
 301 GCGATGGGTG CGGTCGGSAT GCTGCCCGGT ATCCCTCCGT TTTTGGAGCA
 351 GTTCAATCT TTGGGCTAG

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pep
 1 MYRRRVVGLS DGLGDLAAGI DRRRLTAFG SHGNDAQRQ NHPIRRHRGV
 51 LFRVLPVFG WALTMLLDNL GLIGCKERSA QLGFGVRLI PAVGFLILCV
 101 AMGAVGMLPG IPPFLEQFKS LG

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq
 1 ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTGCGC
 51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
 101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
 151 CATCGTGGTG TTCTCTCCG CCTTGTCAT CCGGTTTTCG GCTGGGCGTT
 201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAA GAGCGCAGTG
 251 CGCAATTAGG TTTCGCCGGA CGCGTGTGA TACCCGCACT AGGTTTCTTG
 301 ATCTTGTTG TGGCGATGGG TGGGTCGGG ATGCTGCCCG GTATCCCGCC
 351 GTTTTGGAA CACTTCAAAT CTTTGGGCTA G

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pep
 1 MYRRVMGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGNDAQRQNHPIRR
 51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSALGFAG RVLI PAVGFL
 101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

	10	20	30	40	50	60
m109.pep	MYRRVMGLSDGLGDLAAGIERSLGRRIITAFSGHGNDAQRQNHPIRRHRGVLFRLVN					
	: : :					
g109	MYRRRVVGLSDGLGDLAAGIDR---RRMLTAFGSGHGNDAQRQNHPIRRHRGVLFRLVN					
	10	20	30	40	50	
	70	80	90	100	110	120
m109.pep	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	: :					
g109	PVFGWALTMLLDNLGLIGCKERSAQLGFVGRVLI PAVGFLILCVAMGAVGMLPGIPPFLE					
	60	70	80	90	100	110
m109.pep	HFKSLGX					
	:					
g109	QFKSLGX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq
 1 ATGTATTATC GCCGGGTTGT GGGGCTATCC GATGGACTTG GCGATTGCGC
 51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
 101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
 151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

a109.pep

1 MYRRVVGLS DGLGLAAGI ERLGRRRII TAFSGSHGND AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIPVVGFL
101 ILCVAMGAVG MLPGIPPFLE HFSLG*

		10	20	30	40	50	60
m109.pep		MYYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
		:					
a109		MYYYRRVVLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
		10	20	30	40	50	60
		70	80	90	100	110	120
m109.pep		PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI	PAVGFLILCVAMGAVGMLPGIPPFLE				
a109		PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLI	PVVGFLILCVAMGAVGMLPGIPPFLE				
		70	80	90	100	110	120
m109.pep		HFKSLGX					
a109		HFKSLGX					

g111.seq

1	ATGCCGCTCTG	AAACACGCCT	GCCGAACCTT	ATCCGCGCCT	TGATATTTCG
51	CCTGGGTTC	ATCTTCTGA	ACGCTTGTT	GGaacaacC	GC6CAaaccg
101	TTACCGTGA	AGGCGAAACG	ATGGGTACGA	CctATACCT	CAAAATCCTT
151	TCAAATTAAT	GGGACAAACT	CCCTCCCT	GCCAAAAATAC	AAAAGCGCAT
201	TGATGATGCG	CTTAAAGAAG	TCAACCGGCA	GATGtccaCC	TACCAGACCG
251	ATTCCGAAAT	CAGCGGGTt	atacagacan	atgctggaga	gctcttcgcg
301	tntcatgcag	nttctataac	tgatccgcc	gaagactgtc	tgccataaac
351	gcctatctca	tcggcgctct	ga		

g111.pap

1 MPSETRLPNL IRLALFALGF IFLNACSEQT AQTVTLQGET MGTITYTVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMST YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPTNPISAL *

m111.seq

1	ATGCCGTCTG	AAACACGCCT	GCCGAACTTT	ATCCGCGTCT	TGATATTTCG
51	CCTGGGTTC	ATCTTCCTGA	ACGCTGTTC	GGAACAAACC	GCGCAAACCG
101	TACCCTGCA	AGGCAGAACG	ATGGGCACGA	CCTATa ₇ CGT	CAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCCTACCTT	GCCGAAATAC	AwAAACGCAT
201	CGATGACGC	CTTAAGAAAK	TCAACTCGyA	GATGTCCACC	TATCCAGCCCG
251	ACTCGGAAT	CAGCCGGTTC	AACCAACGA	CAGCCGGCAA	GCCCTTCGCG
301	ATTTCAAGCG	ACTTCGCACA	CGTTACTGCC	GAAGCCGTCC	GCCTGAACCG
351	CCTGACACAC	GGCGCGCTGG	ACGTAACCGT	CGGCCCTTG	GTCAACCTTT
401	GGGGATTCGG	CCCCGACAAA	TCCGTTACCC	GTGAACCGTC	GCCGGAACAA
451	ATCAAACAGG	CGGCATCTTA	TACGGCATA	GACAAATCA	TTTTGAAACA
501	AGGCAAGAT	TACGTTCTCT	TGAGGCAAC	CACCCCCAAG	GCCTATTTTG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGAA

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601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTGC TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGcTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTTYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISR FNOHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWFGPDK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

m111.pep/g111.pep

	10	20	30	40	50	60
m111.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTTYXVKYLSNNRDKLPSP					
	: : : : : : : : : : :					
g111	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m111.pep	AEIXKRIDDALKEXNRXMSTYQPDSEISR FNOHTAGKPLR ISSDFAHVTA EAVRLNRLTH					
	: : :					
g111	AKIQKRIDDALKEVNRQMSTYQTDSEISRFIQT XAGELFAXHAXSITDSABDCLPNTPTIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111.pep	GALDVTVGPLVNLWFGPDKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
g111	SALX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

1  ATGCCGCTCG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTGCG
51  CCTGAGTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCTGCA AGGTGAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAATAATC GGGACAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAATCA TTTTGAAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

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324

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801 TAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAATCTGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGCGG .CTACCGACC GCCATGTCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQT AQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIFLNACSEQT AQTVTLQGETMGTITYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1 ATGCCGCTCG AACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCTTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCTT GCCAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TACCAGACCG

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326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIOKRIDDALKEVNRQMSTYQPDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNRQMSTYQTDSEISRNFQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWCFDPKSVTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPK					
	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVDKVGAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKGFVDKVGAGELEKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAM					
g111-1	GGNTQIIVPLNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVSDSAM					
	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLVFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQEKLVFLIVRDKGGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

g111-1/p44550

sp|P44550|YOJL_HAEIN_HYPOTHETICAL_LIPOPROTEIN_HI0172_PRECURSOR >gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRQMSTYQ 82
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGSGITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRNFQHT-AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFDPKS 141
 DSE+SRNFQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFDP+K
 Sbjct: 75 KDSELSRNFQNTQVNTPIEISADFAKVLAEAIRLNKVTEGALDVTVGPPVNLWGFDPKPR 134

Query: 142 VTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPKAYLDLSSIAKGFVDKVGAGE 201
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVD+VA +L
 Sbjct: 135 PEKQFTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHKGKGNARGEPWRIGIEQPNIVQGGNTQIIVPLNRSLATSGDY 261
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPWQIAIEKPTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A
 Sbjct: 255 RIY-FEENGKREAFHEIDPKTYPIQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDKGGYRTAMSSEFEKL 349
 E+ LAV+LI+R G+ T SS F+KL
 Sbjct: 314 EKNNLAVYLIIRTDNDFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG AAACACGCTT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTT ATCTTCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

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327

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351 CCTGACACAC GGC GCGCTGG ACCTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCATA GGC AAAAACG CGCGCGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAGCGGC AAACGCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG CTTGTCCAC AGGATTATTC GTATTGGCGC AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGCTT CCGAATTGA AAAAGTCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

```

a111-1.pep
1  MPSETRLNPF IRTLIFALSF IFLNACSEOT AOTVTLOGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNROMST YOPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWFGGPK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

	10	20	30	40	50	60
a111-1.pep	MPSETRLNPFIRTLIFALSFI	FLNACSEQTAQVTLOGETM	GTTITYVKYLSNNRDKLPSP			
m111-1	MPSETRLNPFIRVLIFALGF	IFLNACSEQTAQVTLOGETM	GTTITYVKYLSNNRDKLPSP			
	10	20	30	40	50	60
	70	80	90	100	110	120
a111-1.pep	AEIQKRIDDALKEVNROMSTY	QPDSEISRFNQHTAGKPLR	ISSDFAHVTA EAVHLNRLTH			
m111-1	AEIQKRIDDALKEVNROMSTY	QPDSEISRFNQHTAGKPLR	ISSDFAHVTA EAVRLNRLTH			
	70	80	90	100	110	120
	130	140	150	160	170	180
a111-1.pep	GALDVTVGPLVNLWFGGPKSV	TREPSPEQIKQAASYTGIDK	ILKQKGDYASLSKTHPK			
m111-1	GALDVTVGPLVNLWFGGPKSV	TREPSPEQIKQAASYTGIDK	ILKQKGDYASLSKTHPK			
	130	140	150	160	170	180
	190	200	210	220	230	240
a111-1.pep	AYLDLSSIAKFGVDKVAGELE	KYGIQNYLVEIGGELHGKGK	NARGEPRWIGIEQPNIVQ			
m111-1	AYLDLSSIAKFGVDKVAGELE	KYGIQNYLVEIGGELHGKGK	NARGEPRWIGIEQPNIVQ			
	190	200	210	220	230	240
	250	260	270	280	290	300
a111-1.pep	GGNTQIIVPLNNRSLATSGDY	RIFHVDKSGKRLSHIINPN	NKRPISHNLASISVADSAM			
m111-1	GGNTQIIVPLNNRSLATSGDY	RIFHVDKSGKRLSHIINPN	NKRPISHNLASISVADSAM			
	250	260	270	280	290	300
	310	320	330	340	350	
a111-1.pep	TADGLSTGLFVLGETEALKLA	EEREKLAVFLIVRDKGGYRT	AMSSEFEKLLRX			
m111-1	TADGLSTGLFVLGETEALKLA	EEREKLAVFLIVRDKGGYRT	AMSSEFEKLLRX			
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

```

g114.seq
1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCGG

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328

```

101 TAACGGTAGG TTTGTTTGT GTTTCATTA ACTTAACAAT ATCTGTCGAA
151 TACGGTCAAA GCGGCTATTT TACCAGAGCC GCCGAATGTA AAACAGGGTG
201 TCAGGGCATC AGCCCGAGCT GCCTGAACGA ACGGACGGTT TGCGAGGTAA
251 CGATAAAATG GTCGAGCAGC GAAACATCAA CCAGCGACAT GGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTTTCAG GCGAGCCGCC
351 CGGATGGTTG TGCGCGATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

```

g114.pep
  1 MASITSPLHG AQQECSTFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE
 51 YGQSGYFTRA AECKTGCGI SPSCLNERTV CEVTIKWSSS ETSTSDMACA
101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

```

m114.seq
  1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
 51 GACTTTTITA TGTCCACCGG GCGGGACGAG TATAGGGCGG TCAATGTCGG
101 TAACGGTAGG TTTGTTTGT GTTTCATTA ACTTAACAAT ATCTGTTGAA
151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCCGCATGTA AAACAGAGTG
201 TCAGGGCATC AACCAGAGCT GTCTGAACGA ACAGACGCTT TGCGAKGTAA
251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGTTTCsG GCGAGCCGCC
351 CGGATGGTTG TGCGCAATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

```

m114.pep
  1 MASITSPLHG AHRECSKTF CPPGGTSIGR SMSVTVGLFC VSINLTISVE
 51 YGXSGYFIRA AACKTECGI NPSCLEQTL CXVTIKWSSS DTSTSDIACA
101 SRLVNMSSC EXSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

```

m114/g114 90.0% identity over a 140 aa overlap
           10      20      30      40      50      60
m114.pep  MASITSPLHGAHRECSKTF CPPGGTSIGR SMSVTVGLFC VSINLTISVE YGXSGYFIRA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g114       MASITSPLHGAHQECSTFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE YQSGYFTRA
           10      20      30      40      50      60

           70      80      90     100     110     120
m114.pep  AACKTECGINPSCLEQTL CXVTIKWSSD TSTSDIACASRLVNMSSC EXSGEPPGWL
           ||| |||:|||||:| |||||:|||||:|||||:|||||:|||||:
g114       AECKTGCGISPSCLNERTV CEVTIKWSSS ETSTSDMACASRLVNMSSC EGSGEPPGWL
           70      80      90     100     110     120

           130     140
m114.pep  CAIIRLSAYSSNASLTISRMX
           |||||:|||||:|||||:
g114       CAIIRLSAYSSNASLTISRMX
           130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
  1 ATGCCGGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
 51 ACAGGAATGC AGCAAGACTT TTTTATGTCC GCCGGCGGG ACAGTATGG
101 GCGGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTT CATTAACCTA
151 ACGATATCTG TCGAATACGG TTGAAGCGGC TATTTATCA GAGCCGCCGC
201 ATGTAAACA GGGTGTCAAG GCATCAGCCC GAGCTGCCTG AACGAACGGA
251 CGGTTTGCGC CGTTACGATA AAATGGTCGA GCAGCGACAC ATCGACCAGC
301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
351 TTCGGGCGAG CCGCCGGAT GGTGTGCGC GATAATCAGG CTGTCGGCAT
401 ATTCGTCCAA TGCCAGTTTG ACAATTTCAC GGATGTAA

```



```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGCGTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAAACCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTCG GTCCACCGCA AAACCTGCCC
1701 CTCTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAAGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTGA CCGCCGTGCA AACCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTCACG CTCGAAAGTCA AACAAGtCAA CGacCTCCCG
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

```

g117.pep
1 MVDELDLLPD AVAATILLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVVL I KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDILRTEL KKYNIHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGEPDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 GKGDSEYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKIKKG GKTGVLIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTAQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLGDKV GVLSTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

```

m117.seq (partial)
1 ..GTGAACTCA AGAAATACAA TGTCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTTCAC CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTCG
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCGGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAATC TTGGACTGGC GCGAAAACAT GGCGGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAAACGGA CAGCGCTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACGCGCG TCGGACAAGG CGAAATTTC AACCAGCGCA TCCAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCAACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAG
1151 TGCACGCAA AwyyTkCyCG TCTTCCAAC ACCTCGCGA ACACGCGCCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCGGTCGAT ATCGAAATCC GCGCCCAAGA CCGTCCGGG CTTTTCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGA AGCCAGCATG AGGTTCACGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGG GACGTCAAAG
1451 GCGTATTGAG CGTTACCCCG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

```

1...VKLKKYNVHF EVAGRPKHIY SIYKKMVKKK LSFDGLFDIR AVRILVDTV
51 ECYTTLGIVH SLWQPIGGEF DDYIANPKGN GYKSLHTVIV GPEDKGVEVQ
101 IRTFDMHQFN EFGVAHWRY KEGGKGSAY EQKIAWLRQL LDWRENMAES
151 GKEDLAAAFK TELFNDTIYV LTPHGKVLSL PTGATPIDFA YALHSSIGDR
201 CRGAKVEGQI VPLSTPLENG QRVEIITAKE GHPSVNWLYE GWVKSNAKIG
251 KIRAYIRQON ADTVREEGRV QLDKQLAKLT PKPNLQELAE NLGYKKPEDL
301 YTAVGQGEIS NRAIQKACGT LNEPPVPVPS ETTIVKQSKI KKGKNGVLI
351 DGEDGLMTTL AKCCKPAPPD DIIGFVTRER GISVHRKXXX SFQHLAEHAP
401 XKVLDASWAA LQEGQVFAVD IEIRAQDRSG LLRDVSDALA RHKLNVTAVQ
451 TQSRDLEASM RFTLEVQVN DLPRVLSLG DVKGVLSVTR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/g117

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
g117	EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIGGEFDDYIANPKNGYKSLHTVIVG				
g117		SFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQPIGGEFDDYIANPKNGYKSLHTVIVG				
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTFDMHQFNEFGVAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG				
g117		PEDKGVEVQIRTFDMHQFNEFGVAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG				
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
g117		KEDLAAAFKTELFNDTIYVLTTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQRVEIITAKEGHPSVNWLYEGWVKSNAKIGKIRAYIRQONADTVREEGRVQ				
g117		PLSTPLENGQRVEIITAKEGHPSVNWLYEGWVKSNAKIGKIRAYIRQONADTVREEGRVQ				
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLGYYKPPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSE				
g117		LDKQLAKLTPKPNLQELAENLGYYKPPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSA				
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKIKKGKNGVLIIDGEDGLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKXXXS				
g117		TTIVKQSKIKKGKNGVLIIDGEDGLMTTLAKCCKPAPPDDIAGFVTRERGISVHRKTCPS				
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAQT				
	400	410	420	430	440	450

g117
570 580 590 600 610 620
FRHLAEHAPEKVLDA
SAAALQEQGVFAVD
IEIRAQDRSGLLRD
VSDALARHKLNVTA
VQT

m117.pep
460 470 480 490
QSRDLEASMRFTLE
VKQVNDLPRVLASL
GDVKGVLVSVTRLX

g117
630 640 650 660
QSRDLEASMRFTLE
VKQVNDLPRVLAGL
GDVKGVLVSVTRLX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

1	ATGGTTCATG	AACCTGCACCT	GCTCCCCGAT	GCCGTCGCCG	CCACCCTGCT
51	TGCCGACATC	GGACGCTACG	TCCCCGACTG	GAACCTATTG	GTTTCCGAAC
101	GCTGCAACAG	TACCGTTCAG	GAGCTGGTCA	AAGGTGTGGA	CGGAAGTGCAG
151	AAACTACACC	ACTTCGCCCG	GTGGGACAGC	CTCGCCACGC	CGGAAGAAACG
201	CGCCGAGCAG	GCAGAAACTA	TGCGGAAAAA	GCTGCTGGCG	ATGGTTACCG
251	ACATCCGCGT	CGTGTTAATC	AAACTGCGCA	TGCGTACGCG	CACCTTCGAA
301	TTTTTAAGCA	ACGCCCCGCA	CAGCCCCGAA	AAACCGCGCC	TGCCCCAAGG
351	AACCTCGCAC	ATCTTGCGCC	GCTCGCCAA	CCGTTTGGGC	GTGTTGGCAGC
401	TCAAATTGGCA	GCTCGAAGAT	TTGGGCTTCC	GCCATCAAGA	ACCCGAAAAA
451	TACCGCGAAA	TCCGCTGTCT	TTTGGAGCAA	AAACGCACCG	AACGCTCGAA
501	ATACATCGAA	AACTTCTCTA	ATATCTGTGC	TACGGAACCT	AAAAAATACA
551	ATATCCACTT	TGAAGTCGCC	GGCCGCTCGA	AACACTCTA	CTCCATTACG
601	AAAAAAATGG	TGAAGAAAAA	ACTCAGCTTC	GACGGGTTGT	TCGACATCCG
651	CGCCGTGCGG	ATTCTGGTTG	ATACCGTCCC	CGAGTGTTAC	ACCACACTGG
701	GCAATGTCCA	CAGCCTCTGG	CAGCCCAATC	CCGCGCAGTT	CGACGACTAC
751	ATCGCCCAAC	CAGAAAGGCA	CGGCTATAAA	AGTTTGCATA	CCGTTCATGC
801	CGGCCCGGAA	GACAAAGCGC	TGGAAGTGCA	AATCCGCACC	TTCGATATGC
851	ACCAATTCAA	CGAATTCGGT	GTCGCGCGCG	ACTGGCGTTA	CAAAGAGGGC
901	GGCAAGAGCG	ATTCCGCCTA	CGAAACAAAA	ACTGCCCTGG	TAGCCCAACT
951	TTTGGACTGG	CGCGAAAAA	TGGCGGAAAG	CGGCAAGGAA	GACCTCGCCG
1001	CGCCTTCAA	AACCGAGCTT	TTCAACGACA	CGATTATATG	TTTGACCCCG
1051	CACGGCAAAG	TCCTCTCCCT	GCCCACAGGC	GCGACCCCCA	TCGACTTCGC
1101	CTACGCCCTG	CAGTACGCA	TGCGGCACCG	TTGCCGCGGT	GCGAAAGTGC
1151	AAGGGCAGAT	TGTGCGCGTG	TCCACCCCGT	TCGAAAAACG	ACAGCGTGTG
1201	GAATTCATTA	CCGCCAAGA	AGGGCATCCT	TCCGTCAACT	GGCTTTACGA
1251	AGGTGGGGTC	AAATCCAACA	AGGCAATCGG	CAAATCCGCG	GCCTACATCC
1301	GCCACGAAAA	CGCCGACACG	GTGCGCGGAAG	AAGGCCCGAT	CCAACCTGCAC
1351	AAACAGCTTG	CCAACCTCAC	GCCCAAAACC	AACCTGCAAG	AGCTTGCCGA
1401	AAATCTCGGC	TACAAAAAGC	CAGAAGACCT	CTACACCGCC	CTCGGACAAG
1451	GCGAAATTTT	CAACCGCGCC	ATCCAAAAAG	CCTGCGGCAC	GCTGAACGAA
1501	CCGCGCGCCG	TACCCGTACG	CGAAACACCC	ATCGTCAAA	AGTCCAAAT
1551	CAAAAAGAGG	GGCAAAAAAG	CGGTGCTCAT	CGACGGCGAA	GACGGTCTGA
1601	TGACCACGCT	TGCCAAATGC	TGCAAAACCCG	CGCCGCCCGA	CGACATTGTC
1651	GGCTTCGTTA	CCCGCGATCG	CGGCATTTCG	GTACACCGCA	AAACCTGCCC
1701	CTCTTTCCGA	CACCTCGCCG	AACACGCGCC	CGAAAAAGTA	CTGCGACGAA
1751	GTGTTGGCGG	GTTCAGAGAA	GGACAAGTGT	TCCGCGTCGA	TATCGAAATC
1801	CGCGCCCAAG	ACCGCTCGGG	GCTTTTGGCG	GACGTATCCG	ACCGCTCGCG
1851	CGGCCACAAA	CTCAACGTTA	CGCCGCTGCA	AACCCAGTCC	CGCGACTTGG
1901	AAGCGCAGCT	GAGGTTACAG	CTCGAAGTCA	AACAGATTAC	CGACCTCCCA
1951	CGCGTCCCTG	CCAGCCTCGG	CGACGTCAAA	GGCGTATTGA	CGGTTACCCG
2001	GCTTTAA				

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

1	MVHELDLLPD	AVAATLLADI	GRYPDWNLL	VSERCNSTVA	ELVKGVDEVQ
51	KLTHFARVDS	LATPEERAQQ	AETMRKMLLA	MVTDIRVULL	KLAMRTRTEQ
101	FLSNAPDPSPE	KRAVAKETLE	I FAPLANRLG	VWLQKWQLEE	LGRFHRTLEK
151	YREIALLLDE	KRTERLEYIE	NFLNILRTEL	KKYNTHFEVA	GRPKHIYSIY
201	KKMVKKKLSF	DGLFDIRAVR	ILVDTVPECY	TTLGIVHSLW	QPIPGEFDDY
251	IANPKGNQYK	SLHTVIVLPE	DKGVESQIRT	FDMHQFNEFG	VAAHWRYYKEG
301	KGKDSAYEQK	IAWLRQLGDW	RENMAESGKE	DLAAAFKTLE	FNDTYIYLTP
351	HGKVLSLPTG	ATPIDFAYAL	HSSIGDRCRG	AKVEGOIVPL	STPLENGORV

401 EIIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQQNADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTINE
501 PPPVPVSETT IVKQSKIKKG GKNGVLIDGE DGLMTTLAKC CKPAPPDDIV
551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFVAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVAVQTQS RDLEASMRFT LEVKQVTDLP
651 RVLASLGDKV GVLVSVTRL*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKNVHFEVAGR	PKHIYSIYKKMVKKKL	
a117	EKYREIALLLDEKRT	LEYIENFLN	ILRTELKKN	IHFEVAGR	PKHIYSIYKKMVKKKL	
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRIL	VDTVPECYTTL	LGIVHSLWQPI	PGFDDYIANPKG	NGYKSLHTVIVG
a117		SFDGLFDIRAVRIL	VDTVPECYTTL	LGIVHSLWQPI	PGFDDYIANPKG	NGYKSLHTVIVG
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVEVQIRTF	DMHQFNEFGV	AAHWRYKEGKG	DSAYEQKIAWLR	QLLDWRENMAESG
a117		PEDKGVEVQIRTF	DMHQFNEFGV	AAHWRYKEGKG	DSAYEQKIAWLR	QLLDWRENMAESG
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGATPID	FAYALHSSIGDR
a117		KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGATPID	FAYALHSSIGDR
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQ	RVEIITAKEG	HPSVNWLYEG	WVKSNAIGKIR	AYIRQQNADTV
a117		PLSTPLENGQ	RVEIITAKEG	HPSVNWLYEG	WVKSNAIGKIR	AYIRQQNADTV
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPK	PNLQELAEN	LGKYPEDLY	TAVGQGEISN	RAIQKACGT
a117		LDKQLAKLTPK	PNLQELAEN	LGKYPEDLY	TAVGQGEISN	RAIQKACGT
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKI	KKGGKNGVL	IDGEDGLMT	TLAKCKPAP	DDIIGFVTR
a117		TTIVKQSKI	KKGGKNGVL	IDGEDGLMT	TLAKCKPAP	DDIIGFVTR
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPX	KVLDASWA	ALQEGQVFA	VDIEIRAQDR	SGLLRDVSDA
a117		FQHLAEHAPX	KVLDASWA	ALQEGQVFA	VDIEIRAQDR	SGLLRDVSDA
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMR	FTLEVQVND	LPRVLASL	GDKVGLSV	TRLX
a117		QSRDLEASMR	FTLEVQVND	LPRVLASL	GDKVGLSV	TRLX
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCTTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCAAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GGAATAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCCGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTTC GGCTTCCGCC ATCAAGAACCC
651 CGAAAAATAC CGCGAAATCG CCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAA TTCTCGATA TCCTGCGTAC GGAATCAAA
751 AAATAGCAAT TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAACT CAGCTTCGAC GGCCTGTTTCG
851 ACATCCGCGC CGTGGCGGAT CTGGTCGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCATTCGCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGT TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtg aagtgcAAAT CCGCACCTTC
1051 GATATGcacc AATTcAaCga ATTCGGTGTc GCCGCCCACT GGCCTTACAA
1101 AGAAGGCGGC AAAGGCGGAT CCGCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAAAATATG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCATCG
1301 ACTTTCGCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACCCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCAGGCC CAAACCCAAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT CCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAACAGT
1751 CCAAAATCRA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCCGCG TTCTGTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTTC TTTCGACAC CTTGCGCAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCGCG
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCCCTCGCG GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1  MTAISPIQDT OSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPPE KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWRQLLDWR ENMAESGKED
401 LLAAPFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIIDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPV VNWLYEGWVK SGKAIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GGEISNRAI QKACGTLNEP PPVVSATTI VKQSKIKKGG RTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGS CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCGCAAATG GTTCATGAAC TCGACCTGCT CCCGATGCCG GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCAGGCCGG
401 AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACS CCCCAGACAG CCCCAGAAAA CGCGCCGTCG
551 CCAAGAAATC CCTCGACATC TTCGCCCCGC TCGCCAAACG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAATC TTCTCAACA TCCTGCGCGG TGAACCTAAG
751 AAATACAATG TCCATTTCGA AGTCGCCGCG CGCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAATC CAGCTTCGAC GGCCTCTTTG
851 ACATCCGCGC CGTCCGAATT CTGGTTGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCCG CCGGAAGAC AAAGGCGTCG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGIC GCGCCCACT GGCCTTACAA
1101 AGAGGGCGCG AAGGGCGATT CCGCCTACGA ACAGAAAAAT GCCTGGITGC
1151 GCCAACTCTT GGACTGGCGC GAAAACATCG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CTTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAGAGTCC TCTCCTGCC CACGGGCGCG ACCCCATCG
1301 ACTTCGCTTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTCGG
1351 AAAGTCGAAG GGCAGATTGT GCGCTGTCC ACCCGCTCG AAAACGACAA
1401 CGCGTCGAAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCCGTCCA
1551 ACTGCACAAA CAGCTTGCCA AACTCACGCC CAACCCCAAC CTGCAAGAGC
1601 TTGCGGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCGTCC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCT CGCGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGGCGCG AAAAAGCGCG TGCTCATCGA CGGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTATCGGC TTCTGTACCC GCGAGCGCGG CATTTAGTGC CACCGCAAAA
1901 CCTGCCCGTC TTTCACACAC CTCGCGAAGC ACGCGCCGGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCG CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAATC AACGTTACCG CCGTGCAAA CAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAA AAGTCAACGA
2151 CCTCCGCGCG GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPCA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLID FAPLANRLGV
201 WOLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNILRGELK
251 KYNVHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPRKNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHOFNEFGV AAHWRYKEGG KGDSAYEOKI AWLRQLLDWR ENMAESSKED
401 LAAAFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQRV E IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIIG FVTRERGISV HRKTCPSFOH LAEHAPKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDKVG VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRLQFLSNAPDSPEK
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
g117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFRHQKPEKYREIALLLDEKRTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	FLNLRGELKKYNVHFEVAGRPKHIYSIYKMKVKKLSFDGLDIRAVRILVDTVPECYT
g117-1	FLDLIRTELKKYNIHFEVAGRPKHIYSIYKMKVKKLSFDGLDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	TLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTDMHQFNEFGV
g117-1	TLGIVHSLWQPIPGEFDDYIANPKGNGYKSLHTVIVGPEEKGVEVQIRTDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
g117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH
	370 380 390 400 410 420
m117-1.pep	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	VNWLYEGWVKSNKAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTFKPNLQELAENLGY
g117-1	VNWLYEGWVKSGKAIGKIRAYIROQNADTVREEGRVQLDKQLAKLTFKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSETTIVKQSKIKKGGKNSVLIDGED
g117-1	KKPEDLYTAVGQGEISNRAIQACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
	550 560 570 580 590 600
m117-1.pep	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG
g117-1	GLMTTLAKCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWAALQEG
	610 620 630 640 650 660
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR
g117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	VLASLGDVKGVLSTRLX
g117-1	VLASLGDVKGVLSTRLX
	730
m117-1/RelA	

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYPDWNLLVSERCNSTVAELVKGVDVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMDDTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVEQMCAS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKLAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAAQVDNIRRLMSMVDVFRVCVVIKLAERICNLREVQDQDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGFHQQKPEKYREIALLLDEKRTRELEYIENFLNLRGELK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDTYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAQVQGRPKHIYSIWKMKQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEG- 369
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHHW+YKEG
Sbjct: 301 HLPKEFDDYVANPKNGYQSIHTVVLGPEGKTIEIQIRTKMHHESELGVAHHWKYKEG 360

Query: 370 --GKGDSAYEQKIAWLRLQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPHGKVL SLP 427
G SAY++KI WLR+LL W+E M++SG ++ ++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSADEKINWLRLKLLAQEEMSDSG--EMLDELRSQVFDORVYAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQRVEIITAKEGHPSVNWLYE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAKIGIRAYIRQONADTVREEGRVOLDKQLAKL--TPKPNLQELAENLGKRP 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDNIIAGKEILEAEVLKIHATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQACGTLNEPPPPVPVSETTIVKQSKI-----KKGGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLEKLSEASNKQATSHKKPORDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDASW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVDNLMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHAPERI IDTVW 658

Query: 655 AALQEGQGVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLKELTNTLMNEKVKVAGMKSRVDYKKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVL SVTRL 737
+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

a117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACACAGATA
101  AAAAAGTTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GGCAGCAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCGGCCA
251  CCTGTCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGACAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACCGGCAC
501  CCGTCAATTT TTAAGCAACG CCCCCGACAG CCCCCGAAAA CGCGCCGCTG
551  CCAAGAGAAC CCTCGACATC TTCGCCCGCG TCGCCAAACG TTGGGCGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGGTTCGCC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCTGCTTTT GGACGAAAA CGCACCGAAC
701  GCCTCGAATA CATCGAAAA TTCCTTAATA TCCTGCGTAC GGAACTCAAA
751  AAATACAATA TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801  CATTTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGGTTGTTCC

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851 ACATCCGGCG CGTGGCGATT CTGGTTGATA CCGTCCCGGA GTGTTACACC
901 ACACCTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCGGTGTC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGCG AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGTCG AAAACGGACA
1401 GCGTGTCGAA ATCATTACCG CCAACAAGG GCATCCTTCC CTCAACTCGC
1451 TTTACGAAGG CTGGGTCAAA TCCAACAAG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAACCCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAGCCAG AAGACCTCTA CACCGCGGTC
1651 GGACAAGGGG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCCA AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAACGCGC TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATTGTGCGG TTCGTTACCC GCGATCGCGG CATTTGCGTA CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTCGCCGAAC ACGCGCCGCA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTCC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACCGC GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1 MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51 DAATPYGEPL PDHFLGAAQM VHELDLLPCA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VDIRVVLTK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQPEPEY REIALLLDEK RTERLEYIEN FLNILRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVOIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLROLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQQNADTV REEGRVQLDX QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIQGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPSKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

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a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD	SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL				
a117-1	MTAISPIQDTQSATLQELREWFD	SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL				
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPD	AVAATLLADIGRYVPDWNLLV	SERCNSTVAELVKG	DEVQK		
a117-1	PDHFLGAAQMVHELDLLPD	AVAATLLADIGRYVPDWNLLV	SERCNSTVAELVKG	DEVQK		
	70	80	90	100	110	120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAM	VDIRVVLTKLAMRTRTLQFLSNAPDSPEK				
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAM	VDIRVVLTKLAMRTRTLQFLSNAPDSPEK				
	130	140	150	160	170	180
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL	GFRHQPEPEYREIALLLDEK	RTERLEYIEN			
	190	200	210	220	230	240

	250	260	270	280	290	300
m117-1.pep	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
a117-1	FLNILRTELKKYNHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT					
	250	260	270	280	290	300
	310	320	330	340	350	360
m117-1.pep	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPDKGVEVQIRTFDMHQFNEFGV					
a117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPDKGVEVQIRTFDMHQFNEFGV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m117-1.pep	AAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
a117-1	AAHWRYKEGKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH					
	370	380	390	400	410	420
	430	440	450	460	470	480
m117-1.pep	GKVLSTPTGATPIDFAYALHSSIGDRCRGARVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	GKVLSTPTGATPIDFAYALHSSIGDRCRGARVEGQIVPLSTPLENGQORVEIITAKEGHPS					
	430	440	450	460	470	480
	490	500	510	520	530	540
m117-1.pep	VNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY					
a117-1	VNWLYEGWVKSNAIGKIRAYIRQNADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY					
	490	500	510	520	530	540
	550	560	570	580	590	600
m117-1.pep	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
a117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED					
	550	560	570	580	590	600
	610	620	630	640	650	660
m117-1.pep	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFOHIAEHAPEKVLDAASWALQEG					
a117-1	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAASWALQEG					
	610	620	630	640	650	660
	670	680	690	700	710	720
m117-1.pep	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR					
a117-1	QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR					
	670	680	690	700	710	720
	730					
m117-1.pep	VLASLGDKGVLSVTRLX					
a117-1	VLASLGDKGVLSVTRLX					
	730					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1  ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAT TCATTATTG GCAAATGGTA TGATCAGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAGA
251 CTTCCCCTTG GTTGCCCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAPAGACA TAGTCAACGT
351 GCGATTTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1  MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKI ENDLIEVRRK
51  YFYPMDIPRD IVIGIGTIID FLMVFNWELF EIKASFWLPD SVGIHERYER
101 FTTMLRYIFT EKDIYVNVREF YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```

ml18.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCATTG GAATCGGTAC
201 CATATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```

ml18.pep
1  MCEFKDIIRN VPYFEGYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```

ml18/g118
      10      20      30      40      50      60
ml18.pep  MCEFKDIIRNVPYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:
g118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

      70      80      90      100     110     120
ml18.pep  VVIGIGTIIDFLMVPNWKLFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118      IVIGIGTIIDFLMVPNWELFEIKAS PWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD
          70      80      90      100     110     120

ml18.pep  YYNKKX
          |||||
g118      YYNKKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```

a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAATTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```

a118.pep
1  MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRKK
51  YPYPM DIPRD IVIGIGTIID FLMVPNWELF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```

ml18/a118 93.6% identity in 125 aa overlap

```

      10      20      30      40      50      60
ml18.pep  MCEFKDIIRNVPYFEGYDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:
a118      MCEFKDFRRNIPCFEEDENSFIGKWYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10      20      30      40      50      60

```

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	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKAS	PWLPDSVGIHERYERFTTMLRYIFTEK	DIVNVRF			
a118	IVIGIGTIIDFLMVPNWELFEIKAS	PWLPDSVGIHERYERFTTMLRYIFTEK	DIVNVRF			

	70	80	90	100	110	120
m118.pep	YYNKKX					
a118	YYNKKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

```

g120.seq
1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTGCGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGC GCGCGGCGAC GATACGGTAA
551 CGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```

g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```

m120.seq
1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTGCGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGC GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

```

m120.pep
1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
g120	MMKTFKNIFSAAILSAAALPCAYAARLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
g120	VPLYNIRFESGGTVVGNLHPAYYKDIRRGKLYAEAKFADGSVTY GKAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
g120	DLFTLAWQLAANDAKLPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE VVKYRVRRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKP					
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA AKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTTCGAGTCC GCGGGTACGG TTGTCCGCCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAGAAA ACTTTATTC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAACCGGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLHYSYGYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFSAAILSAAALPCAYAAGLPQSAVLXYSYGI PATMTFERSGNAYKIVSTIK					
a120	MMKTFKNIFSAAILSAAALPCAYAAGLPQSAVLHYSYGI PATMTFERSGNAYKIVSTIK					

343

	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFAJGJSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNLHPTYYRDIRRGKLYAEAKFAJGJSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVVKYRVRGD					
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAACAC AGCTTACAT CGGCATTATG TCGGAACCA GTATGGACGG
51  GGCGGATGCC GTGCTGGTAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATTGCTG
151 GATTTCGAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACAGCGCAAAC CGCCGCGCGA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACAGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATT
351 GCGGCTGCTG GCGGAAGTga cgcggatttT TACCGTCggc gacttcCGCA
401 GCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCgcCTTT
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCGCGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cactGGcagc TGCTTACGA CAAAacggt gcAAAGgcgg cacAAGGCaa
651 catatTGcgg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCcacc aaAAAGCAGG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgta- tgcggacgt
801 ttcccgattc accgcgcaaa ccgTttggga cgcgctctca CACGCAGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGCGAGA ATGTTTCGCG ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTTg
1001 cgtggttggC GCGTGTGG ATTAACCGCA TTCCCGTAG TCCGCACAAA
1051 GCGACCGCG CATCAAACC GTGTATTCTG GCGCGGGAT ATTATTATG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSNDGADA VLVRMDGGKW LGAEGHAFT? YPDRLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCQNLAAPC DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAEGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDVAV HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAACAC AGCTTACAT CGGCATCATG TCGGAACCA GCATGGACGG
51  GGCGGATGCC GTAGTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGCGCA GGTACGCGC CCAATTGCTG

```



```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTG
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxGAGC TTCCTTACGA CAAAACGGT GCAAAGTCG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAGACAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCGTTT ACCGCGCAAA CCGTTTGCGA CGCCGCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGSCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILF QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVAVS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQCAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILFQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTPGNMLMDAWTOAHWQLPYDKNGAKAACGNILPOLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIENPV					
	250	260	270	280	290	300

345

	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOQWEAAAFWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPOQWEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
g121	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTAGTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGCGCA GGTACGCGC CAAATTGCTG
151 GATTTCGAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACAGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTGAGAC ACAGCGCGGA ACACAGTTAC AGCGTACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCGGCG GGACAAGGCG CGCCGCTCGT CCCGCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAATCA GCGTACTCCC CCGGACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCACG GGGCGGAAC TGTTGCCCT AAATGGCTC
751 GAAACCTACC TTGACGGCG CGAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATT ACCGCGCAA CCGTTTCGA CGCGTCTCA CACGACGCG
851 CAGATGCCG TCAAATGTAC ATTTGCGGCG GCGCATCCG CAATCCTGT
901 TTAATGGCG ATTTGGCAGA ATGTTTCGGC ACACGCTTT CCCTGCACAG
951 CACCGCGAA CTGAACCTCG ATCCGAATG GGTAGAAGCC GCCGCTTCG
1001 CATGGATGG GCGGTGTTG GTCAACCGCA TTCCCGGTAG TCCGCACAA
1051 GCAACGCGG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATT
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRLKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOQWEA AAFWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRLKLLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRLKLLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSOELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESYISQLADLPLL					
a121	HRSRILSOELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESYISQLADLPLL					
	70	80	90	100	110	120

346

	130	140	150	160	170	180
m121.pep	XX					
		:	:	:	:	:
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVEAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XX					
	:	:	:	:	:	:
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADAROMYICDGGIRNPV					
	:	:	:	:	:	:
a121	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVFCDVSHAAADAROMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	:	:	:	:	:	:
a121	LMADLAECFGTRVSLHSTAEINLDPOWVEAAAFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
	:	:	:	:	:	:
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CGGCAAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCGCGCA GGTTCACGCG CCAATTGCTG
151 GATTTCGAGG ACACAGGCGC AGACGAAC TG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCTTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGCGC ACAGCGCCGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCGCGTGTG GCGGAACGGA CGCGGATTT TACCGTCGGC GACTTCGCA
401 GCGCGACCT TCGGCGCGC GGACAAGGCG CGCCACTCGT CCGCGCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGCGGATT GCCAACATCA GCGTACTCCC CCGCGACGCA CCGCGCTTCG
551 GCTTCGACAC AGGCGCGGCG AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGCGCAG TCCTTACGA CAAAACGGT GCAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCGG TATTTCGCAC
701 ACCCCACCCC TAAAAGCAGC GGGCGCGAAC TGTTCGCCCT AAATTGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCGCTTTT ACCGCGCAAA CCGTTGCGA CGCGCTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG CGCGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTGCGG ACACGCGTTT CCCTGCACAG
951 CACGCGCGAC CTGAACCTCG ATCGCAATG GGTGGAAGCC GCCGNATTTG
1001 CGTGGTTTGG GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGCGCG CATCAAACC GTGTATTCTG ANCGCGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  NETQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFPT YPGRLLRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAFBEHY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVSH HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

```

m121-1.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL
              |||||
g121         METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTPYPDRLRKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
              |||||
g121         HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAFLVPFHEALFRDNRRETRAVLNIGGIANISVLPPDA
              |||||
g121         AELTRIFTVGDFRSRDLAAGGQGAFLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTGPGNMLMDAWTQAHWQLPYDNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||
g121         PAFGFDTGPGNMLMDAWTQAHWQLPYDNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVCDVSHAAADARQMYICGGGIRNPV
              |||||
g121         GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVWDVSHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMADLAEFCGTRVSLHSTADLNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              |||||
g121         LMADLAEFCGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYYX
              |||||
g121         GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCGC CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAA CCGCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTGAGATTTT TACCGTCGCG GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCACGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCCAACC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGCGG CATCCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLP LL AERTQIFTVG DFRSRDLAAG GQGAPLVPFAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMOA

```

348

201 HWQLPYDKNG AKAAQGNILP QLLDRLLAEP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWLGAEGHAFT	PYPGRLRRQLLDLQDTGADEL			
a121-1	METQLYIGIMSGTSM	GADAVLIRMDGGKWLGAEGHAFT	PYPGRLRRQLLDLQDTGADEL			
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSR	LYAQTAELLCSQNLAPSDIT	ALGCHGQTVRHAPEHGY	SIQLADLPLL		
a121-1	HRSRILSQELSR	LYAQTAELLCSQNLAPSDIT	ALGCHGQTVRHAPEHGY	SIQLADLPLL		
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDF	RSRDLAAGGQGAPLVPAFHEAL	FRDNRETRAVLNIGGIANISVLP	PPDA		
a121-1	AERTRIFTVGDF	RSRDLAAGGQGAPLVPAFHEAL	FRDNRETRAVLNIGGIANISVLP	PPDA		
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNMLMDAWTQ	AHWQLPYDKNGAKAAQGNILP	QLLDRLLAHPYFAQPHPKST			
a121-1	PAFGFDTGPGNMLMDAWTQ	AHWQLPYDKNGAKAAQGNILP	QLLDRLLAHPYFAQPHPKST			
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLET	YLDGGENRYDVLRTLSRFTAQTV	CDASHAAADARQMYICGGGIRNPV			
a121-1	GRELFALNWLET	YLDGGENRYDVLRTLSRFTAQTV	CDASHAAADARQMYICGGGIRNPV			
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTAD	LNLDPQWVEAAXFAWLACWINRIPGSPHKATGASKPCIL				
a121	LMADLAECFGTRVSLHSTAD	LNLDPQWVEAAXFAWLACWINRIPGSPHKATGASKPCIL				
	310	320	330	340	350	360
m121-1.pep	XAGYYYYX					
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

1	ATGGCTTTAC	TGAGCATCCG	CAAGCTGCAC	AAACAATACG	GCAGCGTAAC
51	CGCCATCCAA	TCCTTAGACT	TGGACTTGGA	AAAAGGCGAA	GtcatCGTAC
101	TGCTGGGCCC	gTccggetgc	ggCAAATCCA	CCCTcctgcg	ctgcgtcaaC
151	GGTTTGGAGC	CGCACCAagg	cgGCAGCATC	GTGATGGACG	GTgtcgGCCA
201	ATTcggcAAA	GACGTTTCCT	GGCAAACCGC	CCGGCAAAAa	gtcggatatg
251	tctttcaaag	taacgAactg	Tttgcccaca	tgaccgtcat	cgAaaacatc
301	ttcttAggcC	CGGTAAagga	aCAAAAcCgc	gaccgtgccg	aagcaGAGGC
351	gCAAGCCGGC	AAactGttgg	aacgcgTCGG	actgctAGAC	CGCAAAAACG
401	CCTATCCGCG	CGAACTTTCC	GGCGGTCAGA	AACAGCGCAT	CGCCATTGTC
451	CGCGCCCTGT	GCCTGAATCC	GGAAGTCATC	CTGCTGGACG	AAATCACC GC
501	CGCACTTGAC	CCCGAAATGG	TGCGCGAAGT	CITGGAAGTG	GTTTTGGAAC
551	TCGCCCGCGA	AGGGATGAGT	ATGCTCATCG	TAACCCACGA	AATGGGGTTC
601	GCACGCAAAG	TTGCCGACCG	CATCGTCTTT	ATGGACAAAG	GCGGCATCGT
651	CGAATCGTCC	GACCCCGAAA	CCTTTTTTTC	CGCACCAAAA	AGCGAACGCG
701	CCCGCCAATT	TCTGGCAGGT	ATGGACTACT	GA	

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

g122.pep

```

1  MALLSIRKLIH KQYGSVTAIQ SLDLDLEKGE VIVLLGPSGC GKSTLLRCVN
51  GLEPHQGGSI VMDGVGEFGK DVSWQTARQK VGMVFQSNEL FAHMTVIENI
101 FLGPVKEQNR DRAEAEAGAG KLLERVGLLD RKNAYPRELS GGQKQRIATV
151 RALCLNPEVI LLDEITAALD PEMVREVLEV VLELAREGMS MLIVTHEMGF
201 ARKVADRIVF MDKGGIVESS DPETFFSAPK SERARQFLAG MDY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq

```

1  GTTGTCAATGA TTAAATCCG CAATATCCAT AAGACCTTTG GCGAAAACAC
51  TATTTTGCGC GGCATCGATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGcC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAG TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAKGCATG GTGTTTCAAC AATACAaCT CTTTCCGCAC
301 AAAACCGCCT TGGAAAACGT AATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTC CGGCGGTGAG
451 CAGCAGCGCG TCGGCATTGC CCGCGCATTC GCGATTGAGC CTGAACTGAT
501 GCTGTTTGAC GAACCGACTT CCGCGCTCGA TCCTGAATG GTGCAAGATG
551 TTTTGGATmC CATGAAGGAA TTGGCGCAAG AAGGCTGGAC CATGGTTGTC
601 GTTACGCATG AAATCAAGTT CGCCTTAGAA GTGGCAACCA CCGwCGTCGT
651 GATGACrGC GGCCTTATTG TCGAACAAGG CAGCCCGCAA GATTTGTTG
701 ACCACCCCAA ACACCAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.pep

```

1  VVMIKIRNIH KTFGENTILR GIDL DVCKGQ VVILGPSGS GKTTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSXM VFQYNNLFPH
101 KTALENVMEG PVAVQGKPAA QAREEALKLL EKVGLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVLDXMK E LAQEGWTMVV
201 VTHEIKFALE VATTXVMDX GVIVEQGS PQ DLFDPKHER TRRFLSQIQS
251 TKI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng)

from *N. gonorrhoeae*:

m122/g122

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKT	FGENTILRGID	LDVCKGQVVV	ILGPSGSGKT	TFRLRCINALE	MPEDGQI
g122	MALLSIRKLIH	KQYGSVTAIQ	SLDLDLEKGE	VIVLLGPSGC	GKSTLLRCVN	GLEPHQGGSI
	10	20	30	40	50	60
	70	80	90	100	110	120
m122.pep	EFDNERPLKID	FSKKPSKHDIL	ALRRKSXMVF	QYNNLFPHK	TALENVMEGP	VAVQGKPAA
g122	VMDGVGEFGK	DVSWQTA-----	RQKVG	MVFQSNEL	FAHMTVIENI	FLGPVKEQNRDRA
	70	80	90	100	110	
	130	140	150	160	170	180
m122.pep	QAREEALKLLE	KVGLGDKVDL	YPYQLSGGQ	QQRVGIARAL	AIQPELMLFD	EPTSALDPEL
g122	EAEAQAGKLL	ERVGLLD	RKNAYPRELS	GGQKQRIATV	RALCLNPEVI	LLDEITAALDPEM
	120	130	140	150	160	170
	190	200	210	220	230	240
m122.pep	VQDVLDXMKEL	AQEGWTMVV	VTHEIKFALE	VATTXVMDX	GVIVEQGS	PQDLFDPKHER
g122	VREVLEV	VLELAREGMS	MLIVTHEMGF	FARKVADRIV	FMDKGGIVESS	DPETFFSAPKSER

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQISTKIX					
	: : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```
a122.seq
1   GTTGTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTGTGCGC GGCATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGC GCCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTCCGCAC
301 AAAACCGCCT TGGAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTCAGC CCGAGCTGAT
501 GTTGTGTTGAC GAACCCACTT CCGCGCTTGA CCCCAGTTG GTGCAAGACG
551 TGTTGAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGG CAGCCGAAA GAGTTGTTG
701 ACCACCCCAA ACACGAACG ACGCGGAGAT TTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```
a122.pep
1   VVMIKIRNIH KTFGNTILR GINLDVCKGQ VVVLGPSPGS GKTTFLRCLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVMEG PVAVQGKPAQ QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTMNV
201 VTHEIKFALE VATTVVMDG GVIVEQGSPEL FLDHPKHER TRRFLSQIQS
251 TKI*
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFGENTILRGIDLVDCKGQVVVLGPSPGSGKTTFLRCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFGNTILRGINLDVCKGQVVVLGPSPGSGKTTFLRCLNALEMPEDGQI					
	10	20	30	40	50	60
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQ					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQ					
	70	80	90	100	110	120
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSALDPEL					
	130	140	150	160	170	180
m122.pep	VQDVLDMKELAQEGWTVVVVTHEIKFALEVATTXVVMMDXGVIVEQGSPEQLFDHPKHER					
a122	VQDVNLAMKELAREGWTMNVVTHEIKFALEVATTVVVMDGGVIVEQGSPEQLFDHPKHER					
	190	200	210	220	230	240
m122.pep	TRRFLSQISTKIX					

351

|||||||
a122 TRRFLSQIQSTKIX
250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
51 GCGCGGCATC GATTTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACGCGGCC
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
301 GTGTTGGAAA ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGATAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGTGTCCGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTGTT
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVKGQVV VILGPSGSGK TTFLRCLNAL
51 EMPEDGQIEF DNRPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
101 VLENMVEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
201 HEIKFTLEVA TNVVMDGGV IVEQSPKEL FDHLKHERTR RFLSQIQSAK
251 I*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACATTTT
51 GCGCGGCATC GATTTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 CCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCCC GCACAAAACC
301 GCCTTGGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTGAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCCGCG ATTGGCGATT CAGCCTGAAC TGATGCTGTT
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
551 ATACCATGAA GGAATTGGCG CAAGAAGCTT GGACCATGGT TGTCGTTACG
601 CATGAAATCA AGTTCCGCTT AGAAGTGCCA ACCACCGTCG TCGTGATGGA
651 CGGCGGCGTT ATTGTCGAAC AAGGCAGCCC GCAAGATTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVCKGQVV VILGPSGSGK TTFLRCLNAL
51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENMVEGPV AVQGKPAAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
201 HEIKFALEVA TTVVMDGGV IVEQSPQDL FDHPKHERTR RFLSQIQSTK
251 I*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFGENTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALENPEDGQIEF					
g122-1	MIKIRNIHKTFGENTILRGIDLDVKGQVVVILGPSGSGKTTFLRCLNALENPEDGQIEF					

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	10	20	30	40	50	60
m122-1..pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAQA					
g122-1	DNERPLRIDFSKKTSKHDILALRRKSGMVFFQYNLFPHKTVLENVMEGPPVAVQGKPAQA					
	70	80	90	100	110	120
m122-1..pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
g122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
	130	140	150	160	170	180
m122-1..pep	190	200	210	220	230	240
	DVLDTMKELAQEGWTVVVTHEIKFALEVATTVVVMDGGVIVEQGSPPDLFDHPKHHERTR					
g122-1	DVLDMKELAREGWTVVVTHEIKFTLEVATNVVMDGGVIVEQGSPELFDHLKHHERTR					
	190	200	210	220	230	240
m122-1..pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAATAA  TCCGCAATAT  CCATAAGACC  TTCGGCAAAA  ATACCATTTT
51  GCGCGGCATC  AATTTGGATG  TGTGCAAAGG  GCAGGTGGTC  GTCATCCTCG
101  GGCCCTCCGG  CTCAGGCAAA  ACGACGTTTC  TGCGATGCCT  AAACGCGTTG
151  GAAATGCCCG  AAGACGGACA  AATCGAGTTC  GACAACGAGC  GACCGCTGAA
201  AATCGATTTT  TCTAAAAAAC  CAAGCAAACA  CGATATTTTG  GCACTGCGCC
251  GCAATCAGG  CATGGTGTTC  CAACAATACA  ACCTCTTTTC  GCACAAAACC
301  GCCTTGGAAG  ACGTGATGGA  AGGACCGGTT  GCCGTACAGG  GCAAGCCTGC
351  CGCCCAAGCG  CGCGAAGAGG  CTCTGAAACT  GCTGGAAAAA  GTCGGCTTGG
401  GCGACAAAGT  GGATTGTAT  CCCTACCAGC  TTTCCGGCGG  TCAGCAGCAG
451  CGCGTCGGCA  TTGCCCGAGC  ATTGGCGATT  CAGCCCGAGC  TGATGTTGTT
501  TGACGAACCC  ACTTCCGCGC  TTGACCCCGA  GTTGGTGCAA  GAUGTGTGA
551  ACGCCATGAA  GGAATTGGCG  CGGGAAGGTT  GGACGATGGT  CGTCGTTACC
601  CACGAAATCA  AGTTCGCGCT  GGAAGTTGCC  ACGACCGTTG  TCCTGATGGA
651  CGCGGCGGTT  ATCGTAGAGC  AGGCGAGCCC  GAAAGAGTTG  TTCGACCACC
701  CCAACACAGA  ACGGACGCGG  AGATTTTAA  GCCAAATCCA  ATCTACCAAG
751  ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT  FGKNTILRGI  NLDVCKGQVV  VILGPSGSGK  TFLRCLNAL
51  EMPEDGQIEF  DNERPLKIDF  SKKPSKHDIL  ALRRKSGMVF  QQYNLFPHKT
101  ALENVMEGPV  AVQGKPAQA  REEALKLLEK  VLGDKVDLY  PYQLSGGQQQ
151  RVGIARALAI  QPELMLFDEP  TSALDPELVQ  DVLNAMKELA  REGWTMVVVT
201  HEIKFALEVA  TTVVVMDDGV  IVEQGSPEL  FDHPKHHERTR  RFLSQIQSTK
251  I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1..pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGENTILRGIDLVDCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1..pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFFQYNLFPHKTALENVMEGPPVAVQGKPAQA					
	70	80	90	100	110	120
a122-1..pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					
m122-1	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSAIDPELVQ					

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	130	140	150	160	170	180
	190	200	210	220	230	240
a122-1.pep	DVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	PKELFDHPKH	ERTR			
m122-1	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	PQDLFDHPKH	ERTR			
	190	200	210	220	230	240
	250					
a122-1.pep	RFLSQIQSTKIX					
m122-1	RFLSQIQSTKIX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

g125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGGT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TCGCCCCCTT GGGCTGGCAG CGCGGTCTGG CGGCCCTGCT TTGGGGTCAT
151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GTGTGCGCCT GTCGTTCCGC AAATGCGGTT
251 CAGTGCTGTT TTCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGTCGGCGC AacgTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACggc gaATCCTTTG TCTGGTGGGC ATTGGCAAAC GGCGCACTGA
401 TCGTGCTGTG GCTGGTTTTT GCGCACGCA GAACGGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GCTTGCCGTG TTGTGGTTGA GCGTCGAAGT
501 GTTCGCTTCG TCCGGCACAA ACGCCGCGCC CGCCGTTTCA GACGGCATGA
551 CCTTCGGAAC GGCAGTCGAA CTGTCCGCCG TCATGCCGCT TTCCTGGCTG
601 CCGCTGGCCG CCGACTACAC GCGCCAAGCA CGCCGCCCGT TGGCGGCAAC
651 CCGACGGCA ACGCTCGCCT ATACGCTGAC GGGCTGCTGC ATGTATGCCT
701 TGGGTTTGGC GCGGCTCTG TTTACCGGAG AAACCGACGT GCGGAAAATC
751 CTGTTGGGCG CGGCTTTGGG CATAACGGGC ATTCTGGCAG TCGTCCTCTC
801 CACCGTTACC ACAACGTTTC TCGATACCTA TTCCGCCGGC GCGAGTGCGA
851 ACAACATTTT CCGCGTTTTT GCGGAAATAC CCGTCGCTGT CGGCGTTACC
901 CTGatcgca cegtgttgc cgtcatgctg cccgttaccg aatataaaaa
951 cttcctgctg cttatccgct cggatatttg gccgatggcg ggtggttttg
1001 attgccgaCT TTTtgtctt AAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 459>:

m125.seq

```

1  ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCTCCGCCA TCGGGCTGAT
51  TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACGCTGC
101 TTGGCCTTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTACT TTTGGGTCAT
151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTT GCGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAAT
501 CTTTTCACG GCAGGCAGCA CCGCCGACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC CTGGCTGCCG
601 CTTGCCGCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GGCGTTGTTT ACCGGAGAAA CCGACGTGGC AAAAAATCCTG
751 CTGGGCGCAr GTTTGgGTGC GGCAGGCATT TTGGCGGTGC TCCTCTCCAC
801 CGTTACCACA ACGTTTCTCG ATGCCTATTC CGCCGGCGCG AGTGCGAACA

```

851 ACATTTCCGC GCGTTTTGCG GAAACACCCG TCGCTGTCrG CGTTACCCTG
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCC GTTACCGAAT ATGAAAACCTT
 951 CCTGCTGCTT ATCGGCTCGG TATTGCGCC GATGGCGGgC GGTTTTGATT
 1001 GCGGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSVA NMLQLAGWTA
 101 VMYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
 201 LAADYTRHAR RPFATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL
 301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCLFRLE TA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSI AEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA					
	: : : : :					
g125	MSGNASSPSSSSAIGLVWFGAAVSI AEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m125.pep	AYIGALTGRSSMESVRLSFGKRGSVLFSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
	: : : : : :					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFSVANMLQLAGWTAVMIYVAGATVSSALGKVLWDG					
	70	80	90	100	110	120
	130	140	150	160	170	179
m125.pep	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
	: : : : : :					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
	180	190	200	210	220	230
m125.pep	DGMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
	: : : : : :					
g125	DGMTFGTAVELSAVMPLSWLPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	190	200	210	220	230	240
	240	250	260	270	280	290
m125.pep	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
	: : : : : :					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
	300	310	320	330	340	
m125.pep	LIGTVLAVMLPVTEYENFLLLLIGSVFAPMAGGFDCLFRLETA					
	: : : : :					
g125	LIRTVLAVMLPVTEYKNFLLLLIRSVFGPMAGGFDCLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq
 1 ATGTCGGGCA ATGCCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC
 101 TTGCGCCTTT GGGCTGGCAG CCGGCTCTGG CCGCTCTGCT TTTGGGTCAT

```

151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCGGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACCGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATGGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTC GGCGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGCTGA GTGCCGAAGT
501 CTTTCCACG GCAGGCAGCA CCGCCGACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTA TGCCGCTTTC TTGGCTGCCG
601 CTGGCCGCCG ACTACACGCG CCACGCGCGC CGCCCCTTTC CGGCAACCC
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTGGCAGC GCGCTTGTTC ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 TCGGGCGCAG GTTGGGTGTC GGCGGCGATT TTGGCGGTCG TCCTGTGCGA
801 CGTTACCACC ACTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAAAC
851 ATATTTCCGC CAACTTTTCG GAAATACCA TCGCCCTGTC CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCC GTTACCGAAT ATGAAAACCT
951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCG.GC GGTTTTGATT
1001 GCGGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RPFATLTAT LAYTLTGCMW YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

m125.pep      10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA
|||||:|||||
a125          10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA

m125.pep      70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
|||||:|||||
a125          70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLFVANMLQLAGWTAVMIYAGATVSSALGKVLWDG

m125.pep     130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
|||||:|||||
a125         130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD

m125.pep     190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
|||||:|||||
a125         190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF

m125.pep     250     260     270     280     290     300
TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
|||||:|||||
a125         250     260     270     280     290     300
TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV

m125.pep     310     320     330     340
IGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX
:|||||:|||||
a125         310     320     330     340
VGTLLAVLLPVTEYENFLLIGSVFAPMAXGFDCRLFRLETAX

```

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
  1 AtgccgctcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
 51 GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg ctgggcacgG eggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAACTC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGGC
851 ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
  1 MPSETPKARR RLSGDIASDN HTKESIMLTLY YGETFPSRL L LGTAAYPTPE
 51 ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VVPLPNTAGC
101 QSVQEAHTTA QMAREVPETD WIKLELIGDD DTLQPDVFQL VEAAILIKD
151 GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFDGV LLNTAVSRSG DPVNMARAF
251 LAVESGRLAF EAGPVEARTK AQASTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
  1 ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
 51 CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCC GAAATCCTCA
101 AACATCCAT CCAAACCGCC CAGCCTGCGA TGAATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGCGGCGA GCGCACGGT CAGGGGTTT GTTCGCTGCT
201 TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251 TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTTGTCGAAG CGGCGGAAAT CTTGATTAAA GACGGCTTCA
401 AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCCGA TCGGCACGGG
501 TTTGGGCGCG GTTCACGCTT ACACGTTGAA CGTCCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GCGGATCCGG TCAATATGGC ACGCGCCTTC GCACTCGCCG
701 TCGAATCCCG ACGGCTGGCA TTTGAAGCCG GACCGGTGCA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTT GGCATTGCGC
801 GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
  1 ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
 51 RAGSGGEAHG QGFWSLLQET GVPVLPNTAG CQSVQEAHTT AQMAREVPET
```

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101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRLL
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLRL ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDFG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRLERLDPDTPLIIDAGLGLPSQAAQVMEWGFDFGVLLNTAVSRSG
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRLERLDPDTPLIIDAGLGLPSQAAQVMEWGFDFGVLLNTAVSRSG
                  190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMARAFALAVESGRLAFEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLAFEAGPVEARTKAQASTPTVGQPFWHSAEYX
                  250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

a126.seq

```

1   TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CCGCGGCGAG GCGCACGGTC AGGGGTTTTC
201 GTCGCTGCTT CAAGAAACCG GCGTTCCCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GCGGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCUA CGCGTTGAAC GTCCTGCCGC
551 AACGCTGCC CGACACGCCG CTGATTATCG ACGCGGCTT GGGTTTGCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGCG TTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGAAGC CAGCAGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTGCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKPEI MLTYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDGDTLQPD VFQLEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWWSA EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKPEIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           LLIHYTKPEIMLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQLEAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VFQLEAAEILIKDGFKVLPYCTEDLIACRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
              |||||:|||||:|||||:|||||:|||||:|||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
 51  GSCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101  GSCCGCGGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CTTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  C3CAATGGC GCGCGAAGTG TTTGAAACCG ATTGATAAAA ATTGGAATC
301  ATCGGCGAGC ACGACACCTT GCAGCCGGAC GTGTCCAAC TCGTCGAAGC
351  GSCGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCTT TATTGCACCG
401  AAGACCTGAT TGCTTGCCGC CGCTTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCGGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCTA
501  TCGCTCAAAA ATCTTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551  ACGCGGGCTT GGGTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTAAA CACCGCGGT TCCCGCAGCG GCGACCCGCT
651  CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701  TTGAAGCCGG GCCGCTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCGTTTGT GCATTGGCGG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

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```

51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MFWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWWSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1  ATGCTCACCC TATACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  GGCTGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CCGAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATGGGAATC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCGGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CCGGTTGAAC GTCCTGCGCG AAGCGCTGCC CGACACGCGG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCCCG
751 ACAGTCGGAC AACCGTTTGT GCATTCCGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1  MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MFWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGEAHGQGFWSLL					
g126-1						
	10	20	30	40	50	60
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1						
	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1						
	70	80	90	100	110	120
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALNVLRRERLPDTP					
g126-1						
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALNVLRRERLPDTP					
g126-1						
	130	140	150	160	170	180
m126-1.pep	LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESGRLAFEAGPVE					
g126-1						
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSGDPVNMA RAFALAVESGRLAFEAGPVE					
g126-1						
	190	200	210	220	230	240
m126-1.pep	ARDKAQASTPTVGQPFWWSAEYX					
g126-1						
	250	260				
m126-1.pep	ARDKAQASTPTVGQPFWWSAEYX					
g126-1	ARTKAQASTPTVGQPFWWSAEYX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1  ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  AGCCGCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GCGCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGATG CGGCGGCGAG

```


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```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCIT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAATC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCCG CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGCGG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCCGGC GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1  MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51  AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIXLEL
101 ISDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTC LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAQVMWEG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFAEAGPVE ARDKAQASTP
251 TVGQPFWHSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

a126-1.pep	10	20	30	40	50	60
m126-1	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
m126-1	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
m126-1	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
m126-1	190	200	210	220	230	240
a126-1.pep	250	260				
m126-1	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1  ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
51  CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATT CAAACGCTGG
251 CTTTGTGCGT GTTTGCGGTG GCGGCGGCGG TCGTCTGGCC GACAAAAGAA
301 CTGATTATGT GTCTGTCGGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCGCGC ACAATATTTT GGGCGACTAT GTCATCCATA

```

```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGGCC GCGCGTTACC CCGGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGC GCGTACA ATACCGCTG TTAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VQQLAGTTVS FPNLLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51  TGGCGAGGCG GTCGAATCCG TGGCGGCGGT TGGCGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCCGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTGCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TCCCCCAACA GCCTGTGTGT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGsAT TTGAAAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGACC GCGCGTTACC CCGGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGC GCGTACA ATACCGCTG TTAATCACC
851 CCGCCGGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFKRHPDFGI
51  ESKRRFLVAS RNITLLLVL FSLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VQQLAGTTVS FPNLLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAESVAAVAALLLARA_LLLNIHFKRHPDFGIESKRRFLVAS					
	: :					
g127	MEIWNMLNTWPDVPIRAEAESVAAVAALLLARA_LLLNIHFRRHPDFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDCAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDCAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

```

a127.seq
1  ATGGAAATAT  GGAATATGTT  GGACACTTGG  CTCGGTGCCG  TCCCGATACG
51  TCGCGAGGCG  GTCGAATCCG  TGGCGGTGGT  CGCGGCTTTG  CTGCTGGCGC
101 GCGCCCTTCT  GTTGAATATC  CACTTCAAAC  GGCATCCGGA  TTTCGGCATC
151 GAAAGCAAGC  GCGCGTTTTT  GGTGCCAGC  CGCAATATAA  CGCTGCTTTT
201 GGTGCTGTTT  TCGCTGGCAT  TTATCTGGTC  GGCGCAAATC  CAAACGCTGG
251 CTTTGTGCGT  GTTGGCGGTG  GCGGCGGCGG  TCGTCGTGGC  GACGAAGGAA
301 CTGATTATGT  GTCTGTCGGG  CAGCATTTTA  AGGTCTGCCA  CCCAGCAATA
351 CTCGGTCGGC  GACTATATCG  AAATCAACGG  CCTGCGCGGG  CGCGTGGTCG
401 ACATCAACCT  GTTGAACACG  CTGATGATGC  AGTCTGGTCC  GAACCCCTTG
451 GTCGGACAGC  TTGCGGGAAC  CACCGTTTCT  TTCCCAACA  GCCTGTTGTT
501 GAGCCACCCC  GTGCGCCGCG  ACAATATTTT  GGGCGACTAC  GTCATCCATA
551 CGGTCGAAAT  CCCGGTTCCC  ATCCATTGG  ATTCGGATGA  AGCCGTATGC
601 CGTCTGAAAG  CCGTACTCGA  GCCCTGTGTC  GCGCCCTACA  TCCCCGCCAT
651 CCAACGGCAT  TTGGAACACG  TGCAGGCGGA  AAAACTGTTT  ATCACGCCCG
701 CCGCCAAACC  GCGCGTTACC  CGCGTCCGT  ACGATGACAA  GGCATACCGC
751 ATCATCGTCC  GCTTCGCCTC  CCCCCTTCA  AAGCGCTGC  AAATCCAACA
801 GCGCGTTATG  GACGAATTTT  TCGCGTACA  ATACCGCTC  TTAAATTACC
851 CCGCGGCTC  CGAAACACTT  TAA

```

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

```

a127.pep
1  MEIWNMLDTW  LGAVPIRAEA  VESVAVVAAL  LLARALLNI  HFKRHPDFGI
51  ESKRRFLVAS  RNITLLLVLF  SLAFIWSAQI  QTLALSMFAV  AAADVATKE
101 LIMCLSGSIL  RSATQQYSVG  DYIEINGLRG  RVVDINLLNT  LMMQVGNPL
151 VGQLAGTTVS  FPNSLLLSHF  VRRDNILGDY  VIHTVEIPVP  IHLDSDEAVC
201 RLKAVLEPLC  APYIPAIQRH  LENVQAEKLF  ITPAAKPRVT  RVPYDDKAYR
251 IIVRFASPV  KRLEIQQAVM  DEFLRVQYRL  LNYPAGSETL  *

```

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAESVAVVAALLARALLNIHFKRHPDFGIESKRFLVAS					
a127	MEIWNMLDTWLGAVPIRAEAESVAVVAALLARALLNIHFKRHPDFGIESKRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLINTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLINTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASFVSKRLEIQQAVMDEFRLVQYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASFVSKRLEIQQAVMDEFRLVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

```

1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACAtca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATT TCGTATTGAGC GCGCGGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TCGCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa cTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCGGAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAAATG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTaca AAGGCCGCCG CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCAGCC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCGGCAT CAACggcgtA GAATGGGACG CGGTGCAACT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCTGCGGAA AGAACTCTTC GACAAATGTC
1601 TcgCGCCAA AAATTTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 TCcggcGGCT ATTCCGAGG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCGC CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTCTCTGGCA GAAAtccttg ccgtcggegg ctCCCGCAGC
1951 gcgGCGGAAT CCTCAAAGC CTTCGCGGA CGCGAACCGA GCATAGACGC

```

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGCttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1  MIDNALLHLG EEPFRNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTHTGWA
51  NTVERTLGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACC CGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTIG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCG GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAAACTC AACCCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAYTCCCYG TCGGCAAwGT ATTAAACGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGCTC
151 TGGCAAAAG ACGTGCCTA TTKTGAATTG CAACAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CCACTACAAA GGCCGCGCGC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCYTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGCGATCA ACGCGGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTTGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAA AC'TTCAAAG CGGCATGTTC yTsGTCCGCG AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAATCC TTCAAAGCCT TCCGCGGCGG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTHTGWA
51  NTVPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//

1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51  WHKDVRYXEL QQNGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSGDGL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHEGLHH LLTQVDELGV
151 SGINGVXWDA VELPSOFMEN FVWEYNVLAO XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g126

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPAQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLSGAELPPERQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep				340	350	360
				YAGEKLREAKYAFSETEVKKYFPVGKVLG		
m128				YASEKLREAKYAFSETXVKKYFPVGKVLNG		
				10	20	30
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHEGTGHGLHLLTQVDELGV					
m128	GRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHEGTGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHBETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDECRLLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRLLKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRGREPS					
	280	290	300	310	320	330

366

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTGCGG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAACTC AACCACGATC
401 TGCGCGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCCG ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTCACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCTATC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGC CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCGC
1101 CCAATCAAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTC ACGGCGACGC
1301 TGCAACTGCC CACCGCTTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCACGCA
1401 AACCGGACAC GGCCTGCACC ACCTGCCTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCGGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCCCGTCG
1751 TCGACCGGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCGAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCGCCCA
1901 CAGGCAACGC CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDAAAPLAGI PEDALAMFAA
201 LAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLPQ WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VINGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVLPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

	10	20	30	40	50	60
m128.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m128.pep	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130					
m128.pep	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSONVLDTDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
				140	150	
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVGX					
a128	ARRAKPYAEKDIAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160 170 180 190 200 210					
	VLNGLFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370 380 390 400 410 420					
m128.pep	220 230 240 250 260 270					
	NDYKGRRRFS DGTQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFS DGTQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430 440 450 460 470 480					
m128.pep	280 290 300 310 320 330					
	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDXLAAKNFQ					
a128	ELGVSGINGVWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490 500 510 520 530 540					
m128.pep	340 350 360 370 380 390					
	XGMFXVRQXEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550 560 570 580 590 600					

q128-1.seq (partial)

1	ATGATTTGACA	ACGCACTGCT	CCACTTGGGC	GAAGAACCCC	GTTTTAATCA
1	AATCAAAACC	GAAGACATA	AACCCGCCCT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGTAC	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGCGATCACG	GAACCGCTCG	GCAGGATTTG
201	GGGCGTCTGT	TCCCATTCTA	ACTCGTCTCG	CGACACGCCC	GAACTGCGCG
251	CGGTCATAGA	CGAACTGTAT	CCTGAAATCA	CCGCTCTCTT	CACCGAAATC
301	GGACATAGAA	TGCAACTGTA	CACCGCTTCC	AAAACCATCA	AAAATTCCCC
351	CGAATTTGCA	ACGCTTTCCC	CGCACAAAA	AACCAAGCTC	GATCAGGACC
401	TGCGCGATT	CGTATTGAGC	GGCGCGGAAC	TGCCCGCCGA	ACGGCAGGCA
451	GAACTGGCAA	AACCTGAAAC	CGAAGGCGCG	CACTTTCCG	CCAAATTTCT
501	CCAAAACGTC	CTAGACGCGA	CGACCGGTT	CGGCATTTAC	TTTGACGATG
551	CGCGACCGCT	TGCCGGCAAT	CCCCGAAGAC	CGCTCGCCAT	GTTTGC CGCG
601	CGCGCGCAAA	GCGAAGGCAA	AACAGTTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTCACTT	CGCGTTATCC	AATACCGCCG	CAACCGCGAA	TGCAGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTCGCC	GCGAACTTTT	AAACGACGGC
751	AAATTCGACA	ACACCCGCCA	CATCGACCCG	ACGCTCGAAR	ACGCATTGAA
801	AACCCGCAAA	CTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAACTTCCT	GCACGACCTC
901	CGCCGCGCGC	CCAAACCCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAAG
951	CTTCGCCCGC	GAACCTCTCG	GTCCTCGCGA	CCCGCAGCCG	TGGCAATTGA
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCCTGTTGCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	TGCCGAAAAA	ACGCTTCCCC
1151	TCTGGCAAAA	AGACGTCGCG	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGCGCGCG	TTTATATGCA	TTTGTACGCA	CGCGAAGGCA	AACGCGGGCG
1251	CGCGTGGATG	AACGACTACA	AAGCGCCGCG	CCGCTTTGGC	GACGGCACGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGCTCGCA	ACTTCGCCCC	GCGCGTCGCG
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AACCGGCCAC	GGACTGCACG	ACCTGCTTAC	CCAACTGGAC	GAACTGGGCG
1451	TGTCGGGCAT	CACCGCGCTA	AAA		

g128-1.pep (partial)

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	2	3	4	5	6	7	8	9	10	11	12																																																																																								

m128-1.seq

1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCCGCGCT GCAAACCGCC ATCGCCGAG
101 CGCGCGTACA AATCGCGGCC ATCAAGCCCC AAACGCATC CGGCTGGGCA
151 AACCTGTGCG AACCCCTGAC CGGCATACCC GAACCGCAG CGAGGATTG

```

201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAATC AACCCGATC
401 TGGCGGATTT CGTCTCAGC GGGCGGGAAC TGCCGCCCCG ACAGCAGGCA
451 GAACTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CCGCACCGCT TGGCGGCATT CCGAAGACG CGTCGCCAT GTTTGCCGCG
601 GCCGCGCAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCCGTATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTA CGCCGAAAA GACCTCGCGG AAGTCAAAGC
951 CTTCGCCCG GAAAGCCTGA ACCTCGCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGT CAGCGAAACC
1051 GAAGTCAAAA AATACTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAAAAAA CGGCGAAACC
1201 ATAGGCGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGC CCGTTTTCG GACGCGACGC
1301 TGCAACTGCC CACCGCTTAC CTGCTGCA ACTTCGCCCC ACCCGTCGCG
1351 GGCAGGGAAG CCGCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAAGTGGGCG
1451 TATCCGCGAT CAACGGCGTA GAATGGGACG CGGTGCAACT GCCCAGCCAG
1501 TTTATGAAA ATTTCGTTT GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAATCTTC GACAAAATGC
1601 TCBCCGCCAA AAATCTCAA CGCGCATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCGGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTCA
1751 TCCAGCGCGC CGAATAACA CGCTTCGCT TGAGCTTCGG CCACATCTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACCGGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCCGCA
1901 CAGGCAAAAC CTTTGGCAG GAAATCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGCGAGAAT CCTTCAAAGC CTTCGCGCGC CGCGAACCGA GCATAGACGC
2001 ACTCTTCCG CACAGCGTT TGCACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

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1  MTDNALHLHG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESTGY KIGLQIPHYL AVIQYADNRB LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTA LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYPPVVG VLNLGFAQIK KLYGIGFTEK TVPVVHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMPLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESEFKAFRG REPSIDALLR HSGFDNAV*

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m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALHLHGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQTHTGWANTVERLTGIT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      MTDNALHLHGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pep ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m128-1      ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSECKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSECKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGPKNYAELSLATKMADTPEQVLNFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGPKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKYFPVVK					
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQPWDLYASEKLREAKYAFSETEVKYFPVVK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

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1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTC
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTTCAC ACCCTCTCCC ACGCGCAAAA AACCAAACTC AACCACGATC
401 TGCGCGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCGCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCTATC AATACGCCGA CAACGCAAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCGG AAGTCAAAGC
951 CTTCGCCCGC GAAAGCCTCG GCCTCGCGCA TTTGCAACCG TGGGACTTGG
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGCGC TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG

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1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGGCAGGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCGCGTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCGTGACAC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGAAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAAATGTCCGC
1551 CCACGAAGAA ACCGGCGGTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTGCCCTCTT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 CAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGGCG CACAGCGGCT TCGACAACGC GCCTTGA

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This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

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a128-1.pep
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMAADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFEQ EILAVGSGRS
651 AAESEKAFRG REPSIDALLR HSGFDNAA*

m128-1/a128-1 97.8% identity in 677 aa cverlap

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT
m128-1      |||||
          10      20      30      40      50      60
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT

          70      80      90      100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
m128-1      |||||
          70      80      90      100     110     120
m128-1      ERVGRWGVVSHLNSVADTPPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD

          130     140     150     160     170     180
a128-1.pep TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1      |||||
          130     140     150     160     170     180
m128-1      TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY

          190     200     210     220     230     240
a128-1.pep FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV
m128-1      |||||
          190     200     210     220     230     240
m128-1      FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV

          250     260     270     280     290     300
a128-1.pep TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMAADTPQVLNFLHDL
m128-1      |||||
          250     260     270     280     290     300
m128-1      TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMAADTPQVLNFLHDL

          310     320     330     340     350     360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVVGK
m128-1      |||||

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372

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m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLQPWDLGAYASEKLREAKYAFSETEVKKYFPVSK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep  VLNLGFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVMDLYARECKRGGAWM
              |||
m128-1      VLNLGFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVMDLYARECKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep  NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHHLLTQVD
              |||
m128-1      NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep  ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||
m128-1      ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep  RGMFLVRQMEFALFDMMIYSEDEGRLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              |||
m128-1      RGMFLVRQMEFALFDMMIYSEDEGRLKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep  AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||
m128-1      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep  REPSIDALLRHSGFDNAAX
              |||
m128-1      REPSIDALLRHSGFDNAVX
              670

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a128-1/ P44573

sp|P44573|OPDA_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlC) homolog
- Haemophilus influenzae (strain Rd KW20)
>gi|1573174 (U32706) oligopeptidase A (prlC) [Haemophilus influenzae Rd] Length = 681
Score = 591 bits (1507), Expect = e-168
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

Query: 4 NALLHLGEBRFRDQIKTEDIKPALQTXXXXXXXXXXXXXXHTGWANTVEPLTGITERV 63
N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5 NPLLNIGQLPFPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRIWGVSHLSVTDTPELRAAYNELMPEITVFTEIGQDIELYNRFTKKNSPFDTLS 123
R W VSHLSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65 NRWSPVSHLSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIENSLRDFELSGIGLSEKQRYGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243
A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE+YRAY TRA
Sbjct: 185 EAEIAGLPESALQAAQSAESKGLGYRPTLEIPSYLPVMTYCENRALREEMRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLLGPKNYAELSLATKMAADTPEQVLNFLHDLAR 302
SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQGPNAGKWDNSKVMEEILTLRVBLAKLLGFNTYTELSLATKMAENPQQVLDLFLDLAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLQPWDLGAYAGEKLREAKYAFSETEVKKYFFVGKVL 362
RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFF +V+
Sbjct: 305 RAKPQGEKELQELKGyceKEFGVTBLAPWDIGFYSEKQKQHLVAINDEELRPYFFENRVI 364

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QONGETIGGVYMDLYAREGKRGGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVERRKGVDTWHKDVRFDDLIDENDOLRGSFYLDLYAREIHKRGGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEELAFISGHYETGEPLPKEKLTQLLAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRLLQNWQQVLDVSRKEVAVVRPPEYNRPFANSFGHIP 600
 MP++RQ+EF +PD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLSEFIPDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVDWARAPHSPSHIF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAESFKAFR 659
 WAEVLSADAY+ FBE TKG F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSEEPMELEFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq

```

1   ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT
51  TTCATTTCGC TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAATCAAT
101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA
251 TCCGGACAAA CGCGTTGGCA GTCGGAAT CCGGCCGCC GTGTCAAATA
301 ATGCGTACTT TTGGCCGGGT CTTGTCTTTT GTAAGCGGCG GTCTTTTTTT
351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCG ATGCCGCCG
451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGCAT TTAGCCGGT
501 AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep

```

1   MLSPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
51  PTAAAVHPYP RFRHLPFQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
151 TYRAGFCLSD LAAPRPVT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)

```

1   ..TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
51  ACAGGTAGCG GTCAATCCT GTTTCATCCA AATAACACG TTGGTAGTCG
101 GAAAATTCGG CCGCTGTGT CAAATAATGC GTTACTTTGG CCGGCTCTTG
151 TTCTTTGTAA GTGGTGTCT TTTTTCGCG GTTATCCCCA TCTGTTTGAG
201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT
251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCCTA
301 TCCGATTTGA CGGCATTAG ACCGGTAACT TGA

```

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)

```

1   ..YLRFHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
51  FVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
101 SDLTAFRPVT *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

						10	20	30
m129.pep						YLRFHYPFOAAGIGTEQVAVKSCFIQINT		
						: : : :		
g129	RDQNQYRAASSPNRGLPRFPITPTAAAVHPYPRFRHLFPQAAGIGAEQAAVESCFIRTN	30	40	50	60	70	80	
		40	50	60	70	80	90	
m129.pep	LVVGKFGRLCQIMRYFGRVLFVSGGLFLRVIPICLSAXQMVAAVQSKCLAI							SCRXASGC
	: : :							
g129	LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAAAVQSKCLAI	90	100	110	120	130	140	SCROASGC
		100	110					
m129.pep	CPTYXAGFCLSDLTAFRPVTX							
g129	RPTYRAGFCLSDLAAFRPVTX	150	160					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

a129.seq (partial)

1	TATCTGCGCT	TTCACTATTT	GCCCTTTCAG	GCTGCGGGCA	TAGGGACGGA
51	ACAGGTAGCG	GTCAAATCCT	GTTTCATCCA	AATAAACACG	TTGGTAGTCG
101	GAAAATTCGG	CCAGCTGTGT	CAAATAATGC	GTTACTTTGG	CCGGGTCTTG
151	TTCTTTGTAA	GTGGTGGTCT	TTTTTTGCGC	GTTATCCCCA	TCTGTTTGAG
201	TGCATAGCAA	ATGGTGGCTG	CCGTACAATC	AAAATGTTTG	GCGATTTTAT
251	GCAGATAGGC	ATCCTGGTGT	TGCCCAACAT	ATTGAGCCGG	TTTTTGCCCTA
301	TCCGATTGTA	CGGCATTAG	ACCGTAAC	TGA	

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

a129.pep (partial)

1	YLRFHYPFO	AAGIGTEQVA	VKSCFIQINT	LVVGKFGQLC	QIMRYFGRVL
51	FFVSGGLEFLR	VIPICLSA*Q	MVAAVQSKCL	AISCR*ASWC	CPTY*AGFCL
101	SDLTAFRPVT	*			

m129/a129 98.2% identity in 110 aa overlap

						10	20	30	40	50	60
m129.pep	YLRFHYPFOAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVSGGLFLR										
a129	YLRFHYPFOAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVSGGLFLR	10	20	30	40	50	60				
		70	80	90	100	110					
m129.pep	VIPICLSAXQMVAAVQSKCLAI										
a129	VIPICLSAXQMVAAVQSKCLAI	70	80	90	100	110					
	SCRXASGCCPTYXAGFCLSDLTAFRPVTX										
	SCRXASWCCPTYXAGFCLSDLTAFRPVTX										

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

1	ATGAAACAAC	TCCGCGACAA	CAAAGCCCAA	GGCTCTGCAC	TGTTTACCC
51	TGTGAGCGGT	ATCGTTATTG	TTATTGCAGT	CCTTTATTTC	CTGATTAAGC
101	TGGCGGGCAG	TGGATCGTTC	GGCGATGTCG	ATGCCACTAC	GGAAGCGGCA
151	ACGCAGACCC	GCATCCAGCC	TGTCGGACAA	TTGACCATGG	GTGACGGCAT
201	CCCCGTCGGC	GAACGCCAAG	GCGAACAGAT	TTTCGGCAAA	ATCTGTATCC

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```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAACTC AAACGGGCGA TTACCTACAT GCGCAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGACGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCCG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGTTTGTAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLYF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQCHAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPAKG  GAADLTDQEL  KRAITYMANK
151 SGGSFPPNDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAPAVGVDDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKKGKETH  KHALEGFNAM
251 PAKGGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
1  ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
51  CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGGCAA GGCTTCGATA CCTTGTTCCA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGACGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TCGGTCCGCG GTTGACGGTA AAAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACAA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAArG CGgCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
1  ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFOHALNGFN
51  AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAAPAEA KAEDKGAAPA VGVGKRVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPKXG NAGLSDEVK AAVDYMANKS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng)

from *N. gonorrhoeae*:

```

m130/g130
10 20 30
m130.pep GEQIFGKICQCHAADSNVPNAPKLEHNGD
|||||
g130 DATTEAATQTRIQPVGQ LTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
50 60 70 80 90 100

40 50 60 70 80 89
m130.pep XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
|||||
g130 WAPRIAQGFDTLFOHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
110 120 130 140 150 160

```


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```

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
g130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDEVKAAVDYMANQSGAKFX
          |||||
g130      KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC  TCCGCGACAA  CAAAGCCCAA  GGCTCTGCAC  TGTTTACCTT
51  TGTGAGCGGT  ATCGTTATTG  TTATTGCAGT  CCTTTATTTT  CTGATTAAGC
101 TGGCGGGCAG  CGGCTCGTTC  GGCGATGTCG  ATGCCACTAC  GGAAGCAGCA
151 ACGCAGACCC  GTATCCAGCC  TGTCGGACAA  TTGACGATGG  GCGACGGCAT
201 CCCCCTCGGC  GAACGCCAAG  GCGAACAGAT  TTTCGGCAAA  ATCTGTATCC
251 AATGCCACGC  GGCGGACAGC  AATGTGCCGA  ACGCTCCGAA  ACTGGAACAC
301 AACGGCGATT  GGGCGCCGCG  TATCGCGCAA  GGCTTCGATA  CCTTGTTCCA
351 ACACGCGCTG  AACGGCTTTA  ACGCCATGCC  TGCCAAAGGC  GGTGCGGTAG
401 ACCTGACCGA  TCAGGAAGTC  AAACGGGCGA  TTAATTACAT  GGCGAACAAA
451 AGCGGCGGTT  CTTTCCCGAA  TCCTGATGAG  GCTGCGCTTG  CCGACAATGC
501 CGCTTCAGGA  ACAGCTTCTG  CTCCTGCCGA  TAGTGCAGCT  CCGGCAGAAG
551 CGAAGGCAGA  AGACAAGGGT  GCGGCAGCCC  CTGCGGTCGG  CGTTGACGGT
601 AAAAAAGTCT  TCGAAGCAAC  CTGTCAGGTG  TGCCACGGCG  GTTCGATTCC
651 CGGTATTCCC  GGATAGGCA  AAAAAGACGA  TTGGGCACCG  CGTATCAAAA
701 AAGGCAAAGA  AACCTTGCAC  AAACACGCCC  TTGAAGGCTT  TAACGCGATG
751 CCGCCAAAG  GCGGCAATGC  AGGTTTGAGC  GATGACGAAG  TCAAAGCGGC
801 TGTGACTAT  ATGGCAAACC  AATCCGGTGC  AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLYF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQC:HAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPKAG  GAVDLTDQEL  KRAITYMANK
151 SGGSFNPDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAPAVGVVDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKGKETLH  KHALEGFNAM
251 PAKGGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130.pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||||
a130      DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFQHALNGFNAMPKGGAADLTDQELKRAITYMANKSGGSFFNPDEAAP
          |||
a130      WAPRIAQGFDTLFQHALNGFNAMPKGGAVDLTDQELKRAITYMANKSGGSFFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||
a130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDEVKAAVDYMANQSGAKFX

```

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```

a130      |||||
          KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNAGLSDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```

g132.seq
1  ATGGAAGCCT TCAAAACCTT AATTTGGATT ATTAATATTA TTTCCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTtcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCTCTCAG CAGCAGAAAT
351 AACagtTTTt CAAATgccga caTGgtga

```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

```

g132.pep
1  MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```

m132.seq (partial)
1  ATGGAACCTT TCAAAACCTT AATTTGGATT GTTAATTTAA TTTCCGCTTT
51  GGCCGTCCTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...

```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

```

m132.pep (partial)
1  MEAFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

```

m132/g132
          10      20      30
m132.pep  MEAFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG
          || |||||:|:|||||:|||||
g132      MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSGSGSAQGVFGSAGNANFLSRS
          10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

```

a132.seq
1  ATGGAAGCCT TCAAAACCTT AATTTGGATT GTTAATATAA TTTCCGCTTT
51  GGCCGTCATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CTAACCTCCT CAGCCGCTCG ACCGCCGTTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCTCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

```

a132.pep
1  MEAFKTLIWI VNIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRS TAVAATFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*

```

m132/a132 92.1% identity in 38 aa overlap

378

```

      10      20      30
m132.pep  MEPFKTLIWIVNLISALAVFVLVLLQHGKGADAGATFG
           || ||||| |||||:||||| ||||| ||||| |||||
a132      MEAFKTLIWIVNIIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFCSAGNANFLSRS
           10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

```

g134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCCGATGCGG GTAAAACCAC GCTGACCGAA AAATGCTGC
101 TGTTCGCGG  CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGÀ TGCAGTTGCA CTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CAGCCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG  CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCGGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAATCC  GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCGAAT  TGAACAACG
651 CTTTCGTTG  GAAATCCAGC AGTGC GCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGcgg CGAACTCACG
751 CCAGTGTCT  TCGGCTCTGC GATTAACAAC TTCGGCATT  AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCG  GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGC
951 CGTCTGCTCC GGTAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCCTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT  GTCGCACGAC
1051 CGCGAACTGG CGGAAGAAGC CTACGCCGCG GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAATTCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTTACCGG CATCCCATT  TTCGCGCCCG AACTGTTCG  CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAT  CAAACAAC TG CAAAAGGT  TGAACAAC
1251 CGGCGAAGAA GGTGCGGTT  AAGTATTCAA ACCGATGAGC GCGCGGATT
1301 TGATTTGGG  TCGGTCGCG  GTGTGCACT TTGAAGTCG AACCTCACG
1351 CTCGCCAAG  AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGCGCGC  TGGGTATCGT GCGACGACAA GAAAAAATG  GCGGAATTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCG  CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCAACA  TTCGGTCAA  CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

```

g134.pep
1  MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWMD IEKQRGISVA SSVMOFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDBIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG  DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGVAV  FDSASIWSAR WVSCDDKKKL AEFERKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQBRWPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

```

m134.seq
1  ATGTCCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTTGAAGTAA AAATCTTGC
101 TGTTCGCGG  CGCGATTGAG AGCGCGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAACCTT TGGACGAAGT GGAAAACATT TTAATAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGGCGA ACGCTGCGCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCCG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCAATG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGAGC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG
951 CGTCTGCTCC GGCAAAATTC AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGCG GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTCACCGG CATCCCATTC TTCCGACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACG CAAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCTGAATTTG
1451 AAAAAGCCAA CGCGGCAAC CTCGCCATCG ACGCAGCGCG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTGGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

```

m134.pep
1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRNVEPD EPKFSGFIFX
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMShD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYVEAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng)

from *N. gonorrhoeae*:

```

m134/g134
      10      20      30      40      50      60
m134.pep MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
|||||
g134 MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
      10      20      30      40      50      60

      70      80      90     100     110     120
m134.pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
|||||
g134 IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDSALMVIDAAGVEA
      70      80      90     100     110     120

      130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVEDILQIRCAPVTWPIGMGNFKG
	130 140 150 160 170 180
m134 . pep	190 200 210 220 230 240
	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	250 260 270 280 290 300
	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	310 320 330 340 350 360
	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMMSHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMMSHDRELAEAYAG
	310 320 330 340 350 360
m134 . pep	370 380 390 400 410 420
	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	430 440 450 460 470 480
	GAVQVFKPMMSGADLILGAVGVLOFEVVTSLRAN EYGV EAVFDSAS IWSARWVSCDDKKKL
g134	GAVQVFKPMMSGADLILGAVGVLOFEVVTSLRAN EYGV EAVFDSAS IWSARWVSCDDKKKL
	430 440 450 460 470 480
m134 . pep	490 500 510 520 530
	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG  AAATCCTCGA  CCAAGTGCGC  CGCCGCGCGA  CGTTTGCCAT
51  CATCTCCAC  CCTGACGAG  GTAAAACAC  GTTGACTGAA  AACTCTTGC
101  TGTTTTCAGG  TGCATTCAA  AGCGCGGTA  CGGTAAAAGG  CAAGAAAACC
151  GGCAAATTCG  CCACCTCCGA  CTGGATGGAC  ATCGAGAAGC  AGCGCGGCAT
201  TTCCGTGGCA  TCAAGCGTGA  TGCAGTTCGA  CTATAAAGAC  CACACCGTCA
251  ACCTTTTGGA  CACGCCGGA  CACCAAGACT  TCTCCGAAGA  CACCTACCGC
301  GTTTTGACCG  CCGTCGATAG  TGCCTTGATG  GTCATCGACG  CGGCAAAAGG
351  CGTGAAGCG  CAAACCATCA  AACTCTTGAA  CGTCTGCCGC  CTGCGCAATA
401  CGCCGATTGT  TACGTTCATG  AACAAATACG  ACCGCGAAGT  GCGCGATTCC
451  CTGGAATTGC  TGGACGAAGT  GGAAAACATC  CTGCAATCC  GCTGCGGCGC
501  CGTAACCTGG  CCGATCGGCA  TGGGCAAAA  CTTCAAAGGC  GTGTACCACA
551  TCCTGAACGA  CGAAATCTAT  CTCTTTGAAG  CGGGCGGCGA  ACGCTTGCCG
601  CACGAGTTCG  ACATCATCAA  AGGCATCGAT  AATCCCGAAT  TGGAAACAACG
651  CTTTCCGTTA  GAAATACAGC  AGTTGCGCGA  CGAAATCGAA  TTGGTGCAGG
701  CGGCTTCCAA  CGAGTTCAAT  CTCGACGAAT  TCCTCGCGGG  CGAACTCAGC
751  CCCGATTCT  TCGGCTCTGC  GATTAACAAC  TTCGGTATTC  AGGAAATCCT
801  CAATTCAATG  ATTGAATGGG  CGCCCGCGCC  GAAACACGCG  GATGCGACCG
851  TCGGTATGGT  CGAGCCGGAC  GAGCCGAAGT  TTTCCGGATT  TATCTTCAA
901  ATCCAAGCCA  ATATGGACCC  GAAACACGCG  GACCGTATTG  CCTTCTTGCG

```

```

951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTCCG CAGCGTCCG
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGC GCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCACT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTLTE KLLLFSGAIQ SAGTVKGKKT
51 GK FATS DWM D IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAKGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDI IKGID NPELEQRFPLE IQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRRRTFAIISHPDAGKTLTEKLLLFSGAIQSAGTVKGKKTGKFATS DWM					
a134	MSQEILDQVRRRRRTFAIISHPDAGKTLTEKLLLFSGAIQSAGTVKGKKTGKFATS DWM					
	10	20	30	40	50	60
m134.pep	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTA VDSALMVIDAAKGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTA VDSALMVIDAAKGVEA					
	70	80	90	100	110	120
m134.pep	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTA VDSALMVIDAAKGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTA VDSALMVIDAAKGVEA					
	70	80	90	100	110	120
m134.pep	QTIKLLNVCLRDTPIVTFM NKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG					
a134	QTIKLLNVCLRNTPIVTFM NKYDREVRDSLELLDEVENILQIRCAPVTWPIGMGKNFKG					
	130	140	150	160	170	180
m134.pep	QTIKLLNVCLRDTPIVTFM NKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG					
a134	QTIKLLNVCLRNTPIVTFM NKYDREVRDSLELLDEVENILQIRCAPVTWPIGMGKNFKG					
	130	140	150	160	170	180
m134.pep	VYHILNDEIYLFEAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLFEAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
m134.pep	VYHILNDEIYLFEAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLFEAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
m134.pep	LDEFLAGELTPVFFGSAINNFGIQEIILNSLIDWAPAPKPRDATVRMVEPD EPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQEIILNSLIEWAPAPKPRDATVRMVEPD EPKFSGFIFK					
	250	260	270	280	290	300
m134.pep	LDEFLAGELTPVFFGSAINNFGIQEIILNSLIDWAPAPKPRDATVRMVEPD EPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQEIILNSLIEWAPAPKPRDATVRMVEPD EPKFSGFIFK					
	250	260	270	280	290	300
m134.pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEYAG					
	310	320	330	340	350	360
m134.pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEYAG					
	310	320	330	340	350	360

382

	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGVLQFEVVTSLRANEYGVAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGVLQFEVVTSLRANEYGVAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

```

g135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCAGTG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGCGGGCT CGGGTTCCGC AAACGGCACG GCGCGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcCgaaa gcggGGgcag cgttTAtgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

```

g135.pep
1  MKYKRIVFKV GTSSITRSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHINHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

```

m135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```

501 GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCAGT
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACG GCGGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 CTTGGCGTTC TATTCCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
1  MKYKRIVFKV GTSSITHSDG SLSRGIQTI TCQLAALHHA GHLEVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIAA TIAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKWLAF YSESRGSVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng)

from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGIQTIITCQLAALHHAGHELVLVSSGAVAAGFGALG					
	:					
g135	MKYKRIVFKVGTSSITRSDGSLSRGIQTIITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	:					
g135	FKKRPVKIADKQASAAVGGLLMEEYTANLSSDGIVSAQILLSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRAPVPIINENDTVSVEELKIGDNDTLAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	:					
g135	SVLLQRRAPVPIINENDTVSVEELKIGDNDTLAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
	:					
g135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI					
	:					
g135	LAEAAEHQADGSFFVPRAKGLRTQKWLAFYSESGSVYVDESAEHALSEQKACX					
	250	260	270	280	290	
	310	320	330	340	350	360

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTCGGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCA3GGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGGCG AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 CGGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGGTATGC TGACTAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAGAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGCAAAAG GCGAGTCCTG TTCGCCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATGCGTA AGCGGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1  MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TRQLAALHHA GHLEVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIATESGVVP YICSSLKPDA LAEADNQAD
251 GSFFVPRAKG LRTQKWLAF YSESRGGVYV DEGAHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPDA					
a135	NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVVPYICSSLKPDA					
	190	200	210	220	230	240

385

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRGGVYVDEGAEHALSEQGKSLLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKSRKAKGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAEDLLKLRKAKGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

```

1  ATGGAAATCC GGTTCAGAC AGCATTTTTA CGTTTGGTTC AGatgaAAAC
51  AACCGCTtca aTTCTtaccg caACACGCCT TGTATTTCCT GccgCTGCCG
101 CACGGACAGG GATCGTTCCT GCCGgtTTTT TCCCTTCCC TCGGACGGT
151 TTGCGGTTTG TTGATGACCG CCTGCCAGTA GCGGTAGATG Tctgccagcg
201 cgTAAGGCag tTCGGAcgca agttccgcca gctcgcttc ggTGAATTGC
251 AGgcgataa cgccgtttTC CTCTTCGTcG taaatgccgc ccactgccat
301 cacgGGGTAA AACAGCTCTT CAAACGCTTC ATCATCGGCG GCTTCAAACC
351 AATCGGTCCG CACAATGTCC AAACCGTAAA GATAGGCGTT GCACCAAGTG
401 TAAAAATCGC TGCCGCCCTC GCCGTCGTCG TAGAGCCACA AATCGGGCAG
451 CTTTTATCC GACATCGCGG CGGTGTGTTT CATCGCCATT GCCAAACCA
501 GCCGTTTCGAT TTCGGAACGT TCGGCGGCGG TAAATTGCGA TTCGTCGCCC
551 AACACTTCGG GCAGCCAGTC GAGCGGTGCC AATTGTGTCG GCCCGCTCAA
601 CAGCGCCGTC ATAAACCTT GAACCTCGTC GCAACGCATC GTGTTGCCTT
651 GTTCGCTTTT GGCATCCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

```

1  MEIRFQTAFL RLVQMKTNAS ILTATRLVFP AAAARTGIVP AGFFPPFPADG
51  LRFVDDRLPV AVDVCQVRVQ FGRKFRQLAF GELQADNAVF LFVFNAAHCH
101 HRVKQLFKRF IIGGFKPIGR HNVQTVKIGV APSVKIAAAL AVVVEPQIGQ
151 LFIHRGGCF HRHCQNQPF DFGTGGGKLR FVAQHFGQPV ERCQFVRPAQ
201 QRRHKTLLNV ATHRVALFAF GIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

m136.seq

```

1  ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCTTG
101 CGGACGGTTT GCGGTTTGTT GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTCGTCGTA AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC
451 CAAAACCAGC CGTTCGATT CGGAACGTTT GCGGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCGGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCCCTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCTTTT CAAATGGGTT
701 TTGCCCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

386

```

m136.pep
1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRFV  DDCLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVFLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAOPFFGCFG  KFSGIHHFPF  QMGFAPYYRR  NAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

m136.pep	10	20	30	40
	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	10	20	30	40
	MEIRFQTAFRLRLVQMKTNASILTATRLVFPAAAARTGIVPAGFFFPADGLRFVDDRLPV			
m136.pep	50	60	70	80
	AVDIRQCIRQLGFQFRQLAFCELOQTDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	50	60	70	80
	AVDVCQRVRQFGRKFRQLAFGELOADNAVFLFVVNAHCHHGKQLFKRFIIGGFKPIGR			
m136.pep	110	120	130	140
	HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	110	120	130	140
	HNVQTVKIGVAPSVKIAAALAVVVEPQIGQLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
m136.pep	170	180	190	200
	FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQQFAQPFFGCGKFSGIH			
g136	170	180	190	200
	FVAQHFGQPVERCQFVRPAQQRHKTNLNLVATHRVALFAFGIQX			
m136.pep	230	240		
	HFPFQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

```

a136.seq
1  ATGGAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTTCTGC
51  CGTGCCGCA  CGGACAGGGA  TCGTTCCTGC  CTGTTTTTTC  GCCTTCCCTG
101 CGGACGGTT  GCGGCTTGTT  GATGACCGCC  TGCCAGTAGC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTCTCG
201 TGAATTGCAG  ACGGATAGTG  CCGTTGTCTT  CTTCGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAACTCTTCA  AACGCTTCAT  CATCGACGGC
301 TTCAAACCAA  TCGGTCGGCA  CAATATCCAA  ACCGTAAAGA  TAAGCATTCG
351 ACCATGTGTA  AAAATCGCTG  CCGCCGTCTT  CGTTTTTATA  CAGCCACAAA
401 TCGGCGAGT  TTTTATCCGA  CATCGCGCGC  GTTGTTCCTA  TCGCCATTGC
451 CAAAACAGC  CGTTCGATT  CGGAACGTT  GCGGCGGTA  AATTGCGATT
501 CGTCGCCCA  CACTTCGGGC  AGCCAGTCGA  GCGGTGTCAA  TTTGTCCGGC
551 CCGCTCAACA  GCGCCGTCAT  AAAACCTTGA  ACCTCGTCGC  AACGCATCGT
601 GTTGCTTGT  TCGCTTTTGG  CATCCAACAA  TTCGTCACAC  CGCCGTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCTTTT  CCAATGGGTT
701 TTGCGCCCTA  TTATAGTGGA  TAAATTTAA  ATCAGGACAA  GCGCAGCAAG
751 CCGCAGACAG  TACAAATAGT  ACGGCAAGGC  GAGGCAACGC  CGTACTGGTT
801 TAAATTTAAT  CCACTATATC  GCCGCAATGC  CGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

387

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQRRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFFP  PMGFAPYYSG  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

          10      20      30      40      50      60
m136.pep  METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a136      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLPVAVDIRQCIRQLGFQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m136.pep  FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a136      FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          70      80      90     100     110     120

          130     140     150     160     170     180
m136.pep  KIAAAVFVFIQ PIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a136      KIAAAVFVFIQ PIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLRFVAQHFGQPVERCQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m136.pep  FVRPAQRRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFFPMGFAPYYRR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a136      FVRPAQRRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFFPMGFAPYYSG
          190     200     210     220     230     240

m136.pep  NAVX
a136      LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC ATCACcaATT CGATCCCGTC CTCATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCT TAAGCTACAT CCTCGGATTT ATTCTTTTTA
101 CCTTTCTCGG CAGAAAGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TGATTTTGGG
201 CGGACGCTTG GGCTATGTCC TGTTTTACAA ATTCTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTCAGCC GCAAGCACGG
351 CATCGGCTTC CTCAAACCTGA TGGACACGGT CGCGCCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTTA TCAACGGCGA ACTTTGGGGA
451 CGCATTACCG ACATTAACGC ATTTTGGGCA ATGGGCTTCC CGCAAGCGCA
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCCCTTGAAG GCATCTGCCT GTTCGCGGTC GTTTGGCTGT TTTCCAAAAA
651 ACCGCGCCCG ACCGGGCGAG CTGCCGCGCT TTTTCTCGGC GGCTACGGCG
701 TGTTCCGCTT TATTGCCGAA TTGCGCGGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTG GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

m137.seq

This corresponds to the amino acid sequence <SEO ID 532; ORF 137>:

m137.pep

1	MITHPQFDVP	LISIGPLAVR	<u>WYALS</u> YILGF	<u>ILFTFL</u> GRRR	IAOGLSVFTK
51	ESLDDFLTVA	ILGVILGGR	GVYLVFKFSD	YLAHPLDIFK	VWEGGMSFHG
101	<u>GLGV</u> YVIAIR	LFGRKHGIGF	LKMLDVAPL	VPVLGASGR	GNNFINGELWG
151	RVTDINAFWA	MGFPQARYED	AEAAAHNPLW	AEWLQQYGML	PRHPS <u>QLYQF</u>
201	<u>ALEGICLST</u> V	IWLFSKCKRS	TQVASFVFLG	GYGFRFIAE	FARQPPDYLG
251	LLTLGLSMGO	WLSVPMIVLG	IGGVFRFMKG	KQH*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESL	DDFLTWG			
g137	MIIHHQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESL	DDFLTWG			
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF		
g137	ILGVILGGRIGYVLFYKFS	DYLAHPLDIFK	VWEGGMSFHGGFLGVVIAIRL	WFSRKHGIGF		
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLVPLGLASGRIGNF	INGELWGRVTDINAFWAMGFPQARYEDAE	AAAAHNPLW			
g137	LKLMDTVAPLVPLGLASGRIGNF	INGELWGRITDINAFWAMGFPQAHYEDAE	AAAAHNPLW			
	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQQYGMLEPRHPSQLYQFALEGICL	FTVIWLFSSKORSTGOVASLFLGGYGI	FRFIAE			

```

al37.seq
1   ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCPCG TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 GCTTTCFCGG CACAAGCGCG ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTTAGCTCC TGTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG CGGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTCGGTC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGAAACTTCA TCACCGGGCA ACTTTGGGGA
451 GCGGTTACCG ATCATACAGC ATTTTGGGCA ATGGGCTTCC CGACGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCGCGT GTTTGGCTGT TCTCTAAAA
651 ACACGCGCCG ACAGGACAAG TCGCCTCACT CTTTCTCGCG GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTTGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

a137.pep

1	MITHPQFDPV	LISIGPLAVR	WYALSYILGF	ILFTFLGRRR	IAQGLSVFTK
51	ESLDDFLTWG	ILGVILGRLR	GYVLFYKFSD	YLAHPLDIFK	VWEGGMSFHG
101	FLGVVIAIIV	LFRKRGHGIF	LKLMDTVAPL	VPVLGLASRI	GNFINGELWG
151	RVTDINAFWA	MGFPOARYED	LEAAAHNPWL	AEWLQQYQML	PRHPSQLYQF
201	<u>ALEGICLFAV</u>	<u>WVLFSSKKQRP</u>	<u>TQGVASLFLG</u>	<u>GYGIFRFRIAE</u>	<u>FARQPDYDLG</u>
251	LLTLGLSMGO	WLSVPMIVLG	IGVFVRFGMK	KQH*	

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFT	KESLDDFLTWG			
a137	MITHPQFDPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFT	KESLDDFLTWG			
	10	20	30	40	50	60
m137.pep	ILGVILGGRLG	YVLFYKFS	DYLAHPLDIF	FKVWEGGMSFHGG	FLGGVIAIRLF	GGRKHGIGF
a137	ILGVILGGRLG	YVLFYKFS	DYLAHPLDIF	FKVWEGGMSFHGG	FLGGVIAIRLF	GGRKHGIGF
	70	80	90	100	110	120
m137.pep	LKLM	DTVAPL	VPLGL	SLASGR	IGNFINGEL	WG
a137	LKLM	DTVAPL	VPLGL	SLASGR	IGNFINGEL	WG
	130	140	150	160	170	180
m137.pep	RVTDINAF	WAMGFP	QARYEDAE	AAAAHN	PLW	
a137	RVTDINAF	WAMGFP	QARYEDAE	AAAAHN	PLW	
	130	140	150	160	170	180
m137.pep	AEWLQ	QYGML	PRHPS	QLYQ	FALE	GICL
a137	AEWLQ	QYGML	PRHPS	QLYQ	FALE	GICL
	190	200	210	220	230	240
m137.pep	FTVIW	LFSKK	QRSTG	QVASL	FLGGY	GIFR
a137	FTVIW	LFSKK	QRSTG	QVASL	FLGGY	GIFR

390

	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQ	PDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQHX				
a137						
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```

1  ATGGAGTTTG AAAACATTAT TTCCGCCGCGc gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACAtcc gccgGTTTTC CGGTTCCGGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTATCCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCTGA AGCcgcgcgc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```

1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIAKAKL LVDTPEQNSV
151 DTGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAQVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEBAV NGVKATHID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGGTC GCCGTCATCA
101 AATACGCGGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTATCCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCTGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTGATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```

1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

Homology with a predicted ORF from *N. gonorrhoeae*

m138/g138

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

1	ATGGAGTCTG	AAAACATTAT	TTCCGCCGCC	GACAAGGCGC	GTATCCTTGC
51	CGAAGCGCTG	CCTTACATCC	GCCGTTTTC	CGGTTGCGTC	GCGGTCAATCA
101	AATACGCGCG	CAACCGGATG	ACCGAACTTC	CCTTGAAAGA	AGGGTTTGGC
151	CGCGATGTCT	GTCTGCTGAA	CGTGTCGGC	ATTCACTCCG	TCATCGTTCA
201	CGGCGGCGGG	CGCAGATCA	ATGCGATGCT	TGAAAAAGTC	GGCAAAAAGG
251	GTGAGTTTGT	CCAAGGAATG	CGCGTTACCG	ACAAAGAGGC	GATGGATATT
301	GTCGAAATGT	TGTTGGGCGG	CGATTCCAAT	AAAGAAATCG	TGTCGATGAT
351	TAACATCATG	GGCGGACACG	CGGTCCGGCT	AAGCGGACGC	GACGACCATT
401	TCAATTAGCG	GAAGAAACTT	TTGATCGATA	CGCCCGAACA	GAATTGGCGTG
451	GACATCGGAC	AGGTCGGTAC	GGTGGAAAGC	ATCGATACCG	GTTTGGTTAA
501	AGGGCTGATA	GCAAGCTGGT	GCATTCCCGT	CGTCGCCCCC	GTCGGCGTAG
551	GTGAAAAAGG	CGAACGCTTC	AACATCAACG	CCGATTTGGT	AGCAGGCCAA
601	TTGGCGGAAG	AATTGAACGC	CGAAAACTC	TTGATGATGA	CGAATATTCG
651	CGGTGTGATG	GACAAAACGG	GCAATCTGCT	GACCAAACCT	ACGCGGAAAC
701	GGATTGATGA	ACTGATTGCC	GACGGCACGC	TGATGGCGG	TATGCTGCCG
751	AAAATCGCTT	CTGCGGTGCA	CCACGCGCTG	AACGGCGTGA	AAGCCACGCA
801	TATCATCGAC	GGCAGGCTGC	AGCAACCGCT	TTTGCTGGAA	ATCTTTTACCG
851	ATGCCGATAT	CGGTTTCGATG	ATTTTGGGCG	GTGGGGAAGA	TGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
  51  RDVVLKLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
 101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
 151  DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
 201  LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
 251  KIASAVEAAV NGVKATHIID GRVNPALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLKLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLKLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVNPALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
  51  GGCGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
 101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
 151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
 201  AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCTGGGATG
 251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
 301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
 351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
 401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAACTG
 451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAAATTACA
 501  AAAACTATAC GGCCTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
  51  NSRTIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
 101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
 151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

Computer analysis of this amino acid sequence gave the following results:

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

a139.pep
1 MRTTPTEPTK TEKPAANALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS

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```

51  NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETLQTQM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ES VGSI SFPE
151 LYGRKEHGYN ENYXKLYGVY AEGSA*

```

m139/a139 97.1% identity in 175 aa overlap

```

              10      20      30      40      50      60
m139.pep      MRTPTFFPTKTFKPTAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139           MRTPTFFPTKTFKPAAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
              10      20      30      40      50      60

              70      80      90      100     110     120
m139.pep      AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFQTMTHYKNLINLK
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139           AISYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETLQTMTHXKNLINLK
              70      80      90      100     110     120

              130     140     150     160     170
m139.pep      PAIEAGYTGRGVEVGIVDTGESVGSISFPELYGRKEHGYNENYEKLYGVYAEGSAX
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a139           PAIEAGYTGRGVEVGIVDTGESVGSISFPELYGRKEHGYNENYXKLYGVYAEGSAX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

```

g140.seq
1   Atgtcggcac gCGGCAAGGG GGCAGgctat ctcAACAGTA CCGGACGACa
51  TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCAGGATTAT TCTTCTTCA
101 AAAATATCAA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCACTGAAGG CGACACGCCG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACAITCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAGCTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGTGCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCTACGG CGCACAACCT
401 TCCGCACAGC GGCAGCCGTA CAGCATGCGA ATACCGCCGA CGGCGTACGc
451 aTCTTcaaca GTCTCGCCGC TAccgTCTat GccgACAGTG CCGCCGCCCA
501 TGccgATATG CAGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT CGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 TATCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATAGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGTGG GCGATATCGG
801 CATCTCAAAA GGCCTGTTCT CctaCGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGATGAA TATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG TGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTTGAAGGCG GTCTGCGCCA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCagt GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACAC TGGTGCGACT CGCGGTCTG AAAGTGTGCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTCTG CGACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CGCGGTAAAG GCGGCTTTA CCGGCGCGGC TGCAGCAACC
1201 GGCAAGACGG GTGCACGCAA TATGCCGCAC ACCCGCCGGG TTGCCGGTCT
1251 GGGGGTGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACACCGG TTCCAAACAG TACGCAACC ACAGCGGACA AATCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

```

g140.pep
1   MSARGKGAGY LNSTGRHVPF LSAAKIGQDY SFFKNIKTDG GLLASLDSVE
51  KTAGSEGDTP SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAVAD RTDMPGIRLR RTTFRTAAAV QHANTADGVR
151 IFNSLAATVY ADSAAHADMD QGRRKAVSD GLDHNGTGLR VIAQTQDDGG
201 TWEQGGVEGK MRGSTQTIGI AAKTGENTTA AATLGIGRST WSENSANAKT

```

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```

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
451 GYRF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

```

m140.seq
1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
51 TGTTCCTTTC CTGAGTGCCG CCAAATCCGG GCAGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCGAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCAGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCAAAA CCGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGACG CTACAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT
1051 GAAGGCACGC TGGTCGGAAT CGCGGCTCTG AAGCTGTCCG AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGCGCGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCAGCACA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
1251 GGGCGCGGAT GTCGAATTTC GCAACGCTG GAACGCTTG GCACGTTACA
1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

```

m140.pep
1 MSARGKGAGY LNSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVVRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNSLAATVY ADSTAHAADM QGRLKAVSD GLDHNGTGLR VIAQTQDDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

```

m140/g140
10 20 30 40 50 60
m140.pep MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g140 MSARGKGAGYLNSTGRRHVPFLSAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTP
10 20 30 40 50 60
70 80 90 100 110 120

```

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m140.pep	SYVVRGNAARTASAAAH SAPAGLK HAVEEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAH SAPAGLK HAVEEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140.pep	RTDMPGIRPYGATPRAAAVQHANAADGVRI FNSLAATVYADSTAAHADMQGRRLLKAVSD
g140	RTDMPGIRLRRTTFR TAAVQHANTADGVRI FNSLAATVYADSAAHADMQGRRLLKAVSD
	130 140 150 160 170 180
m140.pep	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLIGRST
	190 200 210 220 230 240
m140.pep	WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140.pep	MQLGALGGVNVPPAATGDLTVEGGLRVDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNVPPAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140.pep	KLSQPLSDKAVLFATAGVERDLNGRDYTEVTGGFTGATAATGKTGARNMPHRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAAATGKTGARNMPHRRVAGLGVD
	370 380 390 400 410 420
m140.pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAACACAGC CGTAGAACAG GCGGCAGCA ATCTGGA AAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCCA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCAACA GGACGGTGG
601 ACGTGGGAAC AGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCAAAA CCGGCGAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAA GGCCTGTTCT CCTACGGACG CTACAAAAC AGCATCAGCC
851 GCAGCACC GG TCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
901 ATGACAGCTG GCGCACTGG CGGTGTCAAC GTTCCGTTG CCGCAACGGG

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951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AACAGGATG
1001 CATTCCGCCA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGCTCTG AAGCTGTCTG AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCTGG TTCCGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTT GCACGTTACA
1301 GCTACGCCGG TTCCAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
1 MSAGGKGAGY LNRTGQRPVF LSAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDITL SYYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLG GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
a140	MSAGGKGAGYLNRTGQRPVFLSAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
a140	SYYVRRGNAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLAATVYADSTAAHADMQGRRLKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
a140	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
a140	WSENSANAKTDSISLFAGIRHDAGDIGYLGKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
a140	MQLGALGGVNPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGLTVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

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	370	380	390	400	410	420
	430	440	450			
m140.pcp	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAaccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGCGGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TCGCGAGGCC TTCTTTGGGT
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT AC CGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACGCGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTTga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTtt gGCAATATC TCGTCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAG GCACACGGCG CGATGCGGCG ATTGCTAAAA
751 GATGCGATTA AGCCCAATT GGTGCAAACC ATCGAAGGCA CTCGCGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACC GAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACC GCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGCGGG
1251 CCGGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTCGG TTTCCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTT CAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCGGCG GCGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCGT GCCGAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pep

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFQVKGGA GGGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLE KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAID NQPNNFGFAY DVELGIDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPCMAK TQYSLSDNAK
501 LLGCPGEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVIHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACATG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGCGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TCGCGGAACC TTCTCTGGGG
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCGGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCCTTCGGC CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAATGCCC
951 CCTTGCCCGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGCGCGC GTGGAACGCG CCAACCTCGG CGAAGAAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CCGCGCGGAT TTGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGG TGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCGGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGT CCGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  POKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFGVKGGAA GGYAQVLPD EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNII DGMKPKVDGM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIDDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

	10	20	30	40	50	60
m141.pep	MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKLPOKQGRLLIV					
	:					
g141	MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKLPOKQGRLLIV					
	10	20	30	40	50	60

400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
	130	140	150	160	170	180
	190	200	210	220	230	240
m141.pep	GMGKPDVGVMRPGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPPVYAKDLK					
g141	GMGKPDVGVMRPGFDITVASEVMAVFCLAKDISDLKERFGNILVAYAKDGSPPVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKCRLAGLKPDAAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAEIAMIEKACAEHGVESLTVWKGKGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSADAEIAMIEKACAEHGVESLTVWKGKGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSABASAEIASLEKLG					
g141	LARKVVNAIDNQNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSABASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

```

a141.seq
1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GCGGGGCGAA GGTAACCA CCGTAACCAT CGGTTTGGCG SACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGGCGGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAACTG CTGCGCGCA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCAAA CGCGTGCTGT GCGGCGCGT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAAC ATCGAAGGCA CGCCCGCCTT
801 CGTGACACGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGTTCGCGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTGCGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGCG GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGAAAAAGG TTGCCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGCGCGCGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPVGVDM RPDGEDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAIE SQTNNFGFAY JVELGKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

m141.pep      10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKLPQKQGRLLIV
|||||:|||||
a141          10      20      30      40      50      60
MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKLPQKQGRLLIV

m141.pep      70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGGAAGGGYAQVLPM
|||||:|||||
a141          70      80      90     100     110     120
TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGGAAGGGYAQVLPM

m141.pep     130     140     150     160     170     180
EDINLHFTGDFHGAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
|||||:|||||
a141         130     140     150     160     170     180
EDINLHFTGDFHGAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID

```

402

m141.pep	190	200	210	220	230	240
	GMGKPV DGVMRPDGFDITVASEVMAVFC LAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPV DGVMRPDGFDITVASEVMAVFC LAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAAL LKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAAL LKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGA EKFCDIKCR LAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFCDIKCR LAGLKPDAAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACA EHGVEVSLTEVWGKG GAGGAD					
a141	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACA EHGVEVSLTEVWGKG GAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	L DKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNM MKMPGLPKV					
a141	L DKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNM MKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

g142.seq

```

1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAATGTTC
151 GGCAACATCC TGATGTTCGT CCGCCAGCAT ATTGATGCAG AGCTGCCGT
201 TTTCCGACAG GATeggaATG AttegCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

g142.pep

```

1  MRADFMFADN MPVQVRORAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTPVY AQHHGRRLVG NRRNRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQOF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCCGCGAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCTTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCcC ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
1  MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
51  GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQOF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142

      10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVVGKPLFGRQAGQPGKMFNGNILMFVRQH
          10      20      30      40      50      60

      70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      IDAEAAVFRQDRNDSRTPVYAHGRRLVGNRRNRHCAVTPCRTVCRDDMNACRTGCH
          70      80      90      100     110     120

      130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g142      RITERSLKSFQIRHFSPLNRPPLYKNAAHKASPHVQQFX
          130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCCGCGAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCTTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCGGACAT
501 TTCCGCGCGT TACGGC3TAT TACGAGTTCA ACGCATCCTC GATTTTGGCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAGC
601 TTCTCGATA GCGTCGTAAC GTCGTCCAC TTCTTCGCGG ATTTCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACAG TCGTTGGTCG
701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTTCAG GCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAATGCA CGCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVR NRRNRRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
 151 APPMCSSSDS KSRRSDISAR YGVLVRQIRL DFGKFCQQVF KQHFLLAAQH
 201 FLDSVVTLVH FFADFLIQLL ALGSQKQNT SLVVGGRFQAD NQTRFFKAGQ
 251 DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PELLIGNIRL IQNRPELGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRECNVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRECNVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPYKNAAHKASPHVQQFX					
a142	RITERSLKSFLOIRHFSPLNCPYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQIRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a142	DFGKFCQQVFKQHFLLAAQHFLDSVVTLVHFFADFLIQLLALGSQKQNTSLVVGGRFQAD					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAAG
 51 CTCGCAGATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGTTT TTTATCCTG CCGCGCTGG CCGGGATGCT GGTTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCCTTGTCCT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CCGCGATATG GTCAACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAAA GTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGTTACTG ATTATTACCA GTGCGTTTAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTTCTG CTGGTTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTCTG
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
 851 ACGGCGTTTT GCGCGCGGTG TAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGCGCGGTT ATTTCCGCTG
 951 TTTGGCTTTG GCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
 1001 AATACGCACT CATCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTTGGGCC AACGCTTGT CGGGCAAAACA
 1101 CATGGATACT TATTTGGGCC TGTttaacgg ctctgtCTGT ATGCGcgcaaa
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

405

1201 CAGGCAACCA TGTTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
 1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGD VNEEQKSYAY GIQSFLANTD
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFVTV TPVQFFCWFA
 251 FRYMWYSAG AIAENVHHTT DASSVGHQEA GNRYGVLAIV *SVAAVICSF
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG
 351 IITYPLTIVA NALSGKHMGT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
 151 ATTGTGCGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCGG
 201 CCGTCTGCCG TATCTGCTTT ATGGCAGCGT GATTGCGGTT ATTGTGATGA
 251 TTTTGATGCC GAACCTCGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCTTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTGCTCAAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCACGAGG
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTTCTTAGC AAATACGGGC
 451 GCGGTCGTGG CGGCGATTCT GCCGTTGTG TTTGCGTATA TCGGTTTGCG
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGCTC GTGGCGTTTT
 551 ATGTGGGTGC GCGGTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC
 751 TTCCAATATA TGTGGACTTA CTCGCGAGGC GCGATTGCGG AAAACGCTCTG
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTT
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGCGGGGTT ATTTCGGCTG
 951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTCTTC ATCGGCAACC
 1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
 1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAAA
 1151 TCGTCGCTTC GCTGTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
 1201 CAGGCCACTA TGTCTTGGT AGGGGCGGTC GTCCTGCTGC TGGCGCGGTT
 1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
 1 MLSFGELGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGD VNEEQKGYAY GIQSFLANTG
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFVTV TLVQFFCWFA
 251 FQYMWYSAG AIAENVHHTT DASSVGYQEA GNWYGVLAIV QSVAAVICSF
 301 VLAQVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
 401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

406

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKGVVPQTIV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGKGVVPQTIV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFAFYMWYTSAGAIENVWHTTDASSVGYQEAGNRYGVLAQVAVVICSF
g143	TPVQFFCWFAFRYMWYTSAGAIENVWHTTDASSVGHQEAGNRYGVLAQVAVVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNQYALVLSYTLIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMGLQATMFLVGGVLLLGAFSVC
g143	NALSGKHMDTYLGLFNGSVCMQIVASLLSFVLFPMGLGHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

a143.seq

1	ATGCTCAGTT	TCGGCTTTCT	CGGCGTTCAG	ACGGCCTTTA	CCCTGCAAAG
51	CTCGCAGATG	AGCCGCATCT	TCCAGACGCT	CGGTGCCGAT	CCGCACAGCC
101	TCGGCTGGTT	CTTTATCCTG	CCGCCGCTGG	CGGGGATGCT	GGTGCAGCCG
151	ATTGTGCGCC	ATTACTCCGA	CCGCACTTGG	AAGCCGCGTT	TGGGCGGCCG
201	CCGTCTGCCG	TATCTGCTTT	ATGGCACGCT	GATTGCGGTT	ATTGTGATGA
251	TTTTGATGCC	GAACTOGGGC	AGCTTCGGTT	TCGGCTATGC	GTCGCTGGCG
301	GCTTTGTCTG	TCGGCGCGCT	GATGATTGCG	CTGTTAGACG	TGTCGTCAAA
351	TATGGCGATG	CAGCGTTTAA	AGATGATGGT	CGGCGACATG	GTCAACGAGG
401	AGCAGAAAGG	CTACGCCTAC	GGGATTCAAA	GTTTCTTAGC	GAATACGGGC
451	GCGGTCTGTT	GCGCGATTCT	GCCGTTTGTG	TTTGCCTATA	TCGGTTTGGC
501	GAACACCGCC	GAGAAAGGCG	TTGTGCCGCA	GACCGTGGTC	GTGGCGTTTT
551	ATGTGGGTGC	GCGGTGCTG	GTGATTACCA	GCGCGTTTAC	GATTTTCAAA
601	GTGAAGGAAT	ACAATCCGGA	AACCTACGCC	CGTTACCACG	GCATCGATGT
651	CGCCGCGAAT	CAGGAAAAAG	CCAACTGGAT	CGAACTCTTG	AAAACCGCGC
701	CTAAGGCGTT	TTGGACGGTT	ACTTTGGTGC	AATTCTTCTG	CTGGTTTCGCC

```

751 TTCCAAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
851 ACGGCGTTTT GCGGCGCGTG CAGTCGGTTG CGGCGGTGAT TTGTTCTGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTTCGGCTG
951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTACGG CTCTATCTGT ATGCCGCAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCCTGGT AGGGGCGCTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
  1  MLSFGFLGVQ TAFTLOSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
 51  IVGHYSDRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQGYAY GIQSFLANTG
151 AVVAAILPEV FAYIGLANTA EKGVPVQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYTSAG AIAENVWHTT DASSVGYPEA GNWYGVLAIV QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGFLNGSIC MPQIVASLLS FVLFPMGLGL
401 QATMFLVGGV VLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	:					
	10	20	30	40	50	60
m143.pep	70	80	90	100	110	120
a143	KPRLGRRRLPYLLYGTLIIVIMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	130	140	150	160	170	180
a143	QPFKMMVGDMVNEEQGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV					
	130	140	150	160	170	180
m143.pep	190	200	210	220	230	240
a143	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	250	260	270	280	290	300
a143	TLVQFFCWFAFQYMWYTSAGIAENVWHTTDASSVGYPEAGNWKYGVLAIVQSVAAVICSF					
	250	260	270	280	290	300
m143.pep	310	320	330	340	350	360
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	370	380	390	400	410	420
a143	NALSGKHMGTYLGFLNGSICMPQIVASLLSFVLFPMGLGLQATMFLVGGVVLLGAFSVF					

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a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLOATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGT3C
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTG GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 TGC CGGCGT T CGACATCAAC GGTAGGACTT ACCGCGTGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCcgtTT
351 CAACCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTGGatAtT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGC CGGACAT
551 ATTCGGCCG ATGCCGAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFVSLADGV
51  RENPVVSFDD AASYADNPFF INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGyFLPLGRG RPAyRyLSRH
151 RARRHGVRPD AAHLAAGRG PARCGSAYSA GRtySGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTG GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTG CGGCGT T CGACATCAAC GGCAGGACTT ACCGCGTGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCGTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGg ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAaCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFF INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGFGyFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAHLL AAGRGPARG SAYSAGRtyA
201 GRCRK TARLN GFRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFQFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
g144	AAD-----GRRLSQRFQ--YFLPLGRGRPAYRYSRHRARRHGVRPDAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARGSAYSAGRTYAGRCRKRTARLNGFRRPRSIX					
g144	AAGRGPARGSAYSAGRTYSGRCRKRTARLNGFRRPRSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

a144.seq

1	ATGAGCGATA	CCCCCGCTAC	CCGCGATTTC	GGCCTGATCG	ACGGGCGTGC
51	CGTAACCGGC	TATGTGCTGT	CCAACCGGCG	TGGTACGCGT	GTCTGCGTGC
101	TGGACTTGGG	CGGGATTGTG	CAGGAATTTT	CCGTTTGGC	AGACGGCGTG
151	CGCGAAAACC	TCGTGGTGTC	GTTGACGAT	GCGGCTTCCT	ATGCGGACAA
201	TCCGTTTCAG	ATTAACAAGC	AGATAGGGCG	CGTGGCCGGA	CGCATCCGCG
251	GTGCGGCGTT	CGACATCAAC	GGCAGGACTT	ACCGCGTGGA	GGCCAACGAA
301	GGCAGGAACG	CGCTGCACGG	CGGTTGCGAC	GGGCTGGCCG	TTACCCGTTT
351	CAACGCGGTG	GCGGCAGACG	GCCGTTCGGT	GGTGCTGCGC	AGCCGCGCTG.
401	CAACAGTCGG	CCGACGGTTA	TCCCAACGAT	TTGGATTGG	ATATTTCTTA
451	CCGCTTGGAC	GAGGACGACC	GGCTTACCGT	TACCTATCGC	GCCACCGCGC
501	TCGGCGACAC	GGTGTTCGAC	CCGACGCTGC	ACATTTACTG	GCGGCTGGAC
551	GCGGGCGCTG	ACGATGCGGT	TCTGCATATT	CCGCAGGGCG	GACATATTCC
601	GGCCGATGCC	GAAAACTGC	CCGTCTCAAC	GGTTTCAGAC	GACCTCGAAG
651	TATTTGA				

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

a144.pep

1	MSDTPATRDF	GLIDGRAVTG	YVLSNRRGTR	VCVLDLGGIV	QEFSVLADGV
51	RENLVVSFDD	AASYADNPFQ	INKQIGRVAG	RIRGAADFID	GRTYRVEANE
101	GRNALHGGSH	GLAVTRFNAV	AADGRSVVLR	SRLXTVGRR	SQRFQFGYFL
151	PLGRGRPAYR	YLSRHRARRH	CVRPDAHLL	AAGRGPARG	SAYSAGRTYS
201	GRCKRTARLN	GFRRPRSI*			

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					

410

```

|||||
a144      AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70      80      90      100      110      120

              130      140      150      160      170      180
m144.pep  AADGRSVVLRSLRATVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLRSLRXTVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAHLL
              130      140      150      160      170      180

              190      200      210      219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
              190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51  AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCCGACT GTCCGTCCCG CGCcttTGA GGCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TCGCGGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTATGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLQ VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPFEARG
51  KHVERRRQDK DTDSFRQ RVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNAGT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51  AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCCTT CGACAGCCTC
101 CTTTGGATAA CTCCCCGACT GTCCGTCCCG CGTCCGTGA GGCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCCG CGTATTCCAA AAAAGCTTCC TCGCGGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLDFMPCL RQPPLDNFPT VRPASVEARG
51  KYVERRRQDK DADGFGQ RVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNAGT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

411

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVV	IDHDKVKQYGLLD	FMPCLRQPPLDN	FPTVRPASVEARGKY	VERRRQDK	
g146	MKQIPLRLLOVV	IDHDKVEQYGLFDE	FMPCLRQPPLDN	FPTVRPAPFEARGKH	VERRRQDK	
	10	20	30	40	50	60
	70	80	90	100	110	120
m146.pep	DADGFGQVRVAN	LRRALNVDFQNHVI	ACRRQRIHTLRACA	VIVAKYVG	VFQKSFLRDKRLK	
g146	DTDSFRQVRVAN	LRRALNVDFQNHVI	ACRRQRIHALRACA	VIVAEYVC	VFQKSLLRDKRFK	
	70	80	90	100	110	120
	130	140	150	160	170	180
m146.pep	LFFGNKVIMYAV	CFATRRARRVRH	NAQTMVVCQQPRH	QGFARAGSGRNDK	DVAFSIS	
g146	LFFGNKVIMYAV	CFATRRARRMRH	NAQTMVVCQQPRH	QGFARAGSGRNDK	DVAFSIS	
	130	140	150	160	170	180
	190	200	210			
m146.pep	GHIFYLYIFQPI	VSQWTPSFLFADA	HILPLLFX			
g146	GHIFYLYIFQPI	VSQRTPYFIFADA	HILPLLFX			
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

a146.seq

1	ATGGCGCAAA	TCCTCCTCCG	CCCGCGCCAA	GTCATCATTG	ACCACGACAA
51	AATCGAACAA	TACGGACTGT	TCGATTTCAT	GCCTTGCCCT	CGACAGCCTC
101	CTTTGGATAA	CTTCCCGACT	GTCCGTCCCG	CGTCCGTTGA	GACGCGCAGC
151	AAGCACATCG	AAAGACGGCG	GCAGGATAAA	GATGCCGACG	GCTTCGGGCA
201	GCGCATCTCG	AACCTGAGCC	GCGCCCTGAA	CGTCGATTTC	CAAAATCACG
251	TCATAACCTG	CCGCCGCCAA	CGCATTACAA	CCCTCCGCGC	TTGTGCCGTA
301	ATAGTTGCCG	AACACGTCCG	CGTATTCCAA	AAAAGCCTCC	TGCGCGATAA
351	GCGACTCAAA	CTCTTCTTTG	GAAACAAAGT	GATAATGTAC	GCCGTTTGCT
401	TCGCCTTCAC	GCGGCGGACG	CGTCGTGTGC	GACACGGAAA	CGCGCAAACC
451	GTTATGGTTT	GCCAAACAGC	GCGACACCAG	CGTGGTTTTG	CCCGTGCCCG
501	AAGCGGCCGA	AATGATAAAG	ATGTTGCCTT	TTGATAAGC	GGACATATTT
551	TTTACCTGTA	TATTTTCCAG	CCGATTGTAT	CACAACGGAC	ACCCGGTTTC
601	CTATTTGCCG	ATGCCCATAT	TTTGCCGCTA	TTGTTTTGA	

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

a146.pep

1	MAQILLRPRQ	VIIDHEKIEQ	YGLFDEMPCL	RQPPLDNFPT	VRPASVETR
51	KHIERRRQDK	DADGFGQRI	NLSRALNVDF	QNHVITCRQ	RIHTLRACAV
101	IVAHEVVRVQ	KSLLRDKRLK	LFFGNKVIMY	AVCFATRRRT	RRVRHGNAQT
151	VMVCQQPRHQ	RGFARAGSGR	NDKDVAFSIS	GHIFYLYIFQ	PIVSQRTPGF
201	LFADAHILPL	LF*			

m146/a146 90.6% identity in 212 aa overlap

	10	20	30	40	50	60
m146.pep	MAQILLRSRQVV	IDHDKVKQYGLLD	FMPCLRQPPLDN	FPTVRPASVEARGKY	VERRRQDK	
a146	MAQILLRPRQVI	IDHDKIEQYGLFDE	FMPCLRQPPLDN	FPTVRPASVETR	RSKHIERRRQDK	
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m146.pep  DADGFGQVRANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSLRDKRLK
          |||||::|| |||||::|||::|||::|||::|||::|||::|||::|||::|||
a146      DADGFGQVRISNLSRALNVDFQNHVITCRRQRIHTLRACAVIVAEHVRVVFQKSLRDKRLK
          70      80      90      100     110     120

          130     140     150     160     170     180
m146.pep  LFFGNKVIMYAVCFAETRRARRVRHGNQVTVMVCQPRHQRGFARAGSGRNDKDVAFSIS
          |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
a146      LFFGNKVIMYAVCFAETRRARRVRHGNQVTVMVCQPRHQRGFARAGSGRNDKDVAFSIS
          130     140     150     160     170     180

          190     200     210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLEFX
          |||||::|||::|||::|||::|||::|||::|||::|||
a146      GHIFYLYIFQPIVSQRTPGFLFADAHILPLLEFX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC AACTCAAAC CCATTGTTTT
51 ATCAATTCTT TTAATCAACA CACCCTCCT CGCACAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTCGCC AAAAAAGCCG CAACTTGGGC GACGCTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAGTAT TGAACCATCA
351 CGGCGAAACG GGCATATGCG CGGACTTTTC TCCCGATCAC GCCATTATGG
401 TAGATACCGC CTTGTCGCAA CAGGTTGAAA TCCTGCGCGG GCCGTTACG
451 CTCTTGTAACA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLK?IVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51 RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTTG GAAACGGTCA GCGTCGTCGG
51 CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGACACT TCGACCGCCT
101 CCGACAAAAT CATCTCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GCGGACGCTT TAGACGCGT ACCGGGCATC CACGCTTCGC AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATTT TTCGCCCAGT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGICG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTTGTATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGCGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTCT CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GCGGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGGCC ACGAATACGA TGATTGCCAC
751 GCGGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGGAAGCAA CCGTTCCTCG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG CCGATGCAGT CGAAAACCTT
1051 TTTAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

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1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCAGAC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACCTACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC GACTTCTAC GCGCGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCGGG
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCACCGCTC CTTTCATCGC ACAGGACGAC CAAAATGCC
1901 CCCGTGTTCC GGTGCGCGC CTGGCTTCC ACCTGAAAGC CTCGTGACC
1951 GACCGTATCG ATGCCAATTG GGACTACTAC CGCGTGTTCG CCCAAACAA
2001 ACTCGCCGCG TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG
2051 GCGCAACTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGGCG GTGAACGTGA
2201 AGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNEVL HTEGLYRKSQ DYAVPRYRNL
201 KRLPDSHADS QTSIGLSWV GEKGFIGVAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GREWIDLNRK RYELRAEWKQ PFPGFALRV HLNRRNDYRD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGR LKSGWGVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHSYFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IURENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPPQHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKRSSNN IELALGYEGD RWQYNLALYR NRGNYIYAO
551 TLNDGRGPKS IEDDSEMKL VRYNQSADFY GAEGEYFKP TPRYRIGVSG
601 DYVRGRLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

                                10      20      30
m147.pep                      PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
                                | : ||||| ||||| ||||| ||||| |||||
g147                          MRREAKMAQITLKPVL SILLINTPLLAQA HETEQSVGLETVSVVGKSR PRATSGLLHTS
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m147.pep                      TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g147                          TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m147.pep                      GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKI PEKMPENGVS
                                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g147                          GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNK NPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```

a147.seq
1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCAAGCG CATGGAAC TG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTC CG
151 CGCGCCACTT CGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAATCAT
201 CAGCGCGGAC ACCTTGCAGC AAAAAGCCGT CAACTTGGGT GATGCTTAG
251 ACGGCGTACC GGGCATTCAAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGCGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGATCA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAAACGG CGTATCGGGC GAACCTGGAT
551 TCGGTTTGAG CAGCGGCAAT CTGGAAAAAC TCACGTCGGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACCT TGTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGG
1001 TAGACCTGCG CAACAAACGC TACGAATCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGGTTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACCAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACAGCTT
1351 GAAGCGGCGC TACGCGTGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGCGGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAAACGACG
1751 GAGCGGCGCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCGGTCTGAA AAACCTGCCT TCCCTACCGG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTTCCGGC
2001 TCGCGCCTC GCGTCCACC TGAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTTGGA CTACTACGCG GTGTTGCGCC AAAACAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```

a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVRGOTGRR IKVLNHGET GDMADFSPDH AIMVDSALSQ OVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSF ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNLK RLPDSDHDSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTONARIE LRHQPIGRLE
401 GSWGVQYLGQ KSSALSATSE AVKQPMLLDN KVQHSYFEGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYYNHPL PDLGAHRQTA RSFALSGNWX
501 FTPQHKLST ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

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415

601 YNQSADDFYG AEGEIYFKPT PRYRIGVSGD YVRGRLLNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLOYR VFAQNKLARY
701 ETRTPGHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSRPRATSGLLHTS	
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTS					
	10	20	30	40	50	60
m147.pep		40	50	60	70	80
	TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET					
a147	TASDKIISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET					
	70	80	90	100	110	120
m147.pep		100	110	120	130	140
	GDMADFS	PDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
	130	140	150	160	170	180
m147.pep		160	170	180	190	200
	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ					
a147	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ					
	190	200	210	220	230	240
m147.pep		220	230	240	250	260
	TGSIGLSWVGKEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL				
a147	TGSIGLSWVGKEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHL				
	250	260	270	280	290	300
m147.pep		280	290	300	310	320
	LTEEDIDYDNPGLS	CGFHDDDAHAHNTSGRPWIDLNRKRYELRAEWKQFFPGFEALRVH				
a147	LTEEDIDYDNPGLS	CGFHDDDAHAHNTSGRPWIDLNRKRYELRAEWKQFFPGFEALRVH				
	310	320	330	340	350	360
m147.pep		340	350	360	370	380
	LNRNDYRHDEKAGDAVENFFN	QTNARIELRHQPIGRLKGSWG	VQYLQKSSALSATSE			
a147	LNRNDYRHDEKAGDAVENFFN	QTNARIELRHQPIGRLKGSWG	VQYLQKSSALSATSE			
	370	380	390	400	410	420
m147.pep		400	410	420	430	440
	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYNHNPL				
a147	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHNPL				
	430	440	450	460	470	480
m147.pep		460	470	480	490	500
	PDLGAHRQTARSFALSGN	WYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGN	WYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep		520	530	540	550	560
	HLNKERSNNIELALGYEG	DRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEM				
a147	HLNKERSNNIELALGYEG	DRWQYNLALYRNRFNGNYIYAQTLNDGRGPKSIEDDSEM				
	520	530	540	550	560	570

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	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPPIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPOMGRSETGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPOMGRSETGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1   ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGctgg ttcaTCCCGA
51  AgctATgagt gtcggcgCGC TTGccgAcaa AATCCGCAAA AtcgaAAact
101 gGCCGCAAAA AGgcaTCTTA TTCCACGACA TCACGCCCGT CCTGCAAAGT
151 GCGGAATACT TCCGCCTTTT GGTGATTTG CTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGCTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGtcg gctTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTAcg cgcTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGa tgccgTCAAA CCCGTTTCGC
401 GCGTCTGCT GGTGATGAT TTGGTTGCCA CGGGCGGCAC AATGCTTGCC
451 GGGTGGAAAC TGATCGCAA ACTCGGCGGG GAAATGTGCG AAgcgcgcgC
501 CATTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGCGCAAGTC
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGCAT GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1   MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK
101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK PGSRVLLVDD LVATGGTMLA
151 GLELIRKLGG EIVEAAAIL EFTDLQGGKNI RASGAPLFTL LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1   ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGCTGG TTCATCCCGA
51  AGCTATGAGT GTCGCGCGCG TTGCCGACAA AATCCGCAAA ATCGAAAAC
101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTTCAAAGC
151 GCGGAATACT TCCGCCTTTT GGTGATTTA TTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGTTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGTCG GTTTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA
351 CGGGGAAGCT GCGGTGGAAA TCCACACCGA TGCCGTCAAA CTCGGTTTCGC
401 GCGTCTGCT GGTGATGAT TTGATTGCCA CGGGCGGCAC GATGCTTGCC
451 GGAAGGAAAC TGATCGCAA ACTCGGCGGA GAAATGTGCG AAGCCGCCGC
501 CATTTGGAA TTTACCGACC TTCAAGGCGG CAAGAATATC CGTGCAAGCG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGTAT GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1   MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKGIL FHDITPVLQS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK

```

101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCCGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTCCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCGGCAA	ACTCGGCGGG	GAAATGTGCG	AAGCCGCCGC
501	CATTTTGAA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGGCCCTT	ATTACCCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVGFPVIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

418

```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148      LVYRYMDQKIDIVAGLDARGFIIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
          70      80      90      100     110     120

          130      140      150      160      170      180
m148.pep  AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a148      AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
          130      140      150      160      170      180

          190      200
m148.pep  RASGAPLFTLLQNEGCMKGX
          ||||||||||||||||||
a148      RASGAPLFTLLQNEGCMKGX
          190      200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1  ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGA AAAAC
101 AAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaagA actGtACgca
301 caccggaAGC ACgtcgccac CAACACCTTT GAagtcggca acaaACACCT
351 CAACAAAGAG Cgttccaaca atatcgAACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGAtT CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCCAAAT CCATCgaaga
501 cgacagcgga ATGaagcTCG TGCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACggcgcgga aggcgaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCTT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCcettcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCGCATT ccggtcGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGT
801 CGCCCAAAAC AAATCGCCC GCTACGAAAC GCGTACGCCG GGACACCATA
851 TGCTCAACCT CGGTGCAAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGTTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAc gGGCCGAGC TTtgccgGCG
1001 gcgtaAACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1  MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWRQYNL AAYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVS GDYVRGR LKNLPSLFG R EDPYGRPF I AQADQNAPRI PAARLGFHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1  ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATCTG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGA AAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGCAAAAC ACgtcgccac CAACACCTTT GAAGTCGGCA ACAAAACCTT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```

m149.pep

1	MLLDNKVQHY	SFFGVEQANW	DNFTLEGGVR	VEKQKASIQQ	DKALIDRENY
51	YHNPLPDLGA	HQGTARSFLP	SGNWYFTPOH	KLSLTASHQE	RLPSTQBELY
101	HQAQHVATNTF	EVQGNKHLNKE	RNSNIELAGH	YEGDRWQYNL	ALYRNRFQYNA
151	IYKHTLNDLGR	GPKSIEDDSE	MCLVRYNQSQ	ADFYAAGEBI	YFKPTPRYRI
201	GVSQDGYVRGR	LKNLPSLPGR	EDAYGNRPFI	AQDDONAPRV	PAARLGPHLK
251	ASLTDRIDAN	LDYRYVFAQN	KLARYETRTP	GHHMLNLGAN	YRRNTRYGEW
301	NWYVKADNLL	NOSVYAHSSF	LSDTPOMGRS	FTGGVNGFK*	

Homology with a predicted ORF from *N.gonorrhoeae*

from *N. gonorrhoeae*:

m149/g149

[illegible]

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
1 ATGTCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTTCG GTGTAGAACA
51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAAACTAC
151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA CGCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCACAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
451 ATTTACGCC AAACCTTAAA CGACGGACGC GGCCCAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGG GAAGACGCCT ACGCAACCG CCCACTCATT GCCCAAGCCG
701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCAAAAC AAACCTCGCC GCTACGAAAC GCGCACGCCG GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTACGCCCA
951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51 YNHPLPDLGA HRQTARFAL SGNWYFTPOH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR ZDAYGNRPLI AQADONAPRV PAARLGVHLK
251 ASLTDRIAN LDYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

	10	20	30	40	50	60
m149.pep	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYNHPLPDLGA					
a149	MLLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGA					
	10	20	30	40	50	60
m149.pep	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
a149	HRQTARFALSGNWYFTPOHKLSTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	130	140	150	160	170	180
m149.pep	RSNNIELALCYEGDRWQYNLALYRNRFNGNYIAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
a149	RSNNIELALCYEGDRWQYNLALYRNRFNGNYIAQTLNDGRGPKSIEDDSEMMLVRYNQSG					
	190	200	210	220	230	240
m149.pep	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPFGREDAYGNRPFIAQDDONAPRV					
a149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRRLKNLPSLPFGREDAYGNRPFIAQDDONAPRV					
	250	260	270	280	290	300
m149.pep	PAARLGFLKASLTDRIANLDYRVFAQNKLARYETRTPGHMLNLGANYYRRNTRYGEW					

g149-1.seq

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

g149-1.pap

1	MAQITLKPIV	LSILLINTPL	IQAQHETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTRSDKH	ISGDTLRQRA	VNLGDALDVG	PGIHAQOYGG	GASAPVILYGG
101	TGRRIRVLNI	HGETGDMADF	SPDHANIMDT	ALSQOQEILR	GPVTVLLYSSG
151	NVAGLVADVAD	GRIPEKMPEN	GVSGEAGLRL	SSGNLEKLTG	AGINTGLGKN
201	FVLHTEGLYR	KSGDYAVPRY	RNLKRLPDSH	ADSQTSGISL	SWVGEGKFTG
251	AAYSDDRDRY	GLPAHSHEYD	THCKNIWIQK	SILINKRYLQI	YPHLLHTFII
301	DYDNPGCLSG	FHDGGGAHAH	DHNGPWIIDL	RNKRYELRAE	WKQPFPGFEA

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLAGH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPGKRPFIA
651 QADQNAPIRP AARLGFHLKT SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.00q

```

1 ATGGCACAAA CTACACTCAA ACCCATTTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGCG
101 AAACGGTCAG CGTCGTCCGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTC TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCCG
401 AACAGGTGCA AATCCTGCGC GGGCCSGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAGAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC GCCAATCTGA AACGCTGCC CGACAGCCAC GCGGATTCCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTACGCTACA GCGACCGTCG CGACCAATAT GGTCTGCTCG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAAACGTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATATATG
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACCT CCGTGCCGAA TGAAGCAAC CGTTCCCGCG TTTTGAAGCC
1051 CTGGCGGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCACTC GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTCTGTCTG AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAACCTGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTACT AACCAACCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCGGCTCATT CGCACTTTTC GGCAACTGGT ATTTACGACC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAACACG TCGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAATG AAGCTCGTGC GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGGCG ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCCTAC GCAACCGTCC TTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAACTAC CGCGCAATA CGCGCTATGG
2151 CGAGTGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAGC CAGCTTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGGCGCGC TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALOGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAINVDT ALSQOQVEILR GPVTLLYSYG
151 NVAGLVDVAD GKIPKMPEN GVSSELGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGERGFTG
251 VAYSDDRQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPPGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS AISEAVKOPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLAGH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

```

551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGREG DAYGNRPFIA
651 QDDQNAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

m149-1.pep	10	20	30	40	50	60
g149-1	10	20	30	40	50	60
m149-1.pep	70	80	90	100	110	120
g149-1	70	80	90	100	110	120
m149-1.pep	130	140	150	160	170	180
g149-1	130	140	150	160	170	180
m149-1.pep	190	200	210	220	230	240
g149-1	190	200	210	220	230	240
m149-1.pep	250	260	270	280	290	300
g149-1	250	260	270	280	290	300
m149-1.pep	310	320	330	340	350	360
g149-1	310	320	330	340	350	360
m149-1.pep	370	380	390	400	410	420
g149-1	370	380	390	400	410	420
m149-1.pep	430	440	450	460	470	480
g149-1	430	440	450	460	470	480
m149-1.pep	490	500	510	520	530	540
g149-1	490	500	510	520	530	540
m149-1.pep	550	560	570	580	590	600
g149-1	550	560	570	580	590	600
m149-1.pep	610	620	630	640	650	660
g149-1	610	620	630	640	650	660

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```

      670      680      690      700      710      720
m149-1.pep  AARLGFLKASLTDRIDANLDYIRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
            |||:|||||
g149-1      AARLGFLKASLTDRIDANLDYIRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
            670      680      690      700      710      720

      730      740      750      759
m149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
            |||
g149-1      WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
            730      740      750

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

```

a149-1.seq
1  ATGGCACAAA CTACACTCAA ACCCATTTGT TTATCAATTC TTTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGCTCG
151 CTGCACACTT CTACCGCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAAAGCC GTCAACTTGG GTGATGCTTT AGACGGCGTA CCGGGCATTC
251 ATGCTTCGCA ATACGGCGGC GGCGCATCCG CTCCCGTTAT TCGCGGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGGCGAAA CGGGCGACAT
351 GGCGGACTTC TCTCCAGACC ATGCAATCAT GGTGACAGC GCCTGTGCGC
401 AACAGGTCGA AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTTGCCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAC GCGTATCGG GCGAACTCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCAGCTCC GCGGCATCA ATATCGGTTT GGGCAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGGGTTAC CGCAATCTGA AACGCCTGCC CGACAGCCAC CGCGATTGCG
701 AAACGGGAGC CATCGGGCTG TCTTGGGTG GCGAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCAATAT GGTCTGCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAACCGCTA TTTGCAGCTT TATCCGACCC TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTCAAGACG ACGATGATGC
951 ACACGCCCAT GCCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAC
1001 GCTACGAAC CTGCGCCGAA TGGAGCAAC CGTCCCGGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTA GAAACTTTT TTAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCCGTCTGA AAGCGAGCTG GGGCGTGCAA
1201 TATTTGGGAG AAAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATCGGAC AACTTCACGC TTGAAGCGCG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGCTACGAC AAGCATTGA TTGATCGGGA
1401 AAATACTAC AACCATCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTCC GGCAACTGGT ATTTCACGCC ACAACACAAA
1501 CTCAGCCTGA CCGCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGCG
1801 GACTTCTACG GCGCGAAGG CGAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGGGA GACGCTACG GCAACGCCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGGTTCCG GCTGCGGCC TCGGCGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CAAAACAAA CTCGCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGCGCG TGAACGTGAA GTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

```

a149-1.pep
1  MAQTLKPIV LSILLINTPL LSQAHGTEQS VGLETVSVVG KSRPRATSGL
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQVEILR GPVTLLYSSG
151 NVAGLVDVAD KRIPEKMPEN GVSGLGLRL SSGNLEKLTS GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKFIG
251 AAYSDDRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSGC FHDDDDAHAA AHNGKPWIDL RNKRYELRAE WKQFPFGFEA

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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRKKGSGWVQ
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVVRV
451 EKQKASIRYD KALIDRENY NHELPLDLGAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAGTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA
651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYIRVFAQNK LARYETRTEG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGFVTLTYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGFVTLTYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFTGAAYSDRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFTGAYSDRRDQYGLPAHSHEYDDCHADIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSGCFHDDDDAHAAHNGKPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
m149-1	DYDNPGLSGCFHDDDDAHAAHNGKPWIDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKKGSGVQYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRKKGSGVQYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHLPLDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHLPLDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

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a149-1.pep  DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPLIAQADQNAPRVF
|||||
m149-1       DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFIAQDDQNAPRVF
              610      620      630      640      650      660

              670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
|||||
m149-1       AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

              730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
|||||
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCGCGCCGC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTCCGA TTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCGG GTTGCTCCG
251 CACTGTTATC CCATTCGAA CTCACGCAA ACACCCCGC CTTTGTCAA
301 GGTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTG
401 TGCAACCGCT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGTG
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTT GAACACGAAG
551 GCGCGCCAG GCGGGCGGC GCATCGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGTGCGCCT GTTTGCCGAA CGCAACGAC GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTT CGGCAATCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTGG CAATGGCTGC AGGAAGCGCG
951 GCATATCTAT GTGTGCGGCG ATGCGGCAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGCAG GGCATTGCGA CGAAGACGGC
1051 GCAGAAGGAT ATTGGATAT GCTGCGGAA GAAAAACGCT ATCAGCGTGA
1101 TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YKADPFPA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLGINPAT EIQAGGKTLV VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHFRPAK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDFG LHYRDFAWSR DQEEKIYVQD
301 KIREQAEGWL QWLQEGAHYI VCGDAAKMAK EVEAALLDVI IGAGHSDG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCGGCCCG AAATCAGCA
51  GCTCTGTGCG GGGCTGGACG CGGCACAATG GCGGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCAGA ACCTTTTCC GTAACCGTCC TTCCGCCTC
201 GCAAACCGCG AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCGCGCGG CATCCAAGTC AGTCGCGCGG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGCGGAACG CCGCCTGCTG CTGGTTACCT CCACCAAGG
351 CGAAGGCGAA CCGCGGAAAG AAGCCGTCGT GTCGACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAAACTCC AATTGCGCT ACTGGGTTG

```

m150.pep

Computer analysis of this amino acid sequence gave the following results:

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

	210	220	230	240	250	260
m150.pep	LLKEEAAKNRATPA	QTTPPAGLQTAPD	GRYCKAAFPFAALL	ANQKITARQSDKDV	RHIE	
g150			YCKADFPFAALL	ANQKITARQSDKDV	RHIE	
			10	20	30	
	270	280	290	300	310	320
m150.pep	IDLSGSDLHYLP	GDALGVWFDNDP	ALVREILDLLGID	PATEIQAGGKMMP	VARALSSHFE	
g150	IDLSGSDLHYLP	GDALGVWFDNDP	ALVGEILDLLGIN	PATEIQAGGKTL	PVASALLSHFE	
	40	50	60	70	80	90
	330	340	350	360	370	380
m150.pep	LTQNTPAFVKGY	AAFAHYEELDKII	ADNAVLODFVONT	PIVDVLRHFPAS	LTAEOFIRLL	

1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGCC GCAGAAGAAT
 1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTATTATGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
 1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
 51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
 101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
 151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
 201 LLKEEAAKNR ATPAPQTPP AGLQAPDGR YCKADPFPA LLANQKITAR
 251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT
 301 EIQAGGKTLF VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV
 351 LQGFVQSTPI ADVLHRRPAK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
 401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
 451 SRKPIVMIGS GTGVAPFRAF VQORAAENAE GKNWLFNGP HFARDFLYQT
 501 EWQQFAKDF LHRDYFAWSR DQEEKIYVQD KIREQAEGW QWLQEGAHY
 551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG ABEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
a150	MQNTNPPLPPMPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
	70	80	90	100	110	120
m150.pep	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	LVTSTQGEGE				
a150	VTVLSASQTGNAKSVADKAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	LVTSTQGEGE				
	130	140	150	160	170	180
m150.pep	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDR	RFEELGAKRLLER				
a150	PPEEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKR	FEEELGAKRLLER				
	190	200	210	220	230	240
m150.pep	VDADLDFTASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQAPDGR	YCKAAPFPAA				
a150	VDADLDFAAADGWTDNIAALLKEEAAKNRATPAPQTPPAGLQAPDGR	YCKADFPAA				
	250	260	270	280	290	300
m150.pep	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LDLLGIDPAT				
a150	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LDLLGIDQAT				
	310	320	330	340	350	360
m150.pep	EIQAGGKMPVARALSSHFEELTQNTPAFVKGYAAFAHYEELDKIIADNA	VLQGFVQNTPI				
a150	EIQAGGKTLFVASALLSHFEELTQNTPAFVKGYAPFADDDELDRIAADNA	VLQGFVQSTPI				
	370	380	390	400	410	420
m150.pep	VDVLHRRFPASLTAEQFIRLLRPLAPRLYSISSAQAEVGDEVH	LTGVVRFEHEGRARTGG				
a150	ADVLHRRFPASLTAEQFIRLLRPLAPRLYSISSAQAEVGDEVH	LTGVVRFEHEGRARAGG				
	430	440	450	460	470	480
m150.pep	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAF	VQORAAENAE				
a150	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAF	VQORAAENAE				
	490	500	510	520	530	540
m150.pep	GKNWLIFGNPHFARDFLYQTEWQFAKDFLHRYDFAWSRDQEEKIYVQDKI	REQAEGW				

430

a150	GKNWLF	FGNPHF	ARDFLY	QTEWQQ	FAKDGFL	HRYDF	AWSRDQ	EEKIYV	QDKIRE	QAEG	LW
	490	500	510	520	530	540					
	550	560	570	580	590	600					
m150.pep	QWLQEG	AHIYVC	GDAAKM	KDVEA	ALLDVI	IIGAGH	LDEEGA	EYLDML	REEKRY	QRDVYX	
a150	QWLQEG	AHIYVC	GDAAKM	KDVEA	ALLDVI	IIGAGH	LDEEGA	EYLDML	REEKRY	QRDVYX	
	550	560	570	580	590	600					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TGGAGCGCGT TTTGGGGATG GTGGATTGCG TCGTCTTGTT GGTGGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGCG
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTATAT GACCAGACTT TCGAGTTGTT CGACAACCTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAAccga CGAGAGCAGC GATATGCGCC
551 CGCtggtcga CACCATCCTA AAATACAcgc ctgCACCGAG CCGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCTAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGCG GACATTGTGA TTATTTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGTGACCG AACGTTGCCG TGCGGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GCGGAACTGC ACCTGACGAT
1101 TTTGTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACC cgaacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACCAA TATGGAAGC GACGGCAACG
1301 GacgCACCCG CCTCGAATAC CATAATCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccc tcaAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTactggt GtccccAAGAG CAGGGCGAGG CGGTTGCTTA CGCCTTGTGG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGAcgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGG AATCACGCCG CAAtccatcc
1751 gcctgcat gcgttacctG AGCGaattgg aacgcgccc tcaTTTAAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDITL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRIINMRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DGNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDG YAPVKPDMPG RHNGVLVSQE QGEAVAYALW

```

501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMRYL SELERRRHFK
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCOGGCACA TTCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAATCGAC AAGCCGTCCG
401 CTCGTCCGAG CTGGGTTATC GACCAAACTT TCGAGCTGTT CGACAATTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATGTGTTACG CTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGACGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCCCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGGA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TTATTCCGG TATCGAAGAC ATCGGTATCG
851 CCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
951 GGCGGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TGCGCGTGGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGCGGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAAA
1801 AAGCTGGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFDL YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
g151	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMDSNDLEKERGITILAKNT					
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	70	80	90	100	110	120
	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFEELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESN					
g151	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFEELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESS					
m151.pep	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRIILNGRIKPGQTVAVMN					
g151	190	200	210	220	230	240
	DMRPLFDTILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRIILNGRIKPGQTVAVMN					
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	250	260	270	280	290	300
	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
g151	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR					
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK					
g151	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVVNPLKGGK					
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					

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m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
 51 AACACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAGGCTA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGGCGAAG
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAATCGAC AAACCGTCCG
 401 CCCGTCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACCTG
 451 GCGCGGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTGCACTACG ACAACTACAC
 651 CGGCCGCTC GGTATCGGTG GTATCTTGA CGGACGTATC AAGCCCGGTC
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCTC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATGGAAGAC ATCGGCATCG
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCTGCC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
 951 GGCAGGTACG GAAGGCAAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGCTGGA AGTACCGCC
 1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGCGCAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
 1301 GACGACCCG CCTCGAATAC CATATCCAG CGCGCGGCTT GATCGGCTTC
 1351 CAAGGCGAAT TTATGACCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCGACGAT TACGCGCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA
 1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTT GCCTGACCAC GCCGATTAG CTGACGCTGG AAGGTGCGGT
 1701 CGAGTTATC GACGATGATG AGCTGGTAGA AATCAGCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCG CCATTTCAAA
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQOVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQIAQGRI
 251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLLILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDVPPDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVFD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDGRMFV SPNDKIYEGM IIGIHSRDN LVVNELKGGK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

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```

m151.pep  NKQIRNIAIIAHVDHGKTTLVQDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
           |||
a151       NKQIRNIAIIAHVDHGKTTLVQDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
           10      20      30      40      50      60

           70      80      90      100     110     120
m151.pep  AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
           |||
a151       AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGMPQTRFVTKKALALGL
           70      80      90      100     110     120

           130     140     150     160     170     180
m151.pep  KPIVVINKIDKPSARPSWVIDCTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESN
           |||
a151       KPIVVINKIDKPSARPSWVIDCTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDESN
           130     140     150     160     170     180

           190     200     210     220     230     240
m151.pep  DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
           |||
a151       DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
           190     200     210     220     230     240

           250     260     270     280     290     300
m151.pep  HDQQIAQGRINQLLGFGGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
           |||
a151       HDQQIAQGRINQLLGFGGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
           250     260     270     280     290     300

           310     320     330     340     350     360
m151.pep  VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
           |||
a151       VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR
           310     320     330     340     350     360

           370     380     390     400     410     420
m151.pep  GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
           |||
a151       GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
           370     380     390     400     410     420

           430     440     450     460     470     480
m151.pep  RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
           |||
a151       RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
           430     440     450     460     470     480

           490     500     510     520     530     540
m151.pep  RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMI-GIHSRDNDLVVNPLKGKK
           |||
a151       RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMI-GIHSRDNDLVVNPLKGKK
           490     500     510     520     530     540

           550     560     570     580     590     600
m151.pep  LTNIRASGTDEAVRLTPIKLTLEGAVEFIDDELVEITPOSIRLRKRYLSELERRRHFK
           |||
a151       LTNIRASGTDEAVRLTPIKLTLEGAVEFIDDELVEITPOSIRLRKRYLSELERRRHFK
           550     560     570     580     590     600

m151.pep  KLDX
           |||
a151       KLDX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAaaca aaACCaagt ctgGGacttc cCacccgcc ttTCCactG
51 GctgcttgCC gCATCCetgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

g152.pep

```

1  MKNKTKVWDF PTRLFWLLA ASLPFMWYSA KAGGDMQLQWH TRVGLLVLF
51  LVFRLCWGIW GSDTARFSRF VRGNAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTSTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAAH IAAVAAYRIF KKKNLVLRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAAHA AAAILLLS*

```

m152.seq

1	ATGAAAAACA	AAACCAAAGT	CTGGGACCTC	CCCACCCGCC	TTTTCCTACTG
51	GCTGCTTGCC	GCGTCCCTGC	CCTTTATGTG	GTATAGCGCG	AAAGCCGCGC
101	CGCATATGCT	GCAATGGCAC	ACGCGCGTGC	GGCTGTTCGT	CCTTTTCTCG
151	CTCGTATTTC	GCGTCTGCTG	GGGCACTTGG	GGCAGCGATA	CCGCCCCGTTT
201	TTCCCGTTTC	GTCCAAGGCT	GGGCAGGCAT	ACCGGCGTAT	CTGAAAAACG
251	GTATTCCCGA	ACACATCCAG	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTGCTGCGCG	TTTTTGGCCGC	CGTGTCTCTC	CAAGTCGGCA	CCGGGCTTTT
351	TGCCGCGCAT	GAAACACACT	TCAGCACCAA	CGGCTACCTC	AACCAATTGG
401	TTTCCGAACA	TACGGGCGAG	CTTATGCGGA	AAATCCACCT	CAACTTTTTC
451	AAGCTGCTCG	CCGTTTTTTC	TGCAATCCAC	ATCGCCGCCG	TGCGCCGATA
501	CCGCGTATTC	AAAAAGAAAA	ACCTCATCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCAGGCAA	AGCGCGCGTT
601	GCCGCGCGAT	TATCGGTTGC	CTCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

m152.pep

1	MKNKTKVWDL	PTRLFHWLLA	ASLPMFWYSA	KAGGDMLOWH	TRVGLFVLFL
51	<u>LVFRLCWGIW</u>	GSDTARFSRF	VOGWAGIRGY	LKNGIPEHIQ	<u>PGHNPLGALM</u>
101	<u>VVALLAAVSF</u>	QVGTGLFAAD	ENTFSTNGYL	NHLVSEHTGS	LMRKIHNLFF
151	<u>KLLAVFSALH</u>	<u>IAAVAARYVF</u>	KKKNLILPMI	TGPKYIEGKT	SIRFAGKAAL
201	AAALSVASIA	AAAILLLS*			

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/q152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGGDMQWHTRVGLFVLFLLVFRLCWGIW					
	:					
g152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKAGGDMQWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAA VAAAYRVFKKKNLILPMI					
	: : : : :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFS AVHIAA VAAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	:			
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

```

a152.seq
1  ATGAAAAACA AAACCAAAGT CTGGGACTTC CCCACCCGCC TTTTCCACTG
51  GCTGCTTGCC GCATCCCTAC CCTTTATGTG GTATAGCGCG AAAACCGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTTAT CCTTTTCCTG
151 CTCGTATTCC GCCTCTGCTG GGCATTTCG GGCAGCGATA CCGCCCGTTT
201 CTCCCGTTTC GTCCGCGGAT GGTCGGGTAT CAGAGAGTAT ATGAAAAACG
251 GTATTCCTCGA ACAGTCCAA CCGGACACA ACCCCTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCGCG CGTGTCTTTC CAAGTCGGCA CAGGGCTTTT
351 TGCCGCGGAT GTAAACACCT TCAGCACCAA CGGCTACCTC AACCATTTCG
401 TTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCATCT CAACTTTTTC
451 AACTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGNCG TCGCCGCATA
501 CCGCGTGTTC AAAAAGAAAA ACCTCGTCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

```

a152.pep
1  MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KTGGDMLQWH TRVGLFLEFL
51  LVFRLCWGIW GSDTARFSRF VRGWSGIREY MKNGIPEHVQ PGHNPLGALM
101 VVALLAAYSF QVGTGLFAAD VNTFSTNGYL NHLVSEHTGS LMRKIHLNEF
151 KLLAVFSAVH IAXVAAYRVF KKKNLVLPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAIILLS*

```

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQLQWHTRVGLFVLFLLVFRLCWGIW					
	: : : : :					
a152	MKNKTKVWDFPTRLFWLLAASLPFMWYSAKTGGDMLQWHTRVGLFLEFLVFRLCWGIW					
	10	20	30	40	50	60

	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNIGIPEHIQPGHNPLGALMVVALLAAYSFQVGTGLFAAD					
	: : : : :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAYSFQVGTGLFAAD					
	70	80	90	100	110	120

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AIHIAA VAAAYRVFKKKNLILPMI					
	: : : : :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS AVHIAA VAAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180

	190	200	210	219
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	:			
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX			
	190	200	210	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

g153.seq
 1 atgggggtttg cttacAgat gacgtatatc gaggtCGGga taccggaggc
 51 ggcatccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
 101 attATGGTTT TttggcCGAA GTGATGTTTG TGctgaCTTT cGGCGcgcCG
 151 GTTCTGTtC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
 201 ACAGGCGTAT CTTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
 251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
 301 ATCAAGCTCT CGTCTGTGGC AAAGGTTGCG TTCGGGCGG CGTTTTATCT
 351 GATGTTCCGG CTGTCCGTTA TGCTGATTGG GACTTCGGTA TCGGTTCCCC
 401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGA TAATGCGGTT
 451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTccg
 501 cgacAGTgcc gaatcccCCT GCGGGGTGTg cgCGCgggaA CTgtacggcg
 551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCTgac ggcggcggTT
 601 GTTTTGTAAT TCCctgCcaa TATCctgCcg attaTGAttt cgtccAATCc
 651 tgcgcgcacg GAGGcCAACA CCATCTTTAG CCGCATCGCT TATATGTGGG
 701 ACCagggcga CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
 751 GTGCCGCTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CCGCGGCACG
 801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
 851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
 901 TTGATGTGTT CGTTCaCaC TTATGCCGCG CCGGTCATTc CCGGCAGTGC
 951 GGCAGTCTAT TTCTGCCTGG TCGTGATTT GACGATGCTG TCCGCCTATT
 1001 ATTTGACCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT
 1051 TTCAACGAAA CGGAAAATA TGACTGA

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

g153.pep
 1 MGPAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
 101 IKLSSVAKVR FGPAYFLMFA LSVNLIRTSV SVPQHVVYFQ IGRLTGNNAV
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAAY
 201 VLVFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
 251 VPVLKIAAMS VLIAARFAL PAGAKKLSHL YRITEAVGRW SMIDIFVII
 301 LMCSFHTYAA RVIPGSAAYV FCLVILTML SAYYFDPRL L WDKRASDGLA
 351 FNETBKDY*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

m153.seq
 1 ATGGCGTTTG CTTACGGTAT GACGTATAIC GAGGTGCGGA TACCGGCTGC
 51 GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
 101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
 151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
 201 ACAGGCGTAT CTTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
 251 CACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
 301 ATCAAGCTCT CGTCTGTGGC AGAGGTTGCG TTCGGGCGCG CGTTTTATCT
 351 GATGTTCCGG CTGTCACTTA TGCTGATTGG GACTTCGGTA TCGGTTCCCC
 401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGA TAATGCGGTT
 451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
 501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CCGTGCGGAA CTGTACCGCC
 551 GACGCGCGAA AAGTCTGAGT ATTTGCTCGG CGTTTCTGAC GCGCGCGGTT
 601 ATTTTGTAAT TCCCTGCCAA TATCCTGCCG ATTATGATT CTGCCAATCC
 651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
 701 ACAGGGCGCA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
 751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
 801 CTTCGCTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
 851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
 901 TTGATGTGTT CGTTCACAC TTATGCCGCG CCGGTCATTc CCGGCAGTGC
 951 GGCAGTCTAT TTCTGCCTGG TCGTGATTT GACGATGCTG TCCGCCTATT
 1001 ATTTGACCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CCGCATTGCT
 1051 TTCAATGAAA CGGAAAACA TGACTGA

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

m153.pep
 1 MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
 51 VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY

101 IKLSSVAEVR FGPAPYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV
 151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL ISSAFLTAAY
 201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDRLI AAVIFSASIL
 251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVII
 301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL LWDKRASDGIA
 351 FNTEKHDX

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFPQDYGFLEVMFVLTFGAPVLFLLCLYV					
g153	MGFAYSMYIEVGIPGAASVLSLPEMMRLMVFPQDYGFLEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAPYLMFA					
g153	YAALIRKQAYPALRLATRVMLRQAMVDVFFVSTLVAYIKLSSVAKVRFGPAPYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVFPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
g153	LSVMLIRTSVSVFPQHWVYFQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
g153	LYGGRPKSLSISSAFLTAAVLVYFPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLRYRITEAVGRWSMIDIFVII					
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHLRYRITEAVGRWSMIDIFVII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNTEKHDX					
g153	LMCSFHTYAAARVIPGSAAVYFCLVVILTMLSAYYFDPRLWDKRASDGIAFNTEKYDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 629>:

a153.seq

1	ATGGCGTTTG	CTTACGGTAT	GACGTATATC	GAGGTCGGGA	TACCGGGTGC
51	GGCATCCGTC	CTTTCGCTGC	CCGAGATGAT	GCGCCTGATG	GTGTTTCAGG
101	ATTATGGTTT	TTTGGCCGAA	GTGATGTTTG	TGCTGACCTT	CGGCGCGCCG
151	GTTCTGTTTC	TGCTGCTGTG	CCTGTATGTC	TATGCCGCGC	TGATACGGAA
201	ACAGGCGTAT	CCTGCGCTGC	GTTTGGCAAC	GCGTGTGATG	GTGCGCTTGA
251	GACAGGCGAT	GATGGTGGAT	GTGTTTTTGG	TTTCCACTTT	GGTGGCGTAT
301	ATCAAGCTCT	CGTCTGTGGC	AGAGGTTCCG	TTCGGATCGG	CGTTTTATCT
351	GATGTTCCGG	CTGTCCGTTA	TGCTGATTCG	GACTTCGGTA	TCGTTCCGCC
401	AGCATTGGGT	GTATTTTCAA	ATCGGGCGGC	TGACGGGGGA	TAATGCGGTT
451	CAGACGGCAT	CGGAAGGTAA	AACCTGTTGC	AGCCGCTGCC	TGTATTCCCG
501	CGACAGTGCC	GAATCCCCCT	GCGGCGTGTG	CGGTGCGGAA	CTGTACCGCC
551	GACGGCCGAA	AAGTCTGAGT	ATTTCGTCCG	CGTTTCTGAC	GGCGGCGGTT
601	ATTTTGTATT	TCCTTGCCAA	TATCCTGCCG	ATTATGATT	CGTCCAATCC
651	TGCCGCCACG	GAGGTCAATA	CCATCCTTAA	CGGCATCGCT	TATATGTGGG
701	ACGAGGGCGA	CAGGCTGATT	GCGGCGGTTA	TTTTACAGCG	GAGTATTTTG
751	GTGCCGGTAC	TGAAGATTGC	GGCAATGTCG	GTTTTGATTG	CGTCCGCCCG
801	CTTCGCTTTG	CCAACGGGTG	CAAAGAAATT	GTCGCACCTC	TACCGCATCA

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGSCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTCGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLCLYV YAALIRKQAY PALRLATRV MRLQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL SISAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDR L AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSH LYRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL LDWKASDGI
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSVSPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
a153	LYRRRPKSLSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDRLI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAA RVIPGSAAVYFCLVVILTML SAYYFDPRL LDWKASDGI AFNETEKHDX					
a153	LMCSFHTYAA RVIPGSAAVYFCLVVILTML SAYYFDPRL LDWKASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctctCT CGCCGCTCTG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTATC TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCAACAG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCCGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCT GTcgaATACA AAGGGCTgaA
951 TGTcggCATG GTTTCGGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagcCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACAA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCCTCGCTCG CCGAACTCAA GTCCGCATC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACCAACTGAA CCAAACCTCG AAAGAGTTGC GCATAACCTT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAAgacg TtcaACCGT CATTAACACT TTGAaAGAAa
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAGAcCC tATCCCGAAa
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1  MTDNSPPPNQ HAQARVRKNN TFLSAVVLVP LIALIAGGWL WVKEIRNRGP
51  VVTLMLDSAB GIBVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSLGIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFO
151 VQDIPFVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV QGIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGGK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKPNNL PLDKTVAEIN
451 GSLAEELKSL KSANAALSSI DKLVGNPQTQ NIPNELNQLT KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSKDPPIPK
551 GSR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CAGGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCTCTT CTGCCGCTCG GCTGGTTCGG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCTAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTATC TCCGCCAGCC GTTTTGGCT GGAAGCGGC ATCAATATCG
701 AAACCAACAG CAGCGGCATC AAACCTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCCGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTCCGCC GTGAGTACA AAGGGCTGAA
951 TGTCCGCGTG GTTTCGACG TCCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACAA
1101 ATTTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

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1201 TCACCTAAGC TGGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAAC TTAAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCAACGC GGTGATTTT AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

m154.pep

```

1 MTDNSPPPNQ HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLLMDSAE GIEVNNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFQ
151 VQDIPPVTAI GQSGRLRLNI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPLAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYTTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAEIN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNBLNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNQHAQARVRKNNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
g154	MTDNSPPPNQHAQARVRKNNNTFLSAVWLVP LIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
g154	GIEVNNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNIGKNDRIILNVN					
g154	SGVTGLGTLTSGSYIAFTPGKSDEAKDVFQVQDIPPVTAIGQSGRLRLNIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMVQGVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
g154	SPVLYENFMVQGVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLSAPLPLALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYTTAFFKQ					
g154	KLSAPLPLALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEIANLPDDRSLYTTAFFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLBINADEQS					
g154	SVRGLTVGSPVEYKGLNVGMVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLBINADEQS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
g154	KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATRG					

442

	370	380	390	400	410	420
m154 . pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLOKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPGQTQ					
g154	GGLDDLQVKLADLLDKFNNLPLOKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
m154 . pep	490	500	510	520	530	540
	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
g154	NIPNELNQTLKELRITLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
m154 . pep	550					
	NSSSKDPIPKGSRX					
g154	NSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154 . seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCT GGAAGCGGC ATCAATATCG
701 AAACCAAGG CAGCGGCATC AAATCAATT CCGCCCTCT CTCTGCCCTG
751 CTGTCCGGCG CGATTTCATT TGATTCGCGG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTCGCGCTG GTTTCCGATG TTCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACA
1101 ATTTAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTGG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCTT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CCGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTAAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCACACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154 . pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLV LIALIAGGWL WVKEIRNRGP
51  VVTLMLDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL SSGYIAFTPG KSDEAKDQVQ

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151 VQDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINAEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPGTQ NIPNELNQT LKELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNHQAQARVRKNN	FLSAVWL	VPLIALI	AGGWLWV	KEIRNRGP	VVTLMLDSAE
a154	MTDNSPPPNHQAQARVRKNN	FLSAVWL	VPLIALI	AGGWLWV	KEIRNRGP	VVTLMLDSAE
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVL	SIDVGRV	TRIKLRD	DQKGVET	QAQLNADV	SGLIRSDTQFWVVKPRIDQ
a154	GIEVNNTVIKVL	SIDVGRV	TRIKLRD	DQKGVET	QAQLNADV	SGLIRSDTQFWVVKPRIDQ
m154.pep	130	140	150	160	170	180
	SGVTGLGTL	LLSGSYIA	FTPGKSDE	AKDV	FQVQDIP	PVTAIGQSGRLRLNLIGKNDRIILNVN
a154	SGVTGLGTL	LLSGSYIA	FTPGKSDE	AKDV	FQVQDIP	PVTAIGQSGRLRLNLIGKNDRIILNVN
m154.pep	190	200	210	220	230	240
	SPVLYENFMV	GQVESAH	FDPDQSV	HYTIFI	QSPNDKLI	HSASRFWLESGINIETTSGSI
a154	SPVLYENFMV	GQVESAH	FDPDQSV	HYTIFI	QSPNDKLI	HSASRFWLESGINIETTSGSI
m154.pep	250	260	270	280	290	300
	KLNSAPLPAL	LSGAIS	FDSPKTK	NSKNVKS	EDSFTLY	DSRSEVANLPDDRSLYYTAFFKQ
a154	KLNSAPLPAL	LSGAIS	FDSPKTK	NSKNVKS	EDSFTLY	DSRSEVANLPDDRSLYYTAFFKQ
m154.pep	310	320	330	340	350	360
	SVRGLTVG	SPVEYK	GGLNVGV	SDVPYF	DRNDSL	HLFENGWIPVRIRIEPSRLEINAEQS
a154	SVRGLTVG	SPVEYK	GGLNVGV	SDVPYF	DRNDSL	HLFENGWIPVRIRIEPSRLEINAEQS
m154.pep	370	380	390	400	410	420
	KEHWKQQF	QTALNK	GLTATIS	SNLLTG	SKMIELN	DQPSASP
a154	KEHWKQQF	QTALNK	GLTATIS	SNLLTG	SKMIELN	DQPSASP
m154.pep	430	440	450	460	470	480
	GGLDDLQV	KLADLL	DKFDKL	PLDKT	VAELN	GS
a154	GGLDDLQV	KLADLL	DKFDKL	PLDKT	VAELN	GS
m154.pep	490	500	510	520	530	540
	NIPNELN	QTLKEL	RTTLQ	GVSPQ	SPYGDV	QNTLQSLDKTLKDVQPVINTLKEKPNALIF
a154	NIPNELN	QTLKEL	RTTLQ	GVSPQ	SPYGDV	QNTLQSLDKTLKDVQPVINTLKEKPNALIF

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                    550
m154.pep      NSSSKDPIPKGSRX
               |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtataCCACG CGAGTCatta tcCGGCGAAA cccgcgtagc
51  ctgcAegccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTtggaCGA TGCCCGTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGC GCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCGC ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGCGCGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGCAGC GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTATATCG CGCGGAAATG AAGCTCTTTG CGAACACGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CGGcgatTc aggtTTCcg cgggcccGAG CAAAcgccgt
1151 ctgaAAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgttCCcctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcacccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGTAC CATGTCTGTT GgaacgTCAG CCACTCGCTG
1351 TCACACCCGC TGatgtcggt aaccaaCgcc atctccGGCA tcatgtcggt
1401 cggCGCGCTG CTGCAAAATCG GTCAGGGcaa cgggttcgtT TCgtGCTGT
1451 CGTTTGTTC CATCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTF ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTI V SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTQGITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDLQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKpAPKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNVkiIi GYTDMANRLA QSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMtV TRDGEITfPP PPIQVSARpQ QTPSEKAAPA AKPEPKVPPL
401 WKKLAPAAIA AVLVLWVGAV APAaFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMsvTNA ISGIMVVGAL LQIQGNGfV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMfK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCCACG CGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGGACGA TGCCCGTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

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301 TTGGTCGAAG CTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTGCGCGC CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCGGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGCGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCGTA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGAAAAA AACTCGCGCC CGCCGTCATC GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTGCGACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCTG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDAL SSMANISGYR AVIEAANAAG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFPQES GSGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQF QQTPSEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVYVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIGQGNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155           MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep      AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              |||:|||||
g155           AAVWACPLIYKVNAPSEGELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep      ISRAQALDALSSMANISGYRAVIEAANAAGFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155           ISRAQALDALSSMANISGYRAVIEAANAAGFRFFTGQITAAGKVPPAQVLVIGAGVAGLAA

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	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFAEQAKEVDIIITTAAPGKPAKPLITKEMVESNKSQSVIVDLAAATGGNCELTRPGE					
g155	KLFAEQAKEVDIIITTAAPGKPAKPLITKEMVESNKSQSVIVDLAA-TGGNCELTRPGE					
	250	260	270	280	290	
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYIDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	LSVTGNGVKIIGYIDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	300	310	320	330	340	350
	370	380	390	400	410	420
m155.pep	VTHDGEITFPPPIQVSAQPQQTPEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVVGA					
g155	VTRDGEITFPPPIQVSAQPQQTPEKAAAPAKPEPKPVPLWKKLAPAAIAAVLVLVVGA					
	360	370	380	390	400	410
	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155	VAPAAFLNHFIVFLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
	420	430	440	450	460	470
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
g155	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
	480	490	500	510		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACGTCG CCCTGCTGGG CAAACTGGGC TT'TGAAACG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGCATACCC
201 TTTAATTTAT AAGGTTAAGC CGCCGTCCGA AGACGAGCTG CCGTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCGGC ATTTGCGCGC GCGAGGCTTT GGACGNTTGT TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGCG
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGT'TTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCCG CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCGAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GCATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCAA ACAGGGCGAA
901 TTGTTTCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGCGGAAAT CAGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCAAGC CCGAACCGAA ACCCGTTCCT

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1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTGGGCGCG GTCCGACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTCGCTGCG
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
251 DIIITTAAP GKPAKXXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKVPV
401 LWKKLAPAXI AAVLVLWVGA VAPAAFLNHF IVFVLACVIG YYVWNVSHS
451 LHPTLMSVTN AISGIIVVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

m155/a155 95.3% identity in 513 aa overlap

      10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
a155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK
      10      20      30      40      50      60

      70      80      90     100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPR
a155      AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPR
      70      80      90     100     110     120

      130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQGITAAAGKVPPAQVLVIGAGVAGLAA
a155      ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTQGITAAAGKVPPAQVLVIGAGVAGLAA
      130     140     150     160     170     180

      190     200     210     220     230     240
m155.pep  IGTANSLGAVVRAFDTRLLEVAEQIESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
a155      IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGSGDGYAKVMSDEFIAAEM
      190     200     210     220     230     240

      250     260     270     280     290     300
m155.pep  KLFAEQAQKEVDIIITTAAPGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE
a155      KLFAEQAQKEVDIIITTAAPGKPAKXXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE
      250     260     270     280     290     300

      310     320     330     340     350     360
m155.pep  LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
a155      LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT
      310     320     330     340     350     360

      370     380     390     400     410     420
m155.pep  VTHDGEITFPPIQVSAQPQQTPEKAVPAKPEPKVPVPLWKKLAPAVIAAVLVLWVGA
a155      VTRDGEITFPPIQVSAQPQQTPEKAAPAAKPEPKVPVPLWKKLAPAXIAAVLVLWVGA
      370     380     390     400     410     420

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	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFLACVIGYVVVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
a155	VAPAAFLNHFIVFLACVIGYVVVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
	430	440	450	460	470	480
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRLNMFKKGX					
a155	VSLLSFVAILIASINIFGGFFVTRRLNMFRRGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

g156.seq

1	ATGACTTTCG	CCTATTGGTG	CATTCTGATT	GCCTGCCTAT	TGCCGCTTTT
51	TTGTGCGGCG	TATGCCAAAA	AAGCGGGCGG	ATTCCGGTTT	AAAGACAACC
101	ACAATCCTCG	CGGTTTCTG	GCACATACGC	AAGGCGCAGC	CGCCCGTGCC
151	CACGCCGCGC	AGCAAAACGG	TTTTGAAGCC	TTTGACCCGT	TTGCCGCCGC
201	CGTTTGTACG	GCACACGCAA	CCGGCAATGC	CGGACAAGCA	ACCGTCAACA
251	CGCTTGCCGG	ATTGTTTCATC	CTGTTCCGCC	TCGCCTTTAT	CTGGTGCTAC
301	ATCGCAGACA	AAGCAGCATT	GCGCTCGCTG	ATGTGGGCGG	GCGGATTTGC
351	CTGCACCGTC	GGACTGTTTG	TCGCGGCTGC	TTGA	

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

g156.pep

1	MTFAYWCILI	ACLLPLFCAA	YAKKAGGFRF	KDNHNPRGFL	AHTQGAAARA
51	HAAQQNGFEA	FAPFAAAVLT	AHATGNAGQA	TVNTLAGLFI	LFRLAFIWCY
101	IADKAALRSL	MWAGGFACTV	GLFVAAA*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

m156.seq

1	ATGACTTTCG	CCTATTGGTG	TATTCTGATT	GCCTGCCTAT	TGCCGCTTTT
51	TTGTGCGGCG	TATGCCAAAA	AAGCGGGCGG	ATTCCGGTTT	AAAGACAACC
101	ACAATCCGCG	CGGTTTCTA	GCGCACACGC	AAGGCGCAGC	CGCCCGTGCC
151	CACGCCGCGC	AGCAAAACGG	TTTTGAAGCC	TTTGACCCGT	TTGCCGCCGC
201	CGTTTGTACG	GCACACGCAA	CCGGCAATGC	GGCGCAATCG	ACCATCAACA
251	CGCTTGCTTG	CCTGTTTCATC	CTGTTCCGCC	TCGCCTTTAT	CTGGTGCTAT
301	ATCGCCGACA	AAGCCGCTAT	GCGCTCACTG	ATGTGGGCAG	GCGGATTTGC
351	CTGCACCGTC	GGGCTGTTTG	TCGCGGCTGC	TTGA	

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

m156.pep

1	MTFAYWCILI	ACLLPLFCAA	YAKKAGGFRF	KDNHNPRGFL	AHTQGAAARA
51	HAAQQNGFEA	FAPFAAAVLT	AHATGNAAQS	TINTLACLFI	LFRLAFIWCY
101	IADKAAMRSL	MWAGGFACTV	GLFVAAA*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

	10	20	30	40	50	60
m156.pep	MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
g156	MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAAVLTAAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV					

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```

g156      FAPFAAAVLT AHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70      80      90      100      110      120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCACCGT TTGCAGCCGC
201 CGTTTTCGCG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTGT
351 CTGCACCGTC GGGCTGTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVAA*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10      20      30      40      50      60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
a156           MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10      20      30      40      50      60

              70      80      90      100     110     120
m156.pep      FAPFAAAVLT AHATGNAAQSTINTLACLFI LRLAFIWCYIADKAAMRSLMWAGGFACTV
              |||||
a156           FAPFAAAVLT AHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70      80      90      100     110     120

m156.pep      GLFVAAAX
              |||||
a156           GLFVAAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgccctgcgc cgcaattgC gCgGgcggcg
51 ttcgcAAATg GGcgagacg tGCGggCGGC GGCGgCgata Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCGGCGCA Aaactctatc tgcettATAT CGAACCCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTGGGCATA GACCGCGAAG
401 GCTACCGTTT GGGGCAGGCA GCGGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
 51 PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFTYPY ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGFAQLVD RLPREAHDLP LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
 51 TTCGCAAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GGAATCCGG CGTGATTGG
151 CCGATGGGCA AGGAATTGCG TTGGACGGC TTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACCGCGT TCGGGCGGGA
251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCCGA AAAAGCGTGT
351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGC AAAAACCGTG GCGTGGGCT TTGCCTGCCA
501 GTTGTGGGAC AGGCTGCCGG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAATV KINHLKRYI KKGRKIGVYW
 51 PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFTYPY ADGVKQERKR
101 GRAKLHVPQF AGRKKRVHDL NLLVPPVGM DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGFAQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMGRDVRAAAATVKINHLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMGRDVRAAAAIKINRLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAEKLYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRMWFTYPYPERGEMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
m157.pep	NLLVPPVGMMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
 51 CGCGCAGATG GGGCATCAAG GGCGGTGGC GGCGGGGCAA ACCATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACC GCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGO TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGAFACQFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSOMGRDVR	AAATVKINHLLKRYIKKGRKIGVYW	PMGKELRLDG			
a157	MRNEEKHALRRELRRARAQM	GHQGRLAAGQTINRLLKRYIKRGRKIGVYW	PMGKELRLDG			
	10	20	30	40	50	60
m157.pep	FVRAAQKRGAE	LYLPYIEPRSRMWFTYPYPADGVKQERK	GRAKLHVPQFAGRKRVHDL			
a157	FVRAAQKRGAKLYLPYIEPRSRMWFTYP	PESGMERERIRGRAKLNVPQFAGRKIRVHGL				
	70	80	90	100	110	120
m157.pep	NLLLVVVGMDRLGYRLGQAGGYDATLS	SAMKYRLQAKTVGVGFACQLVDRLPVEA	HDRS			
a157	SVLLVPLVGIDREGYRLGQAGGYDATL	AAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL				
	130	140	150	160	170	180
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGCGC CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGCGC TGTTCGCGCT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACCTATCCG CATATCcgac TTTGCTCGT TCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCTT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACC GGTCTCTAAAT
601 ACATGGGCGG TTTTAGatgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
851 TATTTTGGGA TTTTATTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
901 AATACCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

```

g158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DELVDNDITE
251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNMNR
301 NTK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

```

m158.seq
  1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAGG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
151 AACCGCACCA CGCGGCAACT CAGTCTGACG GAAGAAGCGC CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGGCG GAAACCGAAA
251 TGTGGCAGT GCGTGCACG CCGCAAGCGG TGTGAGCGT GGATTCCGCG
301 ATGCCGATGG TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCCGAA GGCTATATCA
401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TCGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG
551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAT
601 ACATGGGCGG TTTTAGATGC GCAGGGAAT CCCTATAAGA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
751 GGAAAGTTAA TTCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
851 TATTTTGGGA TTTTATTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

```

m158.pep
  1 MKTNSEELTV FVQVVESGSF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFRRA QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHC LGFTEPGSLN
201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DELVDNDIAE
251 GKLIPLLAEQ TSDKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

```

          10      20      30      40      50      60
m158.pep MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT
          |||
g158      MKTNSEELTVFVQVVESGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLNLT
          10      20      30      40      50      60

          70      80      90     100     110     120
m158.pep EEGAQYFRRAQRILQEMAAAETEMLAHVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP
          |||
g158      EEGAQYFRRAQRILQEMAAAETEMLAHVHEVPQGVLRVDSAMPMVLHLLAPLAAKFNERYP
          70      80      90     100     110     120

```

```

a158.00q
1  ATGAAAACCA  ATTCAGAAGA  ACTGACCGTA  TTTGTTCAAG  TGGTGGAAAG
51  CGGCACGCTT  AGCCGTGCGG  CGGAGCAGTT  GGCATGGCCA  AATTCCTGCC
101 TAAGCCGCAT  CGTCAAACGG  CTGGAGGAAA  AGTGTGGGTG  GAACCTGCTC
151 AACCGCACCA  CGCGGCAACT  CAGTCTGACG  GAAGAAGGCG  CGCAATATTT
201 CCGCCGCGCG  CAGAGAATCC  TGCAGAAGAT  GGCAGCGGCG  GAAACCGAAA
251 TGCTGGCAGT  GCACGAAATG  CCGCAAGGCG  TGTTCGCGT  GGATTCCCGG
301 ATGCCGATGG  TGCTGCATCT  GCTGGCGCCG  CTGGCAGCAA  AATTCAACGA
351 ACGCTATCCG  CATATCCGAC  TTTGCTCGT  TTCTCCGAA  GGCTATATCA
401 ATCTGATTGA  ACGCAAAGTC  GATATTGCCT  TAGGGGCGCG  AGAATTGGAC
451 GATTCCGGGC  TCGCTGCACG  CCATCTGTTT  GACAGCCGCT  TCCGCGTAAT
501 CGCCATCTCT  GAATACCTGG  CAAACACGG  CACGCGCGAA  TCTACAGAAG
551 AGCTTGCCEG  CCACCAATGT  TTAGGCTTCA  CCGAACCCGG  TTCTCTAAAT
601 ACATGGGCGG  TTTTAGATGT  CGAGGGAAAT  CCCTATAAGA  TTTCAACGCA
651 CTTTACGCC  AGCAGCGGTG  AAATCTTACG  TCGTGTGTGC  TTTTACGGTT
701 GCGGTATTGC  TTGCTTATCA  GATTTTTTGG  TTGACAACGA  CATCGCTGAA
751 GGAAAGTTAA  TTCCCTTGCT  CGCGGAACAA  ACCTCCAATA  AAACGCACCC
801 CTTTAAATGCT  GTTTATTACA  GCGATAAAGC  CGTCAACCTC  CGCTTACGCG
851 TATTTTGGTA  TTTTTTAGTG  GAGGAACATG  GAAACAATCT  TCTGGGATAA

```

a158.pep

1	MKTNSEELTV	FVQVVESGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NMTTQRLSLT	EEGAQYFRR	QRILQEAMAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSE	GYNLIERVK	DTALRAGEL
151	DSGLRARHLF	DSRFRVIASP	EYLLAGHTPQ	STEELAGHCQ	LGFTPEGSLN
201	TWAVLDAQGN	PKYKSPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYSDSKAVNL	LRRVFLDFLV	EELGNLCG*

	10	20	30	40	50	60
m158.pep	MKTN	SEEL	TVFV	QVVG	SGSFS	RRAEQ
	10	20	30	40	50	60
a158	MKTN	SEEL	TVFV	QVVG	SGSFS	RRAEQ
	70	80	90	100	110	120
m158.pep	EEGA	QYFR	RAQR	ILQE	MAAE	TEML
	70	80	90	100	110	120
a158	EEGA	QYFR	RAQR	ILQE	MAAE	TEML

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHEFTASSGEILRSLCLSGCIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHEFTASSGEILRSLCLSGCIVCLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSNKTDFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSNKTDFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

gl60.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101  AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151  GCGGAAACTT  CCCGCGTCC  GGTCGGCACG  GGCGATATTG  TATTTTCCC
201  GCGCGGCTTG  GGTATGTGT  TGAGCCACGA  CGGAAATAC  GGAGAAAGTT
251  TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301  AACGGGCTGG  ATATGAGCCT  GTTTGCGCC  CGTTTCCGCT  ACGACACCCA
351  CGCGGATTTG  ATGAACGGGC  TGCCGGAAAC  CGTTTTCTG  AACATTGCCC
401  ATCCAAGTTT  GCAGTATGTG  GTTTCATGTC  TGCAACTGGA  AAGCGAAAAA
451  CCTTTGACGG  GGACGGTTC  CGTGGTCAAC  GCATTACCGT  CCGTCCTGCT
501  GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAATCT
551  CCGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601  AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGTTGTC
651  CGCGCCCAAT  ATGTGCGCGC  CGCAACTGAT  GCGCGGCTTC  AAAAGCCAAG
701  TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCTC  GCAAAAAGGC
751  GCATTGCTGC  TGAAGAAAC  CCCGATTCG  GTTTTGAGG  TCGCGCTGTC
801  GGTGGGCTTT  CAGTCGGAAA  CGCATTTCGG  CAAGGCGTTC  AAACGGCAAT
851  ATCACGTTTC  GCCGGGGCAA  TACCGGAAAG  AAGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng> :

```

gl60.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101  NGLDMSLFCA  RFRYOTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151  PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201  KVIDKPEDEW  NIDKMVAARN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251  ALLLKKTPDS  VLEVALSVGF  QSETHFGKAF  KRQYHVSFGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTCGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101  TGAACGCGCA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CCGCTATCTC
151  TGCATCGACG  GCGAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201  ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAAAATGCG
251  GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301  CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCC  GTTTCGCTA
351  CGACACCCAC  GCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401  ACATTGCCCA  TCCGAGTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451  AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTETCGTC

```

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```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGGG TTTTGTGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

	10	20	30	40	50	60
m160.pep	MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP					
	: : : : : : : : : :					
g160	MDILDKLVDF AQLTGSADVQ CLLGGQW--HETLQREGLV HIVTAGSGYL CIDGETSPRP					
	10	20	30	40	50	
	70	80	90	100	110	120
m160.pep	VSTGDIVFFP RGLGHVLSHD GKGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH					
	: : : : : : : : : :					
g160	VSTGDIVFFP RGLGHVLSHD GKGESLQPD IRQNGT FMVKQCGNGLDMSL FCARFRYDTH					
	60	70	80	90	100	110
	130	140	150	160	170	180
m160.pep	ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGT VSMVNALSSVLL VLILRAYLEQ					
	: : : : : : : : :					
g160	ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGT VSVVNALPSVLL VLILRAYLEQ					
	120	130	140	150	160	170
	190	200	210	220	230	240
m160.pep	DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMA AANMSRAQLM RRFKSRVGLS					
	: : : : : : : : :					
g160	DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNIDKMA AANMSRAQLM RRFKSQVGLS					
	180	190	200	210	220	230
	250	260	270	280	290	300
m160.pep	PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ					
	: : : : : : : : :					
g160	PHAFVNHIRL QKGALLLKKTPDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ					
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```


456

```
101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAATATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGC GGCA ACGGACAGGA TATGAGCCTG TTTTGC GCCC GTTTCGGCTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATGTGCGTC
501 CGTCTGCTG GTGCTTATCC TCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGGG TTTTGTGCGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGGAAAGA AGGCGGGCAA
901 AAATAA
```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```
a160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*
```

m160/a160 100.0% identity in 301 aa overlap

```
10 20 30 40 50 60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
a160 MDILDKLVDF AQLTGSVDVQ CLLGGQSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
10 20 30 40 50 60

70 80 90 100 110 120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
a160 VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
70 80 90 100 110 120

130 140 150 160 170 180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
a160 ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
130 140 150 160 170 180

190 200 210 220 230 240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
a160 DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
190 200 210 220 230 240

250 260 270 280 290 300
m160.pep PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
a160 PHAFVNHIRL QKGALLLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
250 260 270 280 290 300

m160.pep KX
a160 KX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGCGCGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTGAC AACCGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTtTtG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTACAGAA
451 CCGCGCGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAATGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCTGCGgt ttgggcgacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tccggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAeg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTtTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TTTLGAAAVL RRDTRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGCGA
251 TGCTGCTGCT GTTTACGCG GTAACGCATC TGCCTTGCG CACTGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTtTtG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCGG TTTACACGCA GCGGTGCTG CTCCTTGGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTACAGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAATGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCTGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCCT GTCCTTTCCA TCGGCAETTT ATCTGTCGTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATCACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTtTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51  TVALGAAAVL RRDxFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSIFL AVFSFLILKE RISVYTQAVL LLGFAGVVLL LNPSFRSGQE

```

m161 / g161 97.0% identity in 300 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 671>:

```

a161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGSGTGGC
51  GGGCGCGCTG TTTACCATTA TGAACGTAAT GATTAAAGAG GCATCGGCAA
101 AATTTGCCCT CGGCAGCGGC GAATTTGCTT TTTGGCGCAT CGTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA CCTTCCGCA
201 GCCCATTGG AAAAACCACT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAAACGCATC TGCCTTTGCG CACCGGGCTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGGTGCTG TCTCTTGGTT
401 TTGCCGCGCT GGTATTGCTG CTTAATCCCT CGTTCGCGAG CGGTCAAGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCAG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACC CGC GTCGCGCTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTATCGGT TTTGGCGAGC
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCG TTTCTATAT GACCCCTGTT
751 TTTTCCGCTC TGTCTGCCG GATTTTTCTG GCCCAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CACGGGTATT TTGAGCAGCA

```

459

851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMFLS
51 TVALGAAAVL RRDTERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVSALSAAFFLAELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51 TTAAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTTt
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGT3C CGGAATTCGG CTTCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGCC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGT TTGGCGGCGG ACCCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCTGTTT CGGCGTTTTCG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACCG CTGCTTTTTCG
1151 AATTCTTTAA TTACCTCCCC CTGCCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCTGTTTTTT TGAACCTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCTG TGGAAAGGCT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TCGGAAAGAG ACGATGCGCG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATAIGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTG ATGTTGTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51  LGFLLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLOEMGW IAENSPGVQV LIIAAVMSLA VVSAISGVGK GVKVLSEINL
251 GLAEFLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAFV GLFIARISKG RTIREFVFGV LLIPGLEFVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVINN ITS RDKGLSA PRWOAVMWGV LMSAVAVLLM
451 RSGGLGNLOS MTLIVSLFFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLEHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCCTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAGAAG
101 TCATTTTTAC CGASTTCAGC TGGTTTTATG TTTAACGTT TCCATTTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCCTGTCG TGGCTGGCGA
251 TGCTGTTTGC GGCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCAATTATT TTCGGACATT ACGGCCGCGA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGAAGGT TCGGCGATGC CATTGATATT ATGGCCTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

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461

```

651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTGTGTT TTGGCGCGCG GACCCACTGT
801 TTACCTGTTG TCGGCATTTCG GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTAAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGGGGGTT TTGCTCATCC CCGGCTGTGT CGGCGTTTTC
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTCG
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTCTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCGG GGATTATGT
1251 CCGTGAACAA ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCTT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTCGCGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTCCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGSTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLT VPQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALARS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGR GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFV CVLVVLVLT VPQVQMWLDR AKEVIFTEFS WFYVLTFSIF LGFLLILSVS					
g163	MVILTTLFFV CVLVVLVLT VPQVQMWLDR AKEVIFTEFS WFYVLTFSIF LGFLLILSVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m163.pep	SLGNIRLGRDE DVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDE DVPEFGFLSWLAMLFAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130 140 150 160 170 180					

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m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
	190 200 210 220 230 240
m163.pep	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
	250 260 270 280 290 300
m163.pep	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
	310 320 330 340 350 360
m163.pep	WFESWTVLYWAWWCWAPFVGLFIARISKGRITREFFVGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCWAPFVGLFIARISKGRITREFFVGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
	370 380 390 400 410 420
m163.pep	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
	430 440 450 460 470 480
m163.pep	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
	490 500 510 520 530 540
m163.pep	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASAMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVIRIMSQTQEODILKFLKHTASAMHELQR
	490 500 510 520 530 540
	550 560 570 580 590 600
m163.pep	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSQDLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSQDLINDGKLPHIR
	550 560 570 580 590 600
	610 620 630 640 650 660
m163.pep	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCCTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGAIGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCCGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCCG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTTGT TTGGCGGCGG GTCCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGAAATC
851 TGGTGCGCCT CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCITTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTTA
1151 AATTCITTTAA TTACCTCCCC CTGCCCAGAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACTTCT GCCGATTCGG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCGTA TGTTCCTCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CCGGTCGATA AGATGTTTCA TCAGGACGAG CCGCAATCG AGTTCGTAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 TACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAACTACGA ACGTATTG ATGTTGTTGG ATGATGTCGG TCAGGAACATG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLEPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIOW IAENSFSVOV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LMLIMCPSL WKGLSADKKY FETRVNPTSV
501 FWTGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCLVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a163       MVILTTLFFVCLVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFISIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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|||||
a163      SLGNIRLGRDEVPFEGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70          80          90          100          110          120

              130          140          150          160          170          180
m163.pep  QALLHTVEHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              |||||
a163      QALLHTVEHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEISGRFGDAIDI
              130          140          150          160          170          180

              190          200          210          220          230          240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              |||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIOWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
              190          200          210          220          230          240

              250          260          270          280          290          300
m163.pep  GVKVLSRLNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              |||||
a163      GVKVLSRLNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250          260          270          280          290          300

              310          320          330          340          350          360
m163.pep  WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              |||||
a163      WFESWTVLYWAWWCSWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
              310          320          330          340          350          360

              370          380          390          400          410          420
m163.pep  WLNDGVAGGMLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              |||||
a163      WLNDGVAGGVLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370          380          390          400          410          420

              430          440          450          460          470          480
m163.pep  ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
              |||||
a163      ITSRDKGLSAPRWQAVMWGVLMASAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL
              430          440          450          460          470          480

              490          500          510          520          530          540
m163.pep  WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKOTASPMHELQR
              |||||
a163      WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPMHELQR
              490          500          510          520          530          540

              550          560          570          580          590          600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              |||||
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              550          560          570          580          590          600

              610          620          630          640          650          660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              |||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              610          620          630          640          650          660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGGCGC TTCCTGTTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGAC GGACAAAAGC
151 CGGCCGCGCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCGC ACTTGGGCGC CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCTg cegatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCCC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTCAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCGCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGGCGA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCATTTTCG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCCTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTCG
1151 GCGAGGACGA aatccgcgcg caccTGCCTA CCGTGTCTGC AAATTTCAAA
1201 ATCCCAAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGCTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SIILVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKRD LIISKQONVY PREIEEIIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACGCGCGGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGT AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGCGGGGCTT AAGGCGCAAA CGCCCCTCGA AAAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCGGCT TCCCCGAAAA ACCCGACTTG GGCGGCCAAC CCCGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCCTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGTGCGG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTTGGTATTT AGATGGTTCA
851 ACCGCATTCT CCGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAATTGCG TGAAGGCTA

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951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTG3TCGA AGTGCCGCGC GCGGAAGTGG GCGAAGTGAT
1101 CGTCAGGGGC GGTTC3GTGA TCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAATCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKEGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNV L
251 KQTLKRA TV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFP RAKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVPR GEVVELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDFIFIV DRKKDLIISK GQNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA
501 TGVKLRVLK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120     130     140     150     160     170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180     190     200     210     220     230
m164.pep  SGTTGHPKALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMAC
g164      SGTTGHPKALISYANLFANLNGIERIFKISKDRDFIVFLPMFHSFTLTAMVLLPIYMAC
          100     110     120     130     140     150

          240     250     260     270     280     290
m164.pep  SIILVKSVPFNSVLKQTLKRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
g164      SIILVKSVPFNSVLKQALLKRA TVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAP
          160     170     180     190     200     210

          300     310     320     330     340     350
m164.pep  LAEQTILDFKAKFPRAKLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
g164      LAEQTILDFKAKFPRAKLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEEL
          220     230     240     250     260     270

          360     370     380     390     400     410

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m164.pep  VEVPRGEVVELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          |||||||
g164      VEVPRGEVVELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDAAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          |||||||
g164      LIISKQNVYPREIEEEIHKLDAAVEAAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          |||||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAACCGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGCGGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGG AAAAACACGG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGGCGGCTTG AAGCGCAGAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCGGATATAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA
951 GTGACTGAGC GAAGCCTCGC CCGTCTGCGC CGTCAATACG CCGAGAGGCG
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTGA AGTGCCGCGC GCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGCTA CCTCAATATG CTTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTGC GACCGCAAAA AAGATTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKN NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPDL GRQPRINDLA HIIYTSGTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDRR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVVELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEGDFIFIV DRKKDLISK GQNVYPREIE EEIYKLDAAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRLTV LANFKIPKQI HFKDGLPRNA

```

468

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
a164	MNRTYANFYEMLTAAACRKNNGTAVFDGKEKTAYRALKQEAEEVAAYLQNIQVKGFDTV					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETG					
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDRIIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKRDRIIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKRAITVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQALLKRAITVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLEGLSEASPVVAVNTPERQKARSVGIPPLGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLEGLSEASPVVAVNTPERQKARSVGIPPLGLEAKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEGFIFIVDRKKDLISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEGFIFIVDRKKDLISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLK EQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLK EQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq
 1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcataatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCTCTTT CCTCGCGCGG GCGGCGGCGC CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CctGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

```

g165.pep
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFKTQKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLQK
251 SGIPKEGKYG GLPVSGLFFR NSNPETAEQH NAKVYQASV GAPFMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

```

m165.seq (partial)
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA cGCGTGGAAC
151 AACCGCGGCA CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCCCGCTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCGC CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGGC GCAGCTCACC CTCCGTACCC
701 GCTTCTCTTT CCTCGCGCGG GCGGCGGCGC CGTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

```

m165.pep (partial)
1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCSYLQKRYD AFKTOKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDENQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSPVPHL
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA					
g165	MAEATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRNKISDWAPLIMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDGQTLRTRFLFLGA					
g165	GRLTRQMVKYLGKGVKTEFNRHVEDIKRESGAWVLKTADTRNPDWQTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
g165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGAAC
151	AACGCCGGCA	CGGGGCATTC	CGCGCTGTGC	GAATTGAACT	ATGCGCCGTT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTGGGCGCA	CGTTGGTCGC	GGAAGGCAAG
301	TTGGAAGACA	ATTCTTCAT	CAATGCCGTG	CCGCATATGT	CTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCCTTTAAAA
401	CCCCAAAAT	TTTGGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCCGCGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCCG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAAA	AACCGAGTTC

```

601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGGCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAAAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACCTATG GATTTGCCCG
1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGT GCAGTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAAGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```

a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GPFVSGLFFR NSNPETAQH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSML DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165/a165 99.7% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
a165	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
a165	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAA N YSAEGTDVDF					
a165	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAA N YSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLQKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTRTRFLFLGA					
a165	GRLTRQMVKYLQKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
a165	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL					
	250	260	270	280	290	300

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	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPJ.TKYLLG				
	310	320	330	340	350
	370	380	390	400	420
a165	ELRKTKEERFASLLEYYPEANPDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGCTTGG  GAAATCACCC
101  TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAA  CCGTGGAAC
151  AACGcCGgca  CGGGGCATT  CGcGCTGTGc  GAATTGAACT  AtgcgccGCT
201  GGGtgcggac  ggcgtcatCA  ATCCGGCGCG  cgCCCTGAAT  ATTGCCGAAC
251  AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctggtCGC  GGAAGGCAAG
301  TTGGAAGACA  ATTCTTCAT  CAATGCCGTG  CCGCATATGT  CTTGGTGAT
351  GAACGAAGAC  CACTGCCGTT  ACCTGCAAAA  ACGCTATGAT  GTGTTAAAA
401  CGCAGAAACT  TTTGAAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451  TCCGATTGGG  CtccgCTGAT  TATGCGCGCG  CGGGACGAAA  ACCAACCCGT
501  CGCCGCCAAC  TATCCGCCG  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551  CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601  AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651  CAAAACCGCC  GATACCGCA  ACCCAGACTG  GCAGCTCACC  CTCCGCACCC
701  GCTTCTCTTT  CCTCGGCGCG  GCGGCGGCG  CACTGACCTT  GCTGCAAAAA
751  TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCCGGCCT
801  GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACACAC  AACGCCAAAG
851  TGACGGGCA  GGCTTCCGTC  GCGCGCGCG  CGATGTCCGT  CCCGCACCTC
901  GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTAIGTTTC  GTCCTTACGC
951  AGGTTTCCGT  TCCAACITCC  TCAAGCAAGG  CTCGTTTATG  GATTTGCCGC
1001  TGTCATCCA  TATGGACAAC  CTCTATCCTA  TGCTGCGCGC  CGGCTGGGCG
1051  AATATGCCCG  TGACCAAATA  CCTGCTGGGC  GAATTGCGTA  AAACCAAGA
1101  AGAACGCTtt  gCCTCCCTGC  TGgaatacta  cccGaggcag  acccGACGAc
1151  tggtagctcat  cagcagggnc  acGCGTcata  tcattanata  tgactCgaaa
1201  ctgcgcgctgc  tgcagttgta  cgagattgtg  ccaCGCGacg  ctgcgtcgcg
1251  cattctggag  cgtcgcggcg  catcacgctn  tgcgctgata  tccgctgatg
1301  acactgctcc  gaGCGcgccc  gtcttggaag  gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSALE  ELNYAPLGAD  GVINPARALN  IAEQFHVSRQ  FWATLVAEGK
101  LEDNSFINAV  PHMSLMNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDNRKI
151  SDWAPLIMRG  RDENPQVAAN  YSAEGTDVDF  GRLTRQMVKY  LQGGKGVKTEF
201  NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLQK
251  SIGPEKGKYG  GLPVSGLFFR  NSNPETAEOH  NAKVYQASV  GAPPMSVPHL
301  DTRNVDGKRH  LMFPGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351  NMPLTKYLLG  ELRKTKEERF  ASLLEYPRQ  TRRLVLITQX  TRHIIXYDSK
401  LRVLLQYEIV  PRDARSRILE  RRGASRXALI  SADDTAPSAP  VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

n165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGCTTGG  GAAATCACCC
101  TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAA  CCGTGGAAC
151  AACGCGCGCA  CGGGGCATT  CGCGCTGTGC  GAATTGAACT  ATGCGCCGTT
201  GGGTGCAAA  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251  AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTCCG  GGAAGGCAAG
301  TTGGAAGACA  ATTCTTCAT  CAATGCCGTG  CCGCATATGT  CTTGGTGAT
351  GAATGAAGAC  CATTGTCTT  ATCTTCAAAA  ACGTTATGAC  GCGTTTAAAA
401  CCCAAAACT  TTTTAAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451  TCCGATTGGG  CTCCGCTGAT  GATGCGCGCG  CGGGACGAAA  ACCAACCCGT
501  CGCCGCCAAC  TACTCCGCCG  AAGGTACGGA  TGTCGATTTC  GGACGGCTGA
551  CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601  AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651  CAAAACCGCC  GATACCGCA  ACCCGACGG  GCAGCTCACC  CTCCGTACCC
701  GCTTCTCTTT  CCTCGGCGCG  GCGGCGGCG  CGCTGACCTT  GCTGCAAAAA
751  TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCCGGCCT
801  GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACACAC  AACGCCAAAG

```

```

851 TGTACGGGCA GGCTTCCGTC GGC GCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTCGCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGAGCA AACCCCGACG
1151 ACTGGGAACT CATCACCGCA GGGCAACGCG TCCAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGAIGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

ml65-1.pep

```

1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEKG
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDENKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVGDKRH LMFGPYAGFR SNFLKQGS LM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKRD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

ml65-1/g165-1 89.7% identity in 428 aa overlap

ml65-1.pep	10	20	30	40	50	60
g165-1	10	20	30	40	50	60
ml65-1.pep	70	80	90	100	110	120
g165-1	70	80	90	100	110	120
ml65-1.pep	130	140	150	160	170	180
g165-1	130	140	150	160	170	180
ml65-1.pep	190	200	210	220	230	240
g165-1	190	200	210	220	230	240
ml65-1.pep	250	260	270	280	290	300
g165-1	250	260	270	280	290	300
ml65-1.pep	310	320	330	340	350	360
g165-1	310	320	330	340	350	360
ml65-1.pep	370	380	390	400	410	420
g165-1	370	380	390	400	410	420
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFFERAPSWEDRLKELVPGYGIKLNENPERADEIIA
:
| | |
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGCGTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGTCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAAC ATGCGCCGTT
201 GGTGCAAAAT GGGATTATCG ATCCGCGCGG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTTCG GGAAGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACT TTTTGAATAA ATGGAATTTT CCACCGATCG GAACAAAAT
451 TCCGATTGGG CTCGCGTGAT GATGCGCGCG CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCGG AAGGCACGGA TGTCGATTTG GGACGGCTGA
551 CGCGCCAAAT GGTGAATAT TTGACGGGCA AGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCG GATACCCGCA ACCCGACGCG GCAGCTCACC TCCGTACCC
701 GCTTCCTCTT CCTCGCGCGG GCGGCGGCGG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGG CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCC GCCCTTACGC
951 AGGCTTCCGT TCCAACTTCC TCAAGCAAGG CTCACTTATG GATTGCGCG
1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCCCAGGCGA AACCCGACG
1151 ACTGGGAAT CATCACCGCA GGGCAACGCG TTCAATCAT TAAAAAGAC
1201 TCCGAAAAAG CGGGCGTGTG GCAGTTTGGT ACGGAGATTG TCGCACACCG
1251 CGACGGCTCG CTCGCGCAT TGCTGGGCGG GTCGCGGGG CGATCGACCG
1301 CCGTGGCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWTALVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAAN YSAEGTDVDF GRLTRQMVY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLOK
251 SGIPEGKGYG GFEVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMEFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKID
401 SEKGVVQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFFERT
451 PSWEGRLKEL VPGYGIKLINE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 486 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
m165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWN	NAGTGHSALC		
	10	20	30	40	50	60
a165-1.pep	ELNYAPLGANGI	IIDPARALNIAEQFHVSQ	FWATLVAEGKLEDNS	FINAVPHMSLVMNED		
m165-1	ELNYAPLGANGI	IIDPARALNIAEQFHVSQ	FWATLVAEGKLEDNS	FINAVPHMSLVMNED		
	70	80	90	100	110	120
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMRGR	DENQPVAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMRGR	DENQPVAANYSAEGTDVDF			
	130	140	150	160	170	180
a165-1.pep						
m165-1						
	190	200	210	220	230	240

a165-1.pep GRLTRCMVKYLQGGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
 |||||
 m165-1 GRLTRCMVKYLQGGKGVKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
 190 200 210 220 230 240

a165-1.pep 250 260 270 280 290 300
 GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
 |||||
 m165-1 GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL
 250 260 270 280 290 300

a165-1.pep 310 320 330 340 350 360
 DTRNVGDKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
 |||||
 m165-1 DTRNVGDKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
 310 320 330 340 350 360

a165-1.pep 370 380 390 400 410 420
 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVAHADGS
 |||||
 m165-1 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVAHADGS
 370 380 390 400 410 420

a165-1.pep 430 440 450 460 470 480
 LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNNPERADEIIA
 |||||
 m165-1 LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEDRLKELVPGYGIKLNNPERADEIIA
 430 440 450 460 470 480

a165-1.pep 489
 YTAKVLDIX
 |||||
 m165-1 YTAKVLDIX

a165-1/p33940

sp|P33940|YOH_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION
 >gi|1736851|gnl|PID|d1016718 (D90850) ORF ID:o372#5; similar to [SwissProt Accession Number
 P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
 to 490 residues of YOH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct
 identical to GB: ECOHU49_33
 ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
 Score = 458 bits (1167), Expect = e-128
 Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

Query: 3 EATDVVLVGGGIMSATLGVLKLELEPSWEITLIERLEDVALESSNAWNNAGTGHSALCEL 62
 + TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
 Sbjct: 30 QETDVLLIGGIMSATLGTYLRELEPEWSMTMVERLEGVAOESSNGWNNAGTGHSALMEL 89

Query: 63 NYAPLGGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLED-NSFINAVPHMSLVNMEDH 121
 NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
 Sbjct: 90 NYTPQNADGSSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMRGRDENOPVAANYSAEGTDVDFG 181
 ++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
 Sbjct: 150 VNFLRARYAALQQSSLFGRMRYSEDHAQIKEWAPLVMEGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLQGGK-VKTEFNHRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
 +TRQ++ LQ K + + V +KR D W + AD +N Q
 Sbjct: 210 EITRQLIASLQKKSNFLQSLSSSEVRALKRNDNTWTVTVADLKNGTAG-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYGOASVGAPPMSVPHL 300
 Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
 Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQLVSENPDVVNHHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVGDKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
 DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
 Sbjct: 329 DTRVLDGKRVVLFPGFATFSTKFLKNGSLWDLMSSTTTSNVMPMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLOFGTEIVXXXXXX 420
 ++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
 Sbjct: 389 QVHLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDSEKGGVLRGTEVVSDDQGT 448

Query: 421 XXXXXXXXXXXXXVPLMIRLMHQCFPER--TFSWEGRLKELVPGYGIKLNNPERADEI 478

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPINLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508

Query: 479 IAYTAKVLDI 488

+ YT++VL +

Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcgccgg cggaataaaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccgtt ctgcacggcg gcatagccgc ttttgcctgc ctgatagggg
 101 tgcaggcgcg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaacaa ggtatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggctt ccaagtctgt gggatgcttt ccggtcagcc ggacggcggt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgtacttt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg c tttgtgccgc
 451 attttgcggc tgttccgcgc tattttcgga tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtcgaaacg tggcaggcgg
 601 aggttcggac ggcatgggt ttatttcaac gggcggatgc cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgc ttttgcgcgc
 701 ctgctgcaa aatctcttcg atttgcgag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRRALCR
 151 ILRLFRIRFG FAAGKQQA A QHGKRYFQH SALLMVSKCR LKRLKRGR
 201 RFRHWVYFN GRMPTASRTL SNNRSASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGCGG CGGAATAAAA ACGCCCCTTC GCTGTCGATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCGATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCAACC TGCCGGAAGT TCCTTATCAT CGGTTTCCAT ACATTGCGCG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
 351 TGGTTTGGC TTCGCTGCTT TGTCCCAAT CCAAACCGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGGCGC TGTACCGCGC TATTTwCGGA TTTGCCGCaC GGCaArgCAG
 501 CAGGCAGCCG CCCAATACCG CAAAFawGT WTTcAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAAACGGG CAGCGGAGG TTCGGACGGC
 601 ATCGGTTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTGTCCA
 651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCTGC CTGCAAAATC
 701 TCTTCGATTT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAABIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
 151 VLRLYRRIXG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFRGR
 201 HRVHFNRMPT TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

m204/q204

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

```

a204.pep
1  MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVIRQFAAVF
51  GDIAHQFGKQ GMAHAVCRPA RRRALSVGFH TFADDGFQVV GMLAQGPDDV
101 LFRQAF . . . . .
151 . . . . .
201 HWVYFNGRIP TASRTLPNNS RASLRAFCAP ACKISSCEG SAVSSL*

```

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSVGFHTFADDFQVVGMLAGQPDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQTGNRRIVDIYDFENRFRRLYRVLRLYRRXGFAATAXQAAAQYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRRRRFGRHRVHFNGRMP TASGTL SNNSRASLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTL PNNRSASLRAFCAPACKISSICEG					
		110	120	130	140	150
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

```

g205.seq
1  atgctgaaaa taccttttgc cgtgttgggc ggctgectgc tgettgcgcg
51  ctgcggcaaa tccgaaaata cggcgaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggttttg ctttgggaca agtagcgaa ggcaaaacca acgacggcaa
201 aaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctggcggg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaacgtac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgcgctgcag aacggacgct atgtgctgga
501 aatgcacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

```

g205.pep
1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51  AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGDAPS GWAENGVCHT LFAKLVGNIA EDGGLTDYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS BGAIFYRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

```

m205.seq
1  ATGCTGAawa CwTyTTTtGC CGTATTGGGC GGCTGCCTGC TGcYtTGCCG
51  tGCGGCAAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CCGTACAAAG
101 CGCGCCGAAA CCGGTTTtCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAAATGTA
301 TGGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC GCCTTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

m205.pep

```

1  MLXTXFAVLG GCLLXCRCCK SXNTAVQPQN AVQSAPKPVF KVIYIDNTAI
51  AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

m205/g205

	10	20	30	40	50	60
m205.pep	MLXTXFAVLGGCLLXCRCCKSXNTAVQPQNAVQSAPKPVFKVIYIDNTA	AGLDLGQSSE				
g205	MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVKYIDNTA	IGLALGQSSE				
	10	20	30	40	50	60
	70	80	90	100	110	120
m205.pep	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDS	PAGWAENGVCHT				
g205	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDA	PSGWAENGVCHT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m205.pep	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEI	DSEGAFYFRRRH				
g205	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEI	DSEGAFYFRRRH				
	130	140	150	160	170	180
m205.pep	YX					
g205	Y					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205.seq (partial)

```

1  TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG
51  CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG
101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGCGGT GTGCCATACC
151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAAC TGAC
201 GGATTACCTG ATTTCGCATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA
251 GCGGCTATGC CGCCGTGCAG AACGGACGCT ATGTGCTGGA AATCGACAGC
301 GAGGGGGCGT TTTATTTCCG CCGCCGCCAT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205.pep (partial)

```

1  SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVC HT
51  LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ AGKSGYAAVQ NGRYVLEI DS
101 EGAFYFRRRH Y*

```

m205/a205 88.3% identity in 111 aa overlap

	50	60	70	80	90	100
m205.pep	KVIYIDNTA	IGLDLGQSSE	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC			
a205			SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC			
			10	20	30	
	110	120	130	140	150	160
m205.pep	METDDKDS	PAGWAENGVC HT	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQ			

g205-1.seq (partial)

g205-1.pep (partial).

m205-1.seq..

m205-1.pgp

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAAGCKSENTAEQPNAAQSAPKPVFKVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAAGCKSENTAEQPNNAVQSAPKPVFKVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQISYPIKGLPEQNVRRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQISYPIKGLPEQNVRRLTGKHPNDLEAVSGKCMETDDKDS PAGWAENGVCHT					

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```

              70      80      90      100     110     120
          130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGA F
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1      LFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNGRYVLEIDSEGA FYFRRRH
          130      140      150      160      170      180
m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
  1 CCTCTTAAAG GCTTGCCGGA ACAAAACGTC GTCCGGCTGA CCGGCAAGCA
  51 TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
 101 AGGGCGCGCC TTGGGGCTGG GCGGCAACG GCGTGTGCCA TACCTTGTTF
 151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGCGCAAAC TGACGGATTA
 201 CCTGATTTCG CATTCCGCCC TGCAACCCTA TCAGGCAGGC AAAAGCGGCT
 251 ATGCCCGCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
 301 GCGTTTATT TCCGCCGCC CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
  1 PLKGLPEQNV VRLTGKHPND LEAVVGKME TDGKGAPSGW AANGVCHTLF
  51 AKLVGNI AED GGKLT DYLI S HSALQPYQAG KSGYAAVQNG RYVLEIDSEG
 101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

              50      60      70      80      90      100
m205-1.pep  KYIDNTA IAGLD LGQSSE GKTNDG KQISYPI KGLPEQNVIRLIGKHPGDLEAVSGKME
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKME
          10      20      30

              110      120      130      140      150      160
m205-1.pep  TDDKDS PAGAENG VCHTLF AKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a205-1      TDGKGAPSGWAANGVCHTLF AKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
          40      50      60      70      80      90

              170      180
m205-1.pep  RYVLEIDSEGA FYFRRRHYX
          |||:|||||:|||||:|||||:|||||
a205-1      RYVLEIDSEGA FYFRRRHYX
          100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
  1 atgttttccc cegacaaaac ccttttcctc tgtctcggcg cactgctcct
  51 cgctcatgc ggcacgacct ccggcaaaac ccgccaaccg aaaccctaac
 101 agacagtcgc gcaaatccaa gccgtccgca tcagccacat eggcgcaca
 151 caaggctcgc aggaactcat gctccacagc ctccgactca tcggcacgcc
 201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcgga
 251 tgattcaatt ggtttacaaa aacgccctca acgtcaagct gccgcgacc
 301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
 351 ggccggcgac atcgatttct tcaacaccgg cggcgcacac cgctactcac
 401 acgtcggact ctacatcggc aacggcgaat tcattcatgc ccccggcagc
 451 ggcaaaacca tcaaaaccga aaaactctcc acaccgtttt acgccaaaaa
 501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
  1 MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq

1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGgAAA ATCCCGGAcA GCCGCTTAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..

1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
 151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSLALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
g206	MFSPDKTLFLCLGALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIGRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFVYKNALNVKLPR	TARDMAAASRKIPDSRXKAGD			
g206	LGLIGTPYKWGGSSTATGFD	CSGMIQLVYKNALNVKLPR	TARDMAAASRKIPDSRLKAGD			
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIG	NGEFIHAPSSGKTIKTEKL	STPFYAKNYLGAHTFFTEX			
g206	IVFFNTGGAHRYSHVGLYIG	NGEFIHAPSGKTIKTEKL	STPFYAKNYLGAHTFFTE			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq

1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
 151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
 201 CTACAAATGG GCGCGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
 251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
 301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCTTAA
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCAGCAGC
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
 501 CTACCTCGGC GCACATACTT TCTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRTQGSQELMLHS
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFYK NALNVKLPR
101 ARDMAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
a206	MFPPDKTLFLCLSALLLASC	GTTSGKHRQPKPKQTVRQIQ	AVRISHIDRTQGSQELMLHS			
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD	CSGMIQFYKNALNVKLPR	TARDMAAASRKIPDSRXKAGD			
a206	LGLIGTPYKWGGSSTATGFD	CSGMIQFYKNALNVKLPR	TARDMAAASRKIPDSRLKAGD			
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEK	LSTPFYAKNYLGAHTFFTEX			
a206	LVFFNTGGAHRYSHVGLYI	GNGEFIHAPSSGKTIKTEK	LSTPFYAKNYLGAHTFFTEX			
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttggcgcggt tgtttttcga
51  tgctgcggtt gatgtgccac tgctggcgga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggttttg gcgaacatcg ttgccgccat aatgatggcg
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccagc tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 tcgctgcggc tatttttctt tgatggtctg cagttcgggt gcggcgccac
501 gcattttcgc catcgaaagg taggaggcgt tggccaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgctggc gatgtttgcg
701 ataacggatg tggtttcggg accggcatac aggttgaccg ccattttcgg
751 ttttgccccc cgggttgga tagcgggtaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
m209.pep
1  MLRHLGNDFA LGALFFDAAV DVPLLDGQVE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDQDQVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQRQTAA QRVDLVEFEK LHHRLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP ERRCEPVYFT VVFCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDGSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGCGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

m209.per

m209/q209

a209.seq

1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

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```
51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGTATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCSGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCCA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAA GAGGGGGGAG GCGAACCAGT
651 GTACGTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTCTGCG CATGTTTGCG
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACCTGACGCG TGGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGCGCG
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTCGGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

a209.pep

```
1 MLRHLGNDEA LGALFFDAAV DVPLLDGQGE VVDHPVQYQT GREEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVQGW IQYGFDDG* NDNRPAFVAD
201 DVVQLVQPK EGGGEPVYFA VVFGQLQVVG DVCNCGGLW AGVEVDGGFG
251 FAPFWIAAKG TLTLVLYSL LRRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

	10	20	30	40	50	60
m209.pep	MLRHLGNDFALGALFFDAAVDVPLLDGQGEVVDHPVQYQTGREEEHDGENQRHDFHHFR					
a209	MLRHLGNDFALGALFFDAAVDVPLLDGQGEVVDHPVQYQTGREEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
	70	80	90	100	110	120
m209.pep	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
a209	LHRVGRRRVQISLGEHRCRHNDGDVVGVAEVEGNPTQPRCLAQFYGGECPIQSDG					
	70	80	90	100	110	120
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
	130	140	150	160	170	180
m209.pep	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
a209	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVQW					
	130	140	150	160	170	180
m209.pep	IQYGFDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
m209.pep	IQYGFDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
a209	IQYGFDDGXNDNRPAFVADDVVQLVQEPVEERGGEVYFAVVFGQLQVVGDVCDGCGLR					
	190	200	210	220	230	240
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLYSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLYSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	AGVEVDGGFGFAPFWMAAKGTLTLVLYSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW					
a209	AGVEVDGGFGFAPFWIAAKGTLTLVLYSLRRLMSIRQSPAAQTLCPPLGWRIQVDMKW					
	250	260	270	280	290	300
m209.pep	CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX					

```
g211.seq
1  atgtttcgga ttgctgctgc caatcagttg gccggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttggcg tggtgctgat aatcaggttg
101 agtttttga aggaaacctg attgtagtcg gcgcgtccgg cgcgtccgct
151 gtaacggtag ccgtggcgca attcgacgt cgtttgtgtg tcttcacgag
201 agaagttacc tctttggcg aagatgatgt tgcgcgcgc gttttgtcc
251 tgttcgcgca ggaacaggtt tttcatgatg ccggttcgg tgtcaaaggt
301 ttcgacgaaa taaccctgc cgttcgctt gcccaagta tgaactcgc
351 cggcttccac caaagacaat tctcgttct gcttcaaat ttcggcatat
401 tcgcggctgc gcagctctgc ccacggtatc acccaaagct gcattgcggc
451 aatcaggtag gcaaacggca cggcaaatcg catgacgggg cgtatccact
501 gtttcaacgc caatcgcgag cgttag
```

g211.pep

1	MLRIAANQL	GGRNGAAVGN	GVDKFGRGAD	NQVEFLIGNL	IVVGASGRAA
51	VTVAVAQFER	AFVVLQREVT	FFGQDDVVA	VFVLFQEQV	FHDAGFGVKG
101	NDEINPAVAL	AQVIELAGFH	QRQFLLLQN	FGIFAAALC	PRYHPKLHDG
151	FDGGRKHGKL	HDGAYPLFOR	QSAG*		

```
m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGACGTG CGGTTTGTTG TCGTTACAGC
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTTGTCC
251 TGTTCCGCGCA GGAACAGGTT TTTCATGATG CCGGATTCCG TATCGAAGGT
301 TTCGACAAAA TAAACCTGCG CGTTGCGCTT GCCCAAAGTG TTGAACTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AATCAAAAACG GCAAAAGGCA CGGCAAAGTG CATCACCGGG CGTATCCATT
501 GTTTCAATGC CAATCGCAaG GATAG
```

m211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFL E GNL	IVVGASGRAA
51	VTVA V AQFER	AFVVQREV T	FFGEDDVVAA	VFVLFAQEQV	FHDAGFGLEG
101	FDKINPAVAL	AQTVELAC LH	QRQ FL LLLLQD	FSVFAAAXLC	PRYHPKLHDG
151	NQNGKRHGKL	HHRAYPLFQC	QSAG*		

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEG	NLI	VVGASGRAAVTV	AVAQFER		
	: : :					
g211	MLRIAANQLGGRNGAAVGNVDFKGRGADNQVEFLEG	NLI	VVGASGRAAVTV	AVAQFER		
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTF	FGEDDVVAAV	FLFAQEQV	FHDAGFGIEG	FDKINPAVALA	QTVELACLH

```

a211.seq
1  ATGTTGCGGG  TTGCTGCTGC  CAATCAGTTG  GGCGGTGCGA  ATGGTACGGC
51  GGTGGGAAAC  GGGGTGCGAT  AGTTTGCGCG  TGGTGCTGAT  AATCAGGTG
101 AGTTTTTGGG  AGGAAACCTG  ATTTGATGTC  GCGCGTCGGG  GCGTGCCGCT
151 GTAACGGTAG  CCGTGCGCGA  ATTCGAGCGT  GCGTTTGTG  TCGTTCAGCG
201 AGAAGTTACT  TTCTTTGGCG  AAGATGATGT  TGTGCGCCGC  GTTTTGTGCC
251 TGTTCGCGCA  GGAACAGGTT  TTTTCATGAT  CCGGATTCGG  TATCGAAGGT
301 TCGACAAAA  TAAACCTGCG  CGTTGCGCTT  GCCAAACTG  TGTAAACGCG
351 CTGCCTCCAC  CAAAGACAAT  TCCTGCTTCT  GCTTCAGGAT  TTCAGCGTAT
401 TCGCGGCTGC  GTAGCTCTGC  CCACGGTATC  ACCCAAAGCT  GCATACGGC
451 AATCAAAACG  GCAAACGGCA  CGGCAAACCT  CATCACCGGG  CGTATCCATT
501 GTTTCATGCG  CAATCCGCGA  GATAG

```

a211.pep

1	MLRVAANQL	GGRNGTAVGN	GVDFEGRGAD	NQVEFLEGNL	IVVGASGRAA
51	VTVAQAQFER	AFVVVQREVT	FFGEDDVVAA	VFVLFQAQEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLL	QRQFLLLLQD	FSVFAAA*LC	PRYHPKLHDG
151	NONGKRHGKLL	HHRAYPLFOC	OSAG*		

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER				
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLI	VVGASGRAAVTVAVAQFER				
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVA	AVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVELAC				
a211	AFVVVQREVTFFGEDDVVA	AVFVLFAQEQQVFHDAGFGIEGFDKINPAVALAQTVEPAC				
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLC	PRYHPK	LHDG	NQNGKR	HGK	LHHRAYPLFCQSAGX
a211	QRQFLLLLQDFSVFAAAXLC	PRYHPK	LHDG	NQNGKR	HGK	LHHRAYPLFCQSAGX
	130	140	150	160	170	

```
g212.seq (partial)
      1  atggacaatc tcgatggga cggcattccc gacatccgca cactcgacca
     51  aaccatccgc aaacacgcac acccgcctcaa cctgatgttc tgccctccccg
    101  ataactcagat tcccgatttt caaacgcgca aagatgtctc ggactcgga
    151  tgcgcgtctga agcacgcttt ggatcaggca acccagtgcc tcaggttcga
    201  cagcatcaac ctcatogaac acatcctgcc cgatgtccgc ttctggctgg
    251  ttcccccttc acgcaacccg cgcttgacag aacacttcca cacatttcc
    301  ttgagacagg aagccatccc gcaaacggaa agcaagtcg cacaacctcg
    351  gtttcgactt ccacaacatc ccgaacggaa aaaaaccgaa cacqctctct
```



```

401 tcatcggtgc aggcattgcc ggcgcacga ccgcccacgc cttagcatca
451 caccggcattt cgtttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccggacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccc aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcaccctcct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 acccgcattht cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 cacattttacc gccacacaca tcattctactg caccggcgcg cacagccctt
1001 gcctgcccga aaccaacctc gcgcacctac ccctcaggca aatacgcgga
1051 caaacccggcc tcacaccgct caccctgttt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgct gtggcacgga ctgcaactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacccgca agcattggca cacttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQTIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRLDQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFFHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNBA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCCTCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCAAGGGC TGCTCTACGC CAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGCT ACGGCTACAC CAAACGCCGT
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTGCTCC
851 GCACCCCTCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATT CCCACGACGG GGAAGAGTGG ATGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCCTAGT CCGCGCACTC
1351 GCGGACATTG CCGCCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAACCTACCG ATCGACACCC CATGCCATA CCGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CGGCACCCGC GGAATCGCCA CCGCCCCCAT CTGCGCCGCC

```

1501 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTACACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep

1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHRLDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHPHHIS
 101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALESSE FAANPNPQKH QGHAAIRCDS PDHPLVLGAL
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)

from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII	CLPDNQIPDFQTAQDASDAECRLKHRLDQA				
g212	MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRKLKHRLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPDKPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	PQTSEKQKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNRQALAHLPALSESSE					

490

```

|||||
g212  SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSNTGWNEAEEASNRQALAHLPALAESL
      370      380      390      400      410      420

      430      440      450      460      470      480
m212 . pep  FAANPNPQKHQGHAAIRCDSPDHLPLVGALGDIAAMRQTYTKLALDKNYRIDTPCPYLPN
      |
g212        F

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

```

a212 . seq
1  ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51  AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCCTCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAC AAGATGCTTC GGACCGGAA
151 TGCCGTCTGA AGCACCCTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCTGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACACTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCG ACAAACCTTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GCGCGGGCAA CCGCCACGCG CTTAGCATCA
451 TACGGCATT T CCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAAGTCTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAAAC ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCAGGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCCTACGCCG AACCATTATG
801 CGGACTGTTT TGGCAGTACG CGGTATGGCT CAATCCTCCC ACATTGCTCC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACGAAGA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCGGA AACCAACCTC GCCACCTGCG CCCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACGCTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGCA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCAAC TTCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCTATGCA ACAAACCTAC GCCAACTCG CGCTGGACAA
1401 AAATATCGC ATCGATGCCC CCTGCCGTA CCTGCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCAT CTGCGCCGCC
1501 CGCGTTGAG CCGAAATCCT AGGCTTGCCC CATCCCTCT CAAAACGCCT
1551 GCGCCACGCC CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738; ORF 212.a>:

```

a212 . pep
1  MDNLAWNGIP DIRTLDQFIR KHAHPLNLIV CLPDNQIPNF QTAQDASDAE
51  CRLKHLRLDQA TQCIQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKPDKPWFAF POTSERQKPE HILVIGAGIS GAATAHALAS
151 YGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHHNH LYRSITQAEA
251 EKIAGIPLNT PYAEPLGLF WQYGVWLNPP TFVRALLSHP LIGLHEDTFL
301 TDISHDGEKW IASTPNGTFT ATHIYCTGA NSPYLPETNL ATLPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
401 EEASNRQALA HLPALSES L FAANPNPQKH QGHAAIRCDSPDHLPLVGAL
451 GDIAAMQQTY AKLALDKNYR IDAPCPYLPN AYANTAHGTR GLATAPICAA
501 AVAAEILGLP HPLSKRLRHA LHPNRAIRA IVRRKDITP*

```

m212/a212 93.7% identity in 539 aa overlap

```

      10      20      30      40      50      60
m212 . pep  MDNLVWDGIPDIRTLDQAIRKHAPPLNLIICLPDNQIPDFQTAQDASDAECRLKHLRLDQA
      |||||:|||||: ||| |||||:|||||:|||||:|||||:|||||:|||||:|||||
a212        MDNLAWNGIPDIRTLDQTIRKHAEPPLNLIVCLPDNQIPNFQTAQDASDAECRLKHLRLDQA

```

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

g214.seq

```

1  atgatacaaa agatatgtaa gctatattgtt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtacgctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag gccggaaggc
251 tcgcccgctc gcttcagcca aacgttggac gggggcacaag ggacggtgag
301 cggtcaggca aacaacgtta cctattcctc cgcagggaagc actgtcgttc
351 tgaccggcaa tgcacaaagt cagcgcggcg gcgacggtgc cgaaggtgag
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

492

```

1  MIQKICKLV LIVIFATSPA FALQSDSRP IQIEADQGS DQANQRTTFS
51  GNVIIRQGT L NISASCVNVT RGRQRRRIE GGRFARPLQ NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ CQSAARRRRC RRCGHYLQHQ NRSLYHQHQH
151 EIGCEIRFQ N RQGRRHPAF KHTKNRITPM PSETETQFR HLPTEMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```

m214.seq (partial)
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTGAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCGCGT
201 CAATGTTACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGT
251 CGCCAGTCCG CTTGAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGTAAT GCCAAGTAC AGCGGCGCG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CCGCAGCACA
451 AAATT...

```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```

m214.pep (partial)
1  MIQKICKLV LIAFFSASPA FALQSDSRP IQIEADQGS DQANQSTTFS
51  GNVIIRQGT L NISAARVNVT RGRQRRRIE GGRFASPLQ DIGRRQRHGA
101 RTGKQRCLEI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQHQH
151 KI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

m214/g214

	10	20	30	40	50	60
m214.pep	MIQKICKLV	LIAFFSASP	FALQSDSRP	IQIEADQGS	LDQANQSTT	FP
g214	MIQKICKLV	LIVIFATSP	AFALQSDSR	PIQIEADQS	LDQANQRTT	FP
	10	20	30	40	50	60
m214.pep	NISAARVNVT	RGRQRRRIE	REGGRFAS	PLQPDIGRR	QRHGARTG	KORCLFIC
g214	NISASCVNVT	RGRQRRRIE	REGGRFAR	PLQPNVGR	QRCGARS	GKORYLFL
	70	80	90	100	110	120
m214.pep	NRX					
g214	RRKHC	RSDRQ				
	130	140	150			
m214.pep	CQSTARRRC	RRRCGDYIQ	HQNRSLYHQ	RQH		
g214	CQSAARRRC	RRRCGHYLQ	HQNRSLYHQ	ROHEIGCE	IRFQNRQ	GRRHPAFK
	130	140	150	160	170	180
g214	PSETETQ	FRRLP	TEMPRRDY			
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```

a214.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTGAGC
151 GGAAACGTCG TCATCAGACA GGTACGCTC AATATTTCCG CCGCCGCGT
201 CAATGTTACA CGCGGCGG AAGCGGCGG AATCCGTGAG GCGGAAGGT
251 TCGCCAGTCC GCTTCAGCCA GACATTGGAC GCGGCAAAG GCACGTGCG
301 CGGACAGGCA AACAACGTTG CTTATTCATC TGCAGGCAGC ACCGTAGTCT

```

493

```

351 TAACCGGTAA TCCCAAAGTA CAGCGCGGCG GCGATGTGCG CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
  1 MIQKICKLV LIAFFSASPA FALQSDSRQP IQIEADQGS LQANQSTTFS
 51 GNVVIRQGT L NISAARVNV T RGXQRRRIE GGRFASPLQF DIGRRQRHGA
101 RTGQRCLEF C RQHRSLNR* CQSTARRRCR RRCGDIYHQ NRSLYHQRH
151 KIRRKIRFQI RQGQRRYPAF EYAKIRIIFM PSET*TWFR HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLV	LIAFFSASP	FALQSDSRQ	PIQIEADQGS	LQANQSTTFS	GNVVIRQGT
a214	MIQKICKLV	LIAFFSASP	FALQSDSRQ	PIQIEADQGS	LQANQSTTFS	GNVVIRQGT
	10	20	30	40	50	60
m214.pep	NISAARVNV	TRGRRRRIE	GGRFASPLQ	PDIGRRQRH	GARTGKQRC	LFIQRHSLNR
a214	NISAARVNV	TRGXRRRIE	GGRFASPLQ	PDIGRRQRH	GARTGKQRC	LFIQRHSLNR
	70	80	90	100	110	120
m214.pep	CQSTARRRC	RRRCGDIYH	QNRSLYHQ	RQHKI		
a214	CQSTARRRC	RRRCGDIYH	QNRSLYHQ	RQHKIRRKIR	FQIRQGRRY	PAFEYAKIRI
	130	140	150			
m214.pep	PSETXTWFR	HLPTEILKRY	LX			
a214	PSETXTWFR	HLPTEILKRY	LX			
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTGTG TTAATTGTAA TTTTGCAC
 51 TTCTCCCGCT TTGCCCCTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGGTACGCTC AACATTCCG CCTCGCGCT
201 CAACGTCACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGT
251 CGCCCGTCCG CTTAGCCAA ACGTTGGACG GGGGCAAAGG GACGGTCCG
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCAG
451 AAATCGGGTG CGAAATCCG TCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
  1 MIQKICKLV LIVIFATSPA FALQSDSRP IQIEADQGS LQANQSTTFS
 51 GNVVIRQGT L NISASRVNV T RGGKGGESV AEGSPVRFSSQ TLDGGKGTVR
101 GQANNVTYSS AGSTVLTGN AKVQRGDDVA EGAVITYNKT TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
  1 ATGATACAAA AGATATGTAA GCTATTGTG TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTGCCCCTC AAAGCGACAG CAGGCAGCCT ATTCAGATG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAGCAC CACATTAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT

```

494

```

201 CAATGTTACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS LDOANQSTTF
51 GNVVIRQCTL NISAAARNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 QQANNVAYSS AGSTVVL TGN AKVQRGGDVA EGAVITYN TK TEVYTISGS
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

```

          10      20      30      40      50      60
m214-1.pep MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS LDOANQSTTFSGNVVIRQCTL
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
g214-1      MIQKICKLFV LIVIFATSPAFALQSDSRRP IQIEADQGS LDOANQSTTFSGNVVIRQCTL
          10      20      30      40      50      60

          70      80      90      100     110     120
m214-1.pep NISAAARNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGTVRGQANNVAYSSAGSTVVL TGN
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
g214-1      NISASRVNVT RGGKGGESVRAEGSPVRF SQ TLDGGKGTVRGQANNVYSSAGSTVVL TGN
          70      80      90      100     110     120

          130     140     150     160     170
m214-1.pep AKVQRGGDVA EGAVITYN TKTEVYTISG STKSGAKSASKS GRVSVVIQPS STQKSEX
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
g214-1      AKVQRGGDVA EGAVITYN TKTEVYTING STKSGAKSASKS GRVSVVIQPS STQKTEX
          130     140     150     160     170

```

g214-1/p38685

sp|P38685|YHBN ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_0185 [Escherichia coli]
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
Score = 97.1 bits (238), Expect = 6e-20
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQP IQIEADQGS LDOANQSTTFSGNVVIRQCTL NISAAARNVT R--GGKGG 76
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
Sbjct: 24 PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKVVT RPPGGEQ GK 83

Query: 77 ESVAEAGSPVRF SQ TLDGGKGTVRGQANNVAYSSAGSTVVL TGN AKVQRGGDVA EGAVIT 136
E + G P F Q D GK V G A + + Y A VVL TGN A +Q+ +G IT
Sbjct: 84 EVIDGYGKPATFYQMDNGK-PVEGHASQMHYELAKDFVVL TGN AY LQOVDS NIKGDKIT 142

Query: 137 YNKTTE 142
Y K +
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTGTGTT TTAATAGCAT TTTTTCGCGC
51 GTCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGCCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCG CCGCCCGCGT
201 CAATGTTACA CGCGGCGGCA AAGCGGCGCA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACC GGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS LDOANQSTTF

```

495

51 GNVVIRQGTI NISAARVNVT RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GOANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTR TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	AFFSASP	AFALQSDSRQFIQIEADQGS	LDQANQSTTFSGNVVIRQGTI		
m214-1	MIQKICKLFVLI	AFFSASP	AFALQSDSRQFIQIEADQGS	LDQANQSTTFSGNVVIRQGTI		
	10	20	30	40	50	60
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGOANNVAYSSAGSTVVLTGN			
m214-1	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGOANNVAYSSAGSTVVLTGN			
	70	80	90	100	110	120
a214-1.pep	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGOANNVAYSSAGSTVVLTGN			
m214-1	NISAARVNVT	RGGKGGESVRAEGSPVRFSSQ	TLDGGKGTVRGOANNVAYSSAGSTVVLTGN			
	70	80	90	100	110	120
a214-1.pep	AKVQRGGDVAEGAVITYNTRKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
m214-1	AKVQRGGDVAEGAVITYNTRKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVAEGAVITYNTRKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
m214-1	AKVQRGGDVAEGAVITYNTRKTEVYTISGSTKSGAKSASKSGRVS	SVVIQPSSTQKSEX				
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq

```

1  atgaaagtaa gatggcggta cggaattgcg ttccattga tattggcggg
51  tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
151 ttggacggaa ggcggtttga cgaacaggga tacttgaaag aacatttgag
201 cgcgaagagt gcgaacagct ttcccgaata cagcgacatc cattttgatt
251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa
351 caacgttgtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaaag
401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaac
451 gatacgcttg tcagtttcca atatggcgcg tcgcaaggtc aggcgggcgg
501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
551 aagccgcgat ttatgataca aaagatatgt aa
```

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep

```

1  MKVRWRYGIA FPLILAVLGL SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS
51  LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG
101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKLH VDTESQYAQT
151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAIYDT KDM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)

```

1  ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
51  CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
151 GCGAAACAGT TTCCGGAAG CAGCGACATC CATTTTGATT CGCCGCATCT
201 CGTGTTCCTC CAAGAAGGCA GGTGTTGTA CGAAGTCGGC AGCGACGAAG
251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG
301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAAAC GATACGCCTG
401 CAGTTTCCA ATATGGTGCA TCGCAGGTC AGGCGGGCGG CATGACTTAC
451 GACCACAwwA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
501 TTATGATACA AAAGATATGT AA
```

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)

```

1  ..SLSAWLGRIS EVEIEEVRNL PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
51  AKQFPENSDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY
```


496

151 DHXTGMLNFS SKVKATIIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
g215	MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
	10 20 30 40 50 60				
	50 60 70 80 90 100				
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
g215	YLKEHLSAKGAKQFPENS DIHFDS PHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				
	70 80 90 100 110 120				
	110 120 130 140 150 160				
m215.pep	LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTVPVSFQYGASHGQAGGMTYDHXTGMLNFS				
g215	LTKTADGRRQAGKVETEKHLHVDTESQYAQTDTVPVSFQYGASHGQAGGMTYNHKTGMLNFS				
	130 140 150 160 170 180				
	170				
m215.pep	SKVKATIIYDTKDMX				
g215	SKVKAIIYDTKDM				
	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATTTGA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GGCGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCTGACT
251	CACCGCATCT	CGTGTCTTTC	CAAGAAGGCA	GGTTGTTGTA	CGAAGTCGGC
301	ASCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCCAAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGTTGCA	TGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTMDS
51	LDGRRFDEQG	YLKEHLSSKG	AKQFPESDI	HFDSPHLVFF	QEGRLLYEVG
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLH	VDTESQYAQT
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG			
a215	MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
	10 20 30 40 50 60				
	50 60 70 80 90 100				
m215.pep	YLKEHLSAKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV				

a215	: :
	YLKEHLSSKGAKQFPPESSDIHFDSPLVFFQEGRLLEYVGSDAEVYHTENKQVLFKNVV
	70 80 90 100 110 120
m215.pep	110 120 130 140 150 160
	LTKTADGKRQAGKVEAEKLVDTESQYAQTDPVSFQYGASHGQAGGMTYDHTGMLNFS
a215	: :
	LTKTADGKRQAGKVEAEKLVDTESQYAQTDPVSFQYGASHGQAGGMTYDHKTGMLNFS
	130 140 150 160 170 180
m215.pep	170
	SKVKATIYDTKDMX
a215	:
	SKVKATIYDTKDMX
	190

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 757>:

q216.seq (partial)

1	..atgatatcga	tttcgcagctc	ggtagccaccg	gacgaaatca	cgcgcacatcat
51	ccccgcactc	aaacgcgaaag	acattaccct	cgtctgcac	accgcccgcgc
101	ccgattcaac	catggcgcgc	catgccgata	tccacatcac	cgcacatcggt
151	tcgcaagaag	cctgcgccgt	ggggcttgcc	ccgaccacca	gcaccaccgcg
201	cgttatggct	tggggcgacg	cgtggcggt	cgtctgctg	cgcgcccgcgc
251	cgttcacgcc	cgacgacttc	gccttgatcc	accctgcgg	cagccttcggc
301	aaacgcctgc	ttttgcgcgt	tgccgcacatt	atgcacaaag	gcggcggcctt
351	gcccgccgctc	cgactcgcga	cgcccttgaa	aggagccatc	gtcagcatga
401	gcgagaaaag	tttgggcctg	ttgggcgggaa	cggacgggca	aaggctgtct
451	gaaagagccctt	tttactga			

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

q216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVCI TARPDSMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHGAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGAI VSMSEKGLGM WAGTDGQRLS
151 ERPEY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

1	ATGGCAATGG	CAGAAAACGG	AAAATATCTC	GACTGGGCAC	GCGAAGTGTT
51	GCACGCCGAA	GCGGAAGGCT	TGCGCGAAAT	TGCAGCGGAA	TTG ₆ ACAAAA
101	ACTTCGTCCT	TGCGGCAGAC	GC ₆ TTGTGTG	AGTGCAAGGG	CAGGGTCGTT
151	ATCACGGGCA	TGGTCAAGTC	GGGACATATC	GCGCGCAAAA	TGGCGGCAAC
201	TATGGCCTCG	ACCGGCACGC	TCGCGT ₆ TTTT	CGTCCACCTC	GCGGAAGCGG
251	CACAC ₉ CGA	TTTGGGTATG	ATTGTGGACA	rCGACGTGGT	CGTCGCGATT
301	TCCAATTCCG	GCGAAAGCGA	CGAAATCGCC	GCCATCATCC	CCGCACTCAA
351	ACGCAAAGAC	ATCACGCTTG	TCTGCATCAC	CGCCCGCCCC	GATTCAACCA
401	TGGCGCGCCA	TGCCGACTTC	CACATCACGG	CGTCGGTTTC	CAAGAAGACC
451	TGCCCGCTGG	GCGTTGCCCC	GACCAACAGC	ACCACCGCGC	TATCGGCTTT
501	GGGCGATGCG	TTGGCGGTG	TC ₆ cGCTGCG	C ₉ cACGCGCG	TTACGCCCCG
551	ACGATTTCGC	CTTGAGCCAT	CCTGCCGGCA	GCCTCGGCAA	ACGCTACTTT
601	TTGCGCGTTG	CCGACATTAT	GCACA ₆ AAAGC	GGCGGCCTGC	CTGCGCTCCG
651	ACTCGGCACG	CCCTTAAAG	AAGCCATCGT	CAGCATAGTG	GA ₆ AAAGGCG
701	TGGGCAATGT	GCGCGTAAAG	GACGGGCAAG	GCGCTGTGAA	AGCGGTATTC
751	ACCGACGGCG	ATTTGCGCGG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTGATA	GACGAAGTCA	TGCATACGCA	TCCTAA ₆ AACC	ATCTCCGCGG
851	AACGCTTCGC	CACCAAGCC	CTGAAAGTCA	TGCAGGCAAA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGATGGCGTG	CTGATCGGCG	CGCTGAATAT
951	GACGACCTG	CTGGCGGCAC	GGATTGTATA	G	

This corresponds to the amino acid sequence <SEO ID 760: ORF 216>:

m216.pep

1 MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALJHCKGRVV

Homology with a predicted ORF from *N. gonorrhoeae*

m216/q216

	70	80	90	100	110	120
m216.pep	TMASTGTPAFFVHPAEAAHGDLGMIVDXDVVVAISNSGESDEIAAII	PALKRKR	DITL	VCI		
g216				::: ::	:: : ::	:: : ::
				MISISSVP	SPSDEITAI	IIPALKRKR
					10	20 30
	130	140	150	160	170	180
m216.pep	TARPDSTMARHADIHITASVSKEACPLGLAPTSTTTAVMA	LGDALAV	LLRARA	FTPD	DF	
g216	:: : ::	:: : ::	:: : ::	:: : ::	:: : ::	:: : ::
	TARPDSTMARHADIHITASVSQEACPLGLAPTSTTTAVMA	LGDALAV	LLRARA	FTPD	DF	
	40	50	60	70	80	90
	190	200	210	220	230	240
m216.pep	ALSHPAGSLGKRLLLLRVADIMHKGGLPAVRLGTPLKEAIV	SMSEKGL	GM	LAVTD	GGRL	
g216						
	ALIHPAGSLGKRLLLLRVADIMHKGGLPAVRLGTPLKGAIV	SMSEKGL	GMWAGT	DG	QRLS	
	100	110	120	130	140	150

a216.seq

1	ATGGCGATGG	CAGGAAACGA	AAAATATCTT	GATTGGGCAC	GCGAAGTGTT
51	GCACACCGAA	GCGGAAGGCT	TGCGCGAAAT	TGCGGCGGAT	TTGGACGAAA
101	ACTTCCGCCCT	TGCGGCGGAC	GGCTTGTTCG	ACTGCCAAAGG	CAGGCGTCGT
151	ATCACCGGCA	TGGGCAAGTC	GCGACATATC	TGCGCGAAAA	TGCGCGGAAA
201	CATGGCCTCG	ACCGGCACGC	CCGCGTTTTT	CGTCCACCCT	GCGGAAGCGG
251	CACACCGCGA	TTTGGGTCAT	ATTGTGGACA	ACGACGTGTT	CGTCGCGATT
301	TCCAATTCCG	GTGAAAGCGA	GCAAAATGCC	GCCATCATCC	CCGCGCTCAA
351	ACGCAAAAGT	ATCACGCTTG	TCTGCATCAC	GCGCCGCCCC	GATTCACCCA
401	TGGCGCGCCA	TGCCGACATC	CACATCACGG	CGTCGGTTTC	CAAAGAAGCC
451	TGCCCCGCTG	GGCTTGCCCC	GACCAACGAC	ACCACCCGCG	TTATGGCTTT
501	GGCGCATGGG	TTGGCGGTTG	TCTCTGTCGG	CGCCCGCGCG	TTACACGCCG
551	ACGACTTTCG	CTTAGGCCAC	CCTGCCGGCA	GCCTCGGCAA	AGCCCTACTT
601	TTGCGCGTTG	CCGACATTAT	GCACAAAGGC	GGCGGCCTGC	CTGCCGTCGG
651	ACTCGCACGG	CCCTTGAAAG	AAGCCATCGT	CAGCATGAGT	GAAAAGAGGG
701	TGGGCGATTG	GGCGGTAAAG	GACGGGCAAG	GCCGCTTGAA	AGGCGTATTC
751	ACCGACGGCG	ATTTGCGCGG	CCTGTTTCAA	GAATGCGACA	ATTTTACCGG
801	TCTTTTCGATA	GACGAAGTCA	TGCATACGCA	TCCTAAAACC	ATCTCCGCCG
851	AACGTCTCGC	CACCGAAGCC	CTGAAAGTCA	TGCAGGCCAA	CCATGTGAAC
901	GGGCTTCTGG	TTACCGATGC	AGATGGCGTG	CTGATCGGGC	CGCTGAATAT
951	GACACGACTT	TTGGCGGCGC	GGATTGTATA	G	

a216.pep

1	MAMAGNEKYL	DWAREVLHTE	AEGLREIAAD	LDENFALAAD	ALLHCKGRVV
51	ITSGMCKSGHI	GRKMAATMAS	TGTPCAFFVHP	AEAAHGDGLGM	IVDNDVVVAI
101	SNSGSEDELA	AIIPALKRKD	ITLVPIATVR	DSTMARHADI	HTIPASVSKEA
151	CPLGLAPTTS	TTAVMALGDA	LAVVLLRARA	FTPDFFALSH	PAGSLGKRLL
201	LRVADIMHKG	GGLPAVRGLT	PLKEAIVSMS	EKGLGMLAVT	DQGGRLKGVF
251	TGDGLRRFLQ	ECDNTTGLSI	DEVMTHTPKT	ISAERLATEA	LKMOVANHVN



301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

m216.pep	MAMAENGKYLDWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVVITGMVKSCHI
a216	MAMAGNEKYLDWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMKKSCHI
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARA
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT
m216.pep	DGQGRKLGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN
a216	DGQGRKLGVFTDGLRRLFQECDNFTGLSIDEVMHHPKTI SAERLATEALKVMQANHVN
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX
a216	GLLVTDADGVLIGALNMHDLAARIVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcgatg acgggttgggt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctgagggt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgagg ttgcccgat atccgggcaa
201 tatccgacag gggttcgagg aaggcgccaa aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgtgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatccccaa
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgg aaacggcgca acacggggcg gggttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcactccaac
551 gcataaaaaa acggttgccg gcggctgatt ttcaagtcgg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgctg tccgaacacg gcttccataa
651 aaggcgataa gggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKRBHFAD FKTAQQQVGH ALQRIKKRLP AADFHVRNGI

```

1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGAATAAT	TGCGCCAATT
51	CGGTTTCCCG	CTrCCATTG	ACCAATTCGT	TTTCAAGGTT	TTGGACTGAC
101	TTTGTGTCAT	CGGCTTCAGC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151	ACGCGCCACC	CATTCCCGCA	CTGTGCGCGT	GTCGCCCAT	ATCCGTCACA
201	TATCCGTCAG	GGTTTCGAGG	AAGGCGCGAA	AACGTCCGAA	CATGCGGTTT
251	TGATTACAGT	CGGCATACCA	CGCGCTGACA	TCCTGCCACA	TCGGATTGCC
301	GCCTTTGGCG	AGCATCCAGC	CCAATATCAT	GCGTCTTACC	GCCTGCTTCC
351	AGGTGAACAG	CTGATCCGTG	CCGCGCGCGA	TTTCTCCGTC	CAAAACCCAG
401	TGGACGTTCA	AATCGGCAAC	CATGTCGTGC	AAAAGCGGTA	AATCGTCTCT
451	AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCAACAAGC
501	CTTTATCGAC	TCAAATCGG	CTTTCCAACA	AGTCGAACAG	GCATGACAAA
551	GCATGAAGCA	GCGGTTGGCG	GCGGCTGATT	TTCAAGTCTG	ACACGGAATA
601	CGGCAATGCC	TGGCGACCgG	gCtGGCGCTT	TCCGAACACG	GCTTCGATAA
651	AAGGCGTATA	GGATTGATA	TTCCGGGGTTA	A	

```

1  MADDGVRRQL SGKLRQFGFR LPFPDPVFKV LDXLLVIGFS LEQCFKQIPA
51 TRHPFADRCG LPPYPYNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXIVL
151 SQSEATAQHGR GFXKHKHKFID FKSAFQQVEQ AXQSMKQRLA AADFHVXHGI
201 ROCRLTGLRLR SEHGFDKRRI GFDIRG*

```

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m217.pep		MADDGVRRLQSLGKLRQFGFRLPFDPFVFKVLDDXLLVIGFSLEQCFKQIPATRHHPFADRCG					
		: : : : :					
g217		MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHHPFADRRR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m217.pep		LPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIAAFGQHPAQYHAFYRLLPGEQ					
g217		LPYPGNIROGFEEGGKTSEHGGLIHVGIPRADILPHRVAAFGQHPAQYHTVCRLLPGKQ					
		70	80	90	100	110	120
		130	140	150	160	170	180
m217.pep		LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFQXKHKHFIDFKSAFQQVEQ					
g217		LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQQVGH					
		130	140	150	160	170	180
		190	200	210	220		
m217.pep		AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
		: : :					
g217		ALQRIKKRLPAADFHVNRNIGRQCLRAGLRLEHGFGHKRRIGFDIRG					
		190	200	210	220		

1 GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT
51 CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTGAGGCT TTGGACTGCC
101 TTTTGTGTCAT CGCCTTCGAC TTGGAACAAT GTTCAAGCA AATCCCGCA
151 ACGCGCCACC CATTCTGCAA CCGTCGCAGG TTGCCGCCAT ATCCGTACAA

291 TATCCGCTCAG GGTTCGAGG AAGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGCG AGCATPCCAG CCAATATCAT GCGTCTTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTCTCCGTC CAAACCCAG
401 CGGACGCTTCA AATCGCGAAC CATGTCGTGC AAAGACGGCA AATCGTCTCT
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCATAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA TCGGTTGTGCG GCGCTGATT TTACATCCG AAACGGATA
601 CGGCAATGCC GCGGCGCCGG GCTGCGCTGT TCCGAACACG GCTTCGATA
651 AAGGCGTATA GGATTCTGATA TTCCGGGTTA A

a217.ppt

```

1 VADDGVQRQL SGKLRQFGFR LPPDFPVFEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRR LPPYPYNIQR GFEEGGKTSE QGLVHVHGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KKHKFID FKSAFQOQVE A*QSMKQRLS AADFHIRNGI
201 ROCLRAGLRL SEHGFDKRRR GFDIRG*

```

	10	20	30	40	50	60
m217.pep	MADDGVRQLSGKLRQFGFRLPFFPFVFKVLDXLLVIGFSLEQC	FKQIPATRHHPFADRCG				
a217	: : : : : : : : : :	: : : :				
	VADDGVRQLSGKLRQFGFRLPFFPFVFEALDCLLVIAFDLEQC	FKQIPATRHHPFVNRRR				
	10	20	30	40	50	60
m217.pep	LPPYPYNIRQGFEEGGKTS	EHGGLIHVGIPRADILPHRI	AAFGQHPAQYHAFYRL	LPGEQ		
a217	: : : : : : : : :	: : : : : : : : :				
	LPPYPYNIRQGFEEGGKTS	EQGGLVHVGIPRADILPHRI	AAFGQHPAQYHAFYRL	LPGEQ		
	70	80	90	100	110	120
m217.pep	LIRAAAHFSVQTPVDVQIGNHVVQKR	XIVLSQSE	TAQHGRGFXKHKH	IFDKSAFQQVEQ		
a217	: : : : : : : : :	: : : : : : : : :				
	LIRAAAHFSVQTPADVQIGNHVVQKR	QIVLSQSEMAQHGRGFXKHKH	IFDKSAFQQVEQ			
	130	140	150	160	170	180
m217.pep	LIRAAAHFSVQTPVDVQIGNHVVQKR	XIVLSQSE	TAQHGRGFXKHKH	IFDKSAFQQVEQ		
a217	: : : : : : : : :	: : : : : : : : :				
	LIRAAAHFSVQTPADVQIGNHVVQKR	QIVLSQSEMAQHGRGFXKHKH	IFDKSAFQQVEQ			
	130	140	150	160	170	180
m217.pep	AXQSMKQRLAAADFHVXHGI	RQCIRTLGRLSEHG	FDKRRIGFDIRGX			
a217	: : : : : : : : :	: : : : : : : : :				
	AXQSMKQRLSAAADFHIRNGI	RQCIRLAGRLSEHG	FDKRRIGFDIRGX			
	190	200	210	220		

q218.seq

1	atgggtgcgg	tggatcctta	tacggcaaaa	gtggtcaaca	ccatgcccgcg
51	caatcagggg	tggatcacaca	ctatggatga	aatccacggc	gatatgatgc
101	tccgtgcggc	agcgcatatt	cttttggaaa	cggcagcttc	actgaccatt
151	attatggttg	tacgcggctt	gtacctttgg	tggcggaaac	agcgcgccat
201	taaacgcgatg	ctgtgtccgc	caaaaagcag	ggcgcttctt	tgtggcgga
251	atctgcacgg	cgcgtttgga	acttgggtgt	cgttgatttt	actgtctgtc
301	tgcctgtcgg	gtattgcttg	ggcaggattt	tggggcggyca	aattcgtgca
351	ggcttgggaat	cagttcccgg	ccggcaaatg	gggtgtcgaa	cgaaccctcg
401	tttcaatcgt	gccgacccac	ggcgaggata	tgaatcacgg	caaggttaag
451	gaagtgccgt	ggattttgga	gcttatgcct	atgctgtctc	cagggacgac
501	tgtgggtgaa	aacggcatta	acccacccga	gccaataaac	attggaiaac
551	gtcgacggtt	tgcgcgggga	aatcggtttc	aaagggcggt	atcagttgaa
601	tttgcccaaa	ggcgaggacg	gggtatggac	tttgtcgag	gattctatga
651	cttatga				

q218.pep

1 MVAVDPYTAK VVNTMPRNOG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWLELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAG NRRQALSVE
 201 FAQRRGRGMD FVAGFYEL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq
 1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCA3TA CCATGCCCGG
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC
 101 TCGGTGCGGC AGGCGATTAT CTTTGGAAA CGGCAGCTTC ACTGACCATT
 151 ATTATGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGC GCGGCAT
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGC GCGTTCT TGGTGGCGGA
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTTGTC
 301 TGCCTGTCGG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA
 351 GGCTTGGAGT CAGTTCCTTG CCGGTAAATG GGGTGTCSAA CCGAACCCCG
 401 TTTCAGTCGT GCCGACCCAC GCGCAGGTAT TGAATGACGG CAAGGTTAAG
 451 GAAGTGCCGT GGGTTTTTGA GCTTACGCCT ATGCTGT'TT CAGGGACGac
 501 yGtgGGCAAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAACCG
 551 TCGACCGCTT TCGCGCGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA
 601 TTTGCCCAAA GCGGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep
 1 MVAVDPYTAK VVSTMPRNQG WYYTMDEIHS DMMLGAAGDY LLETAASLTI
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK
 151 EVPWLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRRQALSVE
 201 FAQRRGRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQG	WYYTMDEIHS	DMMLGAAGDY	LLETAASLTI	IMVVSGLYLW	
g218	MVAVDPYTAKVVNTMPRNQG	WYHTMDEIHG	DMMLGAAGDY	LLETAASLTI	IMVVSGLYLW	
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARS	WWRNLHGTFGTWVSLILLLF	CLSGIAWAGIWGGKFVQAWS			
g218	WAKQRGIKAMLLPPKSRARS	WWRNLHGAFGTWVSLILLLF	CLSGIAWAGIWGGKFVQAWN			
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTH	GEVLNDGKVK	KEVPWVLELTPMPVSGTT	TVGKDGINPDEPMT		
g218	QFPAGKWGVEPNPVSIVPTH	GEVLNDGKVK	KEVPWILELMPMPVSGTT	TVGENGINPTEPNN		
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRRQALSVE	FAQRRGRMD	FVAGFYEL			
g218	IGNRRPFRAGNRRQALSVE	FAQRRGRMD	FVAGFYEL			
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

a218.seq

```

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAAAT GGGTGTGCAA CCGAACCCTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTGGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TGCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTCGAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLF
101 CLSGIAWAGI WGGKFVQAWS OFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVFWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	EHSDMMLGAAGDYLLETAASLTIIMVVSGLYLW				
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYLLLETAASLTIIMIISGLYLW				
	10	20	30	40	50	60
	70	80	90	100	110	120
m218.pep	WVKRRGIKAMLLPSKXARSWWRNLHGT	FVWVSLILLFCLSGIAWAGIWGGKFVQAWS				
a218	WVKRRGIKAMLLPPKGRARSWWRNLHGAF	GTWVSLILLFCLSGIAWAGIWGGKFVQAWS				
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSVPPIHGEVLNDGK	VEVPWVLELTPMPVSGTTVGKGINPDEPMT				
a218	QFPAGKWGVEPNPVSVPPIHGEVLNDGK	VEVPWVLELTPMPVSGTTVGKGINPDEPMT				
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFQALSAEFAQRRGRMD	FVAGFYEL				
a218	LETVDRFARXNRFQALSAEFAQRRGRMD	FVAGFYEL				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

g219.seq

```

1  atgacggcaa ggtaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt ggtgaaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgctc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcggttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtgcaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattatg gcggcaagca ttgcgctgca
351 tatggggact ttgggctggt ggagcgtggt gggaacgct gtgttctgcc
401 ttgccgtgat tttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttctt ccggcgcaaa aaatcaaaact
501 gcccgtcttg tggcgatgg cattgccgct gctgttgatt gcaactgctt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctggt ggataccttg
601 ctgctgtcgc ggattccgt gttgaggaaa tggtttaaat ga

```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

g219.pep

```

1  MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSPTITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWWR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLEPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

m219.seq

```

1  ATGACGGCAA GGTAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCCGACCGCA
251 CGGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTG GCGGAACGTC TTGTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTAAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

m219.pep

```

1  MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTRSXHRWKP TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPTGAVGIVP PAQKVLPVW WMMALPLLAI ALLEPTSLA IAVIWLLDTL
201 LLSRIPVLRR WFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHRWKPSTALRGEIGFKGRYQLNLPKG					
g219	MTARLRKCRGFWSLCLCLSQGRLWVKALTPPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
g219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219 . pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	: : : : :					
g219	LGWWSVLANVVFCLAVIFIGISGCVMMWKRRPSGVAGIVPPAQKIKLPVWAMALPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219 . pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
g219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRKWKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219 . seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTGC GCGG .GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CCGTGATAT  CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTG GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCGG GCGCGGTGGG CATGGTTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219 . pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219 . pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	: : : : :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219 . pep	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	: : : : :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m219 . pep	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	: : : : :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPSGAVGMVPPAQKIKLPVWAMAVPLLLI					
	130	140	150	160	170	180
	190	200	210			
m219 . pep	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	: : : :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng)

from *N. gonorrhoeae*:

```
m221/g221
```

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDVAHDRRLHFGVE				
	: : :				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDYLEMFAYHAEDTFDLFVAQKGA-				
	: :				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGIFAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
            |||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
            130      140      150      160      170      180

m221.pep    GKRFBVX
            |||||
g221        GKRFBVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1  ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51 CGACGCTGAC GGATTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACCTTG GATGCGGTTG ACCGCCGCCT GCACCTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGCGAAGAC
301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTCTTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGAA AGCGGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1  MVVLMRLSLV RQAVNQIDAD GFEPFRARRI DDFGFFVTL DAVDRRLHFG
51 VEILNADAHV VEAESAHEHD GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFKKF DVGIGAAAFV
151 GDDFVAAAVV ADGVAERNVN VKGRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

m221.pep    10      20      30      40      50      60
            MXVLMXRLSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADAHV
            | | | | |
a221        10      20      30      40      50      60
            MVVLMRLSLVRQAVNQIDADGFEPFRARRIDDFGFFVTLDAVDRRLHFGVEILNADAHV

m221.pep    70      80      90      100     110     119
            VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
            | | | | |
a221        70      80      90      100     110     120
            VEAESAHEHDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG

m221.pep    120     130     140     150     160     170
            KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX
            | | | | |
a221        130     140     150     160     170
            KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1  atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51 tttcgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggtc atcgaagccg aaacggcgcg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcgtaa ygagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgct gagcagctct tgttcactga tctctttgcg
301 ccagtatatt tcttggcgca atttcaattc acggaaggcg cgcacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

508

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA
 101 PVFFLGEFQF TEGADTREA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTCCAG TTTTCTCGC
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
 301 CAGTATTTT CTTGTGCGAA TTTCAATTCG CGGAAGGCGC CGACACGCGG
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQRQVLA VEAAGGNRA
 51 GGDLYQVEDVM VESEIXYGNV IGVGSDLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGADTREA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGDLQVEDVM
g223	MEFRHQVVVV	GVEPFGHFD	GELVFVAAR	QLEELFQRQ	VLA	IEAETGGNRARGYLQVEDVM
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGN	IEIGVGS	DLVFPVFL	AQVFSNS	QQFLADFF	FAPVFFLCE
g223	VESEITYSN	IVISVRSS	LVFPVFL	AQVFGNV	EQLLFTDL	FAPVFFLGE
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTCGAAC CATTGGGTCA
 51 TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA
 201 CGGCAACGTA ATCGGCGTTG GCAGCGGCCT GGTGTTTCCA GTTTTCTCG
 251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG
 301 CCAGTATTTT TCTGTGCGA ATTTCAATTC GCGGAAGGCA CCGACACGCG
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQR*VLA VEAAGGNRA
 51 GGDLYQVEDVM VESEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA
 101 PVFFLGEFQF AEGDTREA*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGDLQVEDVM*
a223	VEFRHQVVVV	GVEPFGHFD	SELVFVTAR	QLEELFQRQ	VLA	VEAAGGNRAGGDLQVEDVM
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYGN	IEIGVGS	DLVFPVFL	AQVFSNS	QQFLADFF	FAPVFFLCE
a223	VESEIAYGN	IVIGVGS	GLVFPVFL	AQVFSNS	QQFLADFF	FAPVFFLCE

```
g225.seq
  1  atggattctt  ttttcaaacc  ggcagtttg  gcggtttt  ggctgatgtt
51  tgccgtccgc  cccgccttg  ccgacaggt  gaccaacct  ctccagacc
101  gcgagcagat  tctcagacag  ttatgcgaag  acgaacagc  cgttttacc
151  gtcaaccgag  ccccgcccg  gcgggcggc  aatgccgac  aactcatcg
201  cggcgcgatg  gggcttaac  aacagcccg  tgtacgcgt  aaccgagcc
251  ccgcccgcg  ggcgggcaat  gccgacaaac  tcatcggcg  cgcgatcg
301  cttttgggta  ttgctaccg  ctacggcgc  acatcggtg  ctaccggtt
351  tgactgcagc  ggattcatgc  agcattctt  caaacgcgc  attgggcat
401  acctgccgcg  cactctggcg  gaacaggcg  ggatgggcg  accggttgc
451  cgaagcgaat  tgcagcccg  ggatatggt  tttttcgca  cgtcggcgg
501  cagccgcat  tcccatgtcg  gactttatat  cggcaacaa  cgttcatcc
551  acgcgccgcg  cacggggaaa  aatatcgaaa  tcaccagcc  gagccacaaa
601  tattggagcg  gcaaatatgc  gttcgccgc  cgggtcaaga  aaaacgacc
651  gtcacgctt  ctgaataga
```

g225.pep

1	MDSFFKPAVW	AVLWLMFAVR	PALADELTNL	LSSREQILRQ	FAEDEQPVLP
51	VNRAPARRAG	NADELIGGAM	GLNEQPVVRV	NRAXARRAGN	ADKLIGSAMR
101	LLGIAYRYGG	TSVSTGFDCS	GFMQHIFKRA	MGINLPRTSA	EQARMGAPVA
151	RSELQPGDMF	FFRTLGGSR	SHVGLYIGNN	RFIHAPRTGK	NIETSLSHK
201	YWSGKYAFAR	RVKKNDPSRF	LN*		

```
m225.seq (partial)
1  ..TTTTCAAACC CGGCAGTTTG GCGGTTTTTG TGGCTGAwGT TTGCCGTCGG
51  CCCCGCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTTACC CATCAACCGA
151 GCCCCGCCCC GTCGGGCGGG CAATGCCGAC GAATCATCG CGAGCCGGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCCC GCCCGGCCGG CGGGCAATGC
351 CGACGAACCT ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCCGT
401 ACAGCGCCAC ATCGGTTTCT ACCGGTTTG ACTCGACGGG TTTCATCGAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGGACA
501 ACAGGCACGG ATGGGTACGC CGGTTGCCCG AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCTGA GCCACAAAT TTTGAGCGGC AAATACGCGT
701 TCGCCCGCGG GGTCAGAAAA AACGACCCGT CCGCGTTTCT GAAGTGA
```

```
m225.pep (partial)
  1  ..FSNPVAVWL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQPVLPINR
51  APARRAGNAD ELIGSAMGLN EQPVLVPINRV PARRAGNADE LIGNAMGLNE
101 QPVLVPINRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDCSGFMQ
151 HIFKRAMGIN LPRTSAEQAR MGTFAVSESL QPGDMVFVFT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSEFLN*
```

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

 10 20 30 40 50
m225.pep FSNPVAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPIINRAPARRAG
 | : ||||| | ||||| | ||||| | ||||| | ||||| | ||||| | ||||| |
q225 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPIINRAPARRAG



510

	10	20	30	40	50	60
m225 . pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLVPVNRVPARRAGNADELIGNAMGLNEQPVLVPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVVRVNRAXARRAGNA					
				70	80	90
m225 . pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225 . pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225 . pep	240	249				
	VKKNDPSRFLNX					
g225	VKKNDPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225 . seq
1  ATGGATTCTT TTFTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151 ATCAACCGAN CCCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTACC CGTCAACCGA GCCCCGCCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACCGCAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225 . pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQVLPV
51  INRXPARRAG NADELIGSAM GLNEQPVLVP NRXPARRAGN ADXLIGNAMG
101 LNEQPVLVPV RVPARRAGNA DELIGNAMGL NEQPVLVPNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225 . pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRXPARRAG				
	10	20	30	40	50
m225 . pep	60	70	79		80
	NADELIGSAMGLNEQPVLVPNR-----VPARRAGNA				

511

```

      |||
a225  NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
      70      80      90      100     110     120

      90      100     110     120     130     140
m225.ppep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      |||
a225  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
      130     140     150     160     170     180

      150     160     170     180     190     200
m225.ppep MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      |||
a225  MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      190     200     210     220     230     240

      210     220     230     240     249
m225.ppep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
      |||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLNX
      250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt tttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag ttgcccgaag acgaacagcc cgttttacc
151  gtcaaccgag ccccgcccg gcggcgccgc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccgt tgcacgcgtc aaccgagccn
251  ccgcccggcg ggcgggcaat gccgacaaac tcacggcgag cgcgatgccc
301  cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401  acctgccgcg cagtcggcg gaacaggcgc ggtggggcgc acccgttgcc
451  cgaagcgaat tgcagcccgg ggatatgggt tttttccgca cgctcgccgg
501  cagcccgatt tcccatgtcg gactttatat cggcaacaac cgcttcaccc
551  acgcccgcgc caggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAV AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAFPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RPIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDPSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCCT TTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCCGC CCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTGCGGAAG ACGAACAGCC CGTTTACCC
151  ATCAACCGAG CCCCCCGCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCGGCG GCGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGC
351  GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCGCCA AGCGAATTGC
551  AGCCCGGAGA TATGGTGT TTCCGACGCG TCGGCGGCAG CGCATTTCC
601  CATGTCCGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTTG
751  AACTGA

```


This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVWLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQPVLPV NRVPARRAGN ADELIGNAMG
101 LNEQPVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*
```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep  MDSFFKPAVWAVWLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPINRAPARRAG
              |||||
g225-1      MDSFFKPAVWAVWLWLMFAVRPALADELTNLSSREQILRQFAEDEQPVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep  NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
              |||
g225-1      NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
              70      80      90

              130     140     150     160     170     180
m225-1.pep  DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |||||
g225-1      DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep  SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              |||||
g225-1      SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep  VKKNDPSRFLNX
              |||||
g225-1      VKKNDPSRFLNX
              220
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTACCC
151 ATCAACCGAN CCCCGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTACGAAC AGCCCGTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTACC CGTCAACCGA GCCCCCGCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTG GGTATTGCTT ACCGCTACGG
501 CCGCACATCG ATTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAA AC GCGGTTTCG
801 CCGCCGGGTC AAGAAAACG ACCCGTCCCG CTTTCTGAAC TGA
```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVWLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *
```

513

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADKLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70	80	90			
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLLGGSRIHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLLGGSRIHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX					
m225-1	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGATTA TCGTGCGCAC GCGCAGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttatatta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcga
451 tttctgttgc ctccgcctct cctgcgcgc ctcggcccg atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Cggggcctcg cccctccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILROPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLPR LGPHTLRRFT ILPKLRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGATTA TCGTGCGCAC GCGCAGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCGGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCGTTGGGT ATGTCGCTCG
551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
651 CGCGCTGATT GCGCCGCTGC TCATCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

```
m226.pep
1  MNEILRQPSV LLFLTLAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFWLK PAVVLAVPL YQNRKKIFNQ WLPVVISQLA
101 GSVTGIVTGM YFAKWGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
151 AATVVIAGLV GFQIYGYKML NTVMPSSVVG MSLGTASHAM GIAASLERSR
201 RMAAYAGLGL TGNGVLTALI APTLLPVLGF *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

```

m226/g226

      10      20      30      40      50      60
m226 .pep  MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIA YLKILGIDYAVYHN
g226       MNEILRQPSVLLFLT LAVYALAIIVRTRTGNIFCNPVLVSTIVLIA YLKILGIDYAVYHN
      10      20      30      40      50      60

      70      80      90     100     110     120
m226 .pep  AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGI VTGMYFAKWLGAE
g226       AAQFIDFWLKPAVVVLAVPLYQNRRIKFNQWLPVIVSQLAGSVTGI VTGMYFAAWLGPD
      70      80      90     100     110     120

      130     140     150     160     170     180
m226 .pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPS
g226       EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPS
      130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

```

a226.seq
1  ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
51  CGTGTACGCG CTTGCGATTA TCGTGCAGC CCGCACGGGT AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTG CTGATTGCCTA CTGAAAACT
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
201 CTGGCTCAAG CCCGCCGTGC TCGTGCTTGC CGTCCCGCTC TACCAAAACC
251 GCGCTAAAA CTTCACCAAA TGGTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACGGGGAT TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAAGTCGTC TCTCGCTCGC GTCCAAATCT GTTACCAATC
401 CTATCGCCAT CGAAATCACC CGCTCCATCG CGCGCATTCG CGCCATTACC
451 GCGGCCACCG TCATATTGTC CGGCTTGGT GGACAGATTG CCGGTTACAA
501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
551 GCACGGCTTC GCACGCGATG GCGATTGCCG CCTCGCTCAG ACGCAGCCGC
601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG CGGTACTGAC
651 CGCGCTGATT GCGCCGCTGC TTATCCCGT TTTGGGATTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

```
a226.pep
1  MNEILRQPSI LLFLTAVYA LAIIVRTRTG NIFCNPVLS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKKIFNQ WLPVIVSOLA
101 GSVTGIVTGM YFAKWGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
151 AATVIIAGLV GQIAGYKMKL NTVVMPSSVG MSLGTASHAM GIAASLERSR
201 RMAAYAGLGL TFGNVLTALI APLLIIVLGF *
```

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep  MNEILRQPSVLELTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          |||||||:|||||
a226      MNEILRQPSILLELTLAVYALAIIVRTRTGNIFCNPLVSTIVLIAYLKILGIDYAVYHN
          10      20      30      40      50      60

          70      80      90      100     110     120
m226.pep  AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          |||||||:|||||
a226      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
          70      80      90      100     110     120

          130     140     150     160     170     180
m226.pep  EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
          |||||||:|||||
a226      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVVMPSVVG
          130     140     150     160     170     180

          190     200     210     220     230
m226.pep  MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          |||||||:|||||
a226      MSLGTASHAMGIAASLERSRRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgcggc
51  cgaaaccgcc gtttctctag caggcatcaa actgcccgcc agcatcgctc
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctc
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF LQAGWLKTS
51  WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGTCTTtKGC TGCAACAGCT TACCGACGCG CTGATGTCGA ACCTGACGCT
51  GTtCCTCGTG CCGCC.TGCG TGGCGGTCAT CAGCTATTtG GATTtGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCOG CCTCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTLFLV PCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227

          10      20      30
m227.pep  TSXLQQLTDALMSNLTLFLVPPCVAVISYL
          || |||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
          20      30      40      50      60      70

          40      50      60

```

516

```

m227.pep    DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||||||||||||||||||||||||||:|
g227        DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAACCAGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTGCG CTTTTCAGG CGGGTTGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TCGTGCGCG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGTTTACAG GCAAGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLF LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSLV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep                                10      20      30
                                TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||:|||||
a227      TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
            20      30      40      50      60      70

m227.pep      40      50      60
            DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
            |||||||||||||||||||||||||:|
a227      DLJADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE BAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

a228.pep
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
 101 KMKDAAK*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq
 1 atggctgccg tategggcgg cggcgccggtc ttcctgataa tgcttcaca
 51 tattgccgcg gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
 101 aaatcgcat tgaagccgcc ggcgaaattg tatcggtcgc cgccaagag
 151 gttttgcccg acaaacggca cggcgccgaa cgagcgcgtt accgaacggt
 201 tttgatggcc gaacgacagg cgcagggttct gttcgctgaa atctttgtta
 251 tcccaataat gcacgccgcg gctgatgccg ccgtagagga aatgatgcc
 301 gcccgcatcg atttcgcgcg acacgcccaa gccgtagcgc aaaccgtgtg
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
 401 tcaatcgttt tttcggacga agcgttggtt atagcggatt aacaaaaatc
 451 aggacaaggc ggcgggccgc aggcagtagc gatggtagcg aaccggttcg
 501 cccggtgctt ggacgcctta gggaaccgtt ccttttgagc cggggcgggg
 551 caaccgtac cggttttgtg tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep
 1 MAAVSGGAV FLIMLPHIAR VQROPFAFAQ ASGEIGIEAA GEIVSAAAE
 51 VLPDKRHGAE RARYRTLMA ERQAQVLFAE IFVIPIMHAA ADAAVEEMMP
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKE
 151 RTRRAAGST DGETPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
 251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTGCG CGGTTTTCGT
 301 CCAGCTTCTG CCCGCAAAAT CAATCGTTT TCGGACGAA GCGTTGTTTA
 351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
 401 AATAGTACGG AACCGATTCA CTGGTGCTT CAGCACCTTA GAGAATCGTT
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)
 1 ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAEROAQLF
 51 AEIFVIPIMH AAAADA VEE MMPARIDFAR HAXALACTVC LLRQAVGGFR
 101 PASARKFNRF FGRSVVYSGL TKIRTRQRSA DSTNSTEPIH LVLQHLRESR
 151 SLFCSSAILC *

Computer analysis of this amino acid sequence gave the following results:

m229/q209

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQAIGEIGIEAADEIVSAAAXEVLLDKRHDAE
                               ||| |||| |||| |||| |||| |||| |||| ||||
a229    MAVVSGGGAVFLITLPHIAHVQRQPPKFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                               10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep    RARYRTVFIAERQAQALFAEIFVPIPMHAAAADAAVEEMMPARIDFARHAXALAQTVCLL
              ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
a229        XARYXTVFIAERQAQALFAEIFVLIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
              70      80      90      100     110     120

```

519

```

          100      110      120      130      140      149
m229.pep  RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---
          |||||
a229      RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX
          130      140      150      160      170      180

          150      160
m229.pep  -----RSLFCSSAILCX
          |: |||:|
a229      AKARQRRRTGFCSSII
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttcatt ccatcgaaaa atacagaaca cccgccaag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttccatc
101 cgggcgccga ctacatcgtc caagtggcg acgaaaaat cagcgagcac
151 tcaatcaaca acgcatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtccgcg
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtgtg
401 tcgaagaaat ccgcgatcag ttgacctgac agaatttggg aagcctcgtc
451 caaacaggcg tattggtcgg cgacgcgcag gcggaacagc tgatcagggt
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgcagaa atttataat
601 gcgaacaaaa aagactatct gctgcgcgag gcggtcaaat tggatatgt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcatatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaaa gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaac acctaataca tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tcgcgcgcaa agaagtccgc gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tcgctcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ ABQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELMKKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR ERKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCAC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC

```


520

```

451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTGCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACCG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATGGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTITGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGT ATGCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

m230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAKLMGI SVSSEIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFPN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDVAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRakeVR EEKTLPPFAE KDAVRQAYIR TEAAKL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

m230.pep	10	20	30	40	50	60
	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	70	80	90	100	110	120
	ADGGGSPDPAVFQSLQRAYLKQGAKLMGISVSSEIKQIIVDDPNFHDANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAKLMGISVSSEIKQIMIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230.pep	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRIRSHTFN					
	130	140	150	160	170	180
m230.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFPYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDVAVNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGSGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTCCTTGC AGAATTGGT AAACCTCGTC
451 CAAACGCGC TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGEC AGGATGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCET ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGSPSRDA VFQSLQRAY LKQGA KLMI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHNSVLTINSET
351 AWWVVRKEVR EEKTLPF AEAKDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGSPDAVFQSLQRAYLKQGA KLMI SVSSEQIKQII VDDPNFHDANGKFDHALLN					
a230	ADGGGSPDAVFQSLQRAYLKQGA KLMI SVSSEQIKQII VDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m230.pep  RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          |||||||
a230      RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN
          130      140      150      160      170      180

          190      200      210      220      230      240
m230.pep  PDEFIAQVKVSEADLQKFYNANKKDYL LPQAVKLEYVALNLKDFADKQTVSETEVKNAFE
          |||||||
a230      PDEFIAQVKVSEADLQKFYNANKKDYL LPKAVKLEYVALNLKDFADKQTVSETEVKNAFE
          190      200      210      220      230      240

          250      260      270      280      290      300
m230.pep  ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS
          |||||||
a230      ERVARLPANEAKPSFEQEKAAVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS
          250      260      270      280      290      300

          310      320      330      340      350      360
m230.pep  GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR
          |||||||
a230      GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSEVLTINSETAWVVRakeVR
          310      320      330      340      350      360

          370      380
m230.pep  EEKTLPF AEAKDAVRQAYIRTEAAKL
          |||||||
a230      EEKTLPF AEAKDAVRQAYIRTEAAKL
          370      380

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCGGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACTTTTC TCGGCTTCGG CGTCAGCACG GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTGCTTTCGC AGAATTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTCAAC CCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATG
651 CCGCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCGTTTGGC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAGAGGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAGAAAGAA AAGCTGGGCG
851 ACGATGCGTI CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAACAAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 CAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGGC AAACGGCAAA CCGCCTATG TCACACTGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCTCCGG AGGATATTGC
1401 CACACAGCTT CCTCTGCGA AACAGGCTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGCGAT GGTACGTA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV OVGDEKISEH
51  SINNAMQNEQ ADGGSFWRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSDQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQOAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPFEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIRQT
501 KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAAGC CCCGCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CCGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGGCCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAAAT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCGA TATGCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCGCA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAT TCGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACCGG
701 AAGTGAAAAA TGCATTGAA GAGCGCGTGG CGCGTTTGCC GCGAATGAA
751 GCGAACCTTT CTTTCGAGCA GGAAGAGGCC GCGGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTGCGCG ACTTCAACAA GGCAAAAGAA AAATGGGCG
851 AAGTATGCGT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTACGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGCG AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTGCAAGT ACAGGCTGTA ACCCGCGCG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGGCAACAG CAGTCTGCCA
1451 ATACITTCGA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGCGGAC GGTACGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLFFAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQOAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPFDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIRQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

	10	20	30	40	50	60
m230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230-1	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230-1.pep	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
g230-1	ADGGSPWRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFSHALLS					
	70	80	90	100	110	120
m230-1.pep	RYLSQRHSEDDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180

a230-1.seq

1	ATGTTCCCA	TCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTPAACCTTC	TCGGTCTCGG	GGTCAGCAGC	GTATCCCACAT
101	CGGGTCGCCA	CTACATCTGC	CAAGTGGGCG	ACGAAAAAAT	CAGCGACATC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	GCGGACGGCG	CGGGCCCTTC
201	CGCGCAGCGC	GTGTTCCAAT	CCCTGCTCA	ACGCGCCTAC	CTGAACACAGG
251	CGCGGAAGCT	GATGGGCAAT	TCGGTTTCTT	TCGACAAAT	CAACGAGAT
301	ATCGTGGACG	ATCCCAATTT	CCACGACGCA	AACGGCAAT	TCGACACGCG
351	CGCTTTTAAAC	CGCTACCTTT	CCCAACGCA	TATGTCGAA	GACCACTTTG
401	TGGAAGAAAT	CGCGATCAG	TTTGCCTTGC	AGAATTTGGT	AAACCTCGTC
451	CAAAACGGCG	TATTGGTCGG	GACGCGCAG	CGGGAACAGC	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCGTTGACCA	CACTTTCAAC	CCCGACGAAT
551	TCATCGCCCA	AGTCAAAGTG	TCTGAAGCCG	ATTTCGAGAA	GTGTTATAAC
601	GCAACAAAAA	AAGACTACTC	GCCTCCCAAA	CGGGTCAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTCGACAGAA	ACAGACCTTC	AGCGAAACAC
701	AAGTGA AAAA	TGCGTTTGA	GAGCGCGTGG	CGCGTTTGCC	GGCAATTGAA
751	GCCAACCTTT	CTTTCGAGCA	GAGAAAAGCC	CGCGTCGAAA	ACGAAATTGAA
801	AATGAAAAAG	GGCGTTGCCG	ACTTCAATAA	GGCAAAAGAA	AAGCTGGGCG
851	ATGACCGGTT	CAACCATCCT	TCCCTCGCTT	CCGAAAGCCG	CAAAAAACGC
901	GGTTTGAAGT	TCGAAACCCA	GAAACTTTGG	CTAGCAGGCG	AGGATTGCGCA
951	AATGTCGGGT	ATGCCCGAAA	ACCTGATCAA	TGCGCTATTCT	AGCGACAGCC
1001	TATTGAAGAA	AAAAACAAT	TCCGAAGTGC	TGACCATCAA	CACCGAAGCG
1051	CGGTGGGTGC	TCGCGGCCAA	AGAAGTCCGC	GAGAGAGAAA	CCCTGCGGTT
1101	TGCCGAAGCC	AAAGACCGGG	TACGTCAGGC	TTATATTCGT	ACCGAAAGCCG
1151	CCAAACTTGC	CGAAAACAG	GCAAAAGACG	TGCTTACCCA	ACTGAACGGC
1201	GGCAAGGCTG	TGTGACTGAA	ATGGTCCGAA	GTGTCGGTT	TGGGCGSCAA
1251	GCAGGCAAGC	CAGTCCATGC	CGCCCGTAGC	TTATGCGGAA	CTGCTGAAAG
1301	CAAAACCGGG	AAACGCCAA	CCCGCCTAGC	TCAGGCTGAT	CGGCTTCGCG
1351	GCACCGGTGA	TGTGCGAAGT	ACAGGCTTGA	ACCCCGCGGG	ATGATATTCG
1401	CGCACAGCTT	CGCCTTGCAA	AACAGGCTTT	GGCGAACAG	CAGTCTGCCA
1451	ATACTTTTCA	CTTGTGTGTA	CGTTATTTCA	ACGGCAAAAT	CAACAGAGCC
1501	AAAGGAGCCG	AATCGGTCGA	CAACGCGTAC	GGTCAGTA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFGVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMGI SVSSEIQIKOI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINA VF SDDVLKKKH SEVLTINSET
351 AWVVRakevr EEKTLPFaea KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVkwe VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPDIDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVdngd GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

	10	20	30	40	50	60
a230-1.pep	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
m230-1	MFHSIEKYRTPAQVLLGLIALTFVGFGVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a230-1.pep	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEIQIKQIIIVDDPNFHDANGKFDHALLN					
m230-1	ADGGGPSRDAVFQSLQRAYLKQGAKLMGISVSSEIQIKQIIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a230-1.pep	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
m230-1	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a230-1.pep	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
m230-1	PDEFIAQVKVSEADLQKFYNANKKDYLLPKAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a230-1.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
m230-1	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300
	310	320	330	340	350	360
a230-1.pep	GLKVETQETWLSRQDAQMSGMPENLINA VF SDDVLKKKHSEVLTINSETAWVVRakevr					
m230-1	GLKVETQETWLSRQDAQMSGMPENLINA VF SDDVLKKKHSEVLTINSETAWVVRakevr					
	310	320	330	340	350	360
	370	380	390	400	410	420
a230-1.pep	EEKTLPFaeakDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVkweVSVLGAQQAR					
m230-1	EEKTLPFaeakDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVkweVSVLGAQQAR					
	370	380	390	400	410	420
	430	440	450	460	470	480
a230-1.pep	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPDDIDIAAQLPLAKQALAQQ					
m230-1	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEQAVTPDDIDIAAQLPLAKQALAQQ					
	430	440	450	460	470	480
	490	500	510			
a230-1.pep	QSANTFDLLIRYFNGKIKQTKGAQSVdngdGQX					
m230-1	QSANTFDLLIRYFNGKIKQTKGAQSVdngdGQX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```
g231.seq
1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cggcgctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 ggcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtctt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgcgcgtcc tgccctgccg gcggtacgcc cagggcgctt gcggattttt
301 agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351 catagtcggc aaaatccgac ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgccccgtc ctgcacctgc atcaggttca aatcggtttt
451 gccggcggtt acctgcgcca cttcgcgctg atagcggctg gtttcaaaca
501 cagctacact gactttccta ccctccgccc ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacgccat
601 ccgaatttta tgtttcgcgc cgtcccgctc gatgacgtga aggggtatcg
651 cgtcatagac tttggacacc gtgctgtgtg agctgtggcc ggatttcgcc
701 gatgccgctc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgcgcgtcc caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgac gtctgaacat
901 ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```
g231.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA OPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLSVGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAAC
51  GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCAGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACATTTCG GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFVAV QGRAVSLPNA QPFG.....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng)

from *N. gonorrhoeae*:

m231/g231

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFVAV					
g231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFVAV					
	10	20	30	40	50	60
	70					
m231.pep	QGRAVSLPNAQPFG					
	:					
g231	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLSVGIVG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

527

a231.seq (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGAACA
501 CGCGGACGCT GACTTTCCTG CCTCCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGTC GATAACGTGA AGGCTGTCCG
651 CGTCATAGAC TTTGGACACC GTGCTGTGT AGCGGTGGCC GGATTTGCGC
701 GATGCTCGGC GCGGCGCGG CGCGTCGGA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTT
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQTGF
151 ADRNLRHFAL VAVGVEHADA DFFAFRRRAQ VVAETRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFEDFFNLH IFQMPMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFPG					
a231	QSRVSLPNAQPFHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG cgegcgcCAG GTTGtcgcGC
551 GAACgTGTAC CGTAagcgtg Ttcatctcc GGTGcgtcGA TATACCCaT
601 cCgAATTTta tGTTtcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgccgtcgt AGctGTGGCC GGAtttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```


528

101 SFQSFAPFF RLNLVGIIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFTRLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGCGGAACT
 51 GCCGCGCTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGCG ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
 201 ACCAATGCCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACTTTAA
 401 TAATGCCACG CGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
 451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTG GTATCGAACA
 501 GCGCACGCT GACTTTCCTG CCTTCGCGC CCGCGCGCAG GTTGTCGCGC
 551 GAACGCGTG CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTA AGGTTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCCTGTG AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCGCTCCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFQSFAPFF RLNLVGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFFAFERRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRVAV DNVKGVAVD FGHRACVAVA GFRRCSAAGG RVGTEVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLIH IFQMMPSEH
 301 IGIGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAGHIHPILIAAPACPAVRPRRLRIFSFQSFAPFRLNLVGIIVG					
m231-1	QSRVSLPNAQPFAGHIHPILIAAPACSAVRPRRLRIFSFQSFAPFRLNLVGIIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFTRLRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRNLRFHFAVAVGIEHAHADFFAFRRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLIHIFQMMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAC GAAATCCAT AAACCGTCCG TATCAAAAC CGCGGAACT
 51 GCCGCGCTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG

529

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTGC CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCCTGCCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTGGAACA
501 CGCGGACGCT GACTTTCCCTG CCTTCCGCGC CGCGCGCGAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCACTCC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT ACCGCTGGCC GGATTTCGCC
701 GATGCTCGGC GCGCGCGCGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGCTCCG CACCGCTCCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILLFIS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVD FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNHLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAPAACPAPVRPRLRIFSFQSFAPFRLNLVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAACPACSAVRPRLRIFSFQSFAPFRLNLVGIIG					
	70	80	90	100	110	120
a231-1.pep	KIRLILLFSSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGVEHADDFPFRRAQ					
m231-1	KIRLILLFSSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHADDFPFRRAQ					
	130	140	150	160	170	180
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNLVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNHLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNHLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt tttgctggtc gccgtcggag gaacggccgg cagcctgttt

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530

```

151 atgccgtccg taccgcccaa ggctgccgat acccaaatcg agtggaaat
201 tgtccgtggg acaaaatccc tgctgcgtga aacggtgcgg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggg tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggt attgccgccc
401 gtccggtact gtgtgccaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgcggcctgg ttttgggtgt
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggatgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaacgc
651 cagcagcgag actttccgcg cccgcgcgct tgccgccaac aatatcgtaa
701 acggcatctt tatggtttcc gccgccgttt tgagcgcggt attgctgttt
751 ttggttgaca gcattttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgca aaggcggttt ttaggcgcgg
851 cggaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

```

g232 . pep
1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLRETIVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGNLGI FWFLSQGWAY PVMAVMTLIG
201 PFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

```

m232 . seq
1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCTG CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCAGC CATTATCGGT ATTTCTGGT TTTGGTTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAkGG AACGCCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGCGGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTtGTTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTCTC CGTTCCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGaTT TCCGCGCCCg GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGG TTTCCGCTGC CGTTTGTAGC GCGGTGTGTC TGTTTGTGT
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTtagg CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

```

m232 . pep
1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLRETIVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGNLGI FXFLSQGWAY PVMAVMTLIG
201 PFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m232 . pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
g232        MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

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	10	20	30	40	50	60
m232.pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPNVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	70	80	90	100	110	120
m232.pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	130	140	150	160	170	180
m232.pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	190	200	210	220	230	240
m232.pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLI VALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLI VALGNIPLAVFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTGTGATG ATTGGGTTT ACGGTTTGGG GCAAAACGGC
151 TTCCTGCCTG CCGGACAGAT GTTGAACCTG GCGCGTTGC TGTATTATTT
201 GCCGTATTTC CTGTTTTCCT CGCTGTCGGG GCAGTTGGGT AACAAATTCG
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCGCG TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTGTGTCGC ATCCTGTTTCG GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATGTCGGG ATACTGGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAAATTGAG TGAATATATG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CGGTGCGGCA CAAGCCCGTT TTTACCGCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTG GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCTCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTTA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGTG TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCGGT
1251 ATTTTGTGAT AAGCGCGAAA GCGGTTTTT AGCGCGGCG GCAATCAGGA
1301 AAAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGLGL VKSRRFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAQOMLNL GALLFILPYF LFSLSGLQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLACLFL CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLFMPSV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNLML ALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTILFGPLKYAILPDYLDKELMMGNSLIESGTFVAILFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNMLALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFXFLSQGWAYPVMAMVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGNLGIFWFLSQGWAYPVMAMVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232		VFLIKRERRFLGAAAIRKKPX					
		420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcggggtgcg
51  ttctcgggtcgc gacaaaccca agcaatatgt cgaaatcgga agcaaaacccg
101 ttttagaaca tgtacttggg atttttgaa ggcatgaggc cgtcgtattg
151 accgctcgttgc tcgtctcgcc cgaagacacg tttgccgata aggttcagac
201 ggcatattcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacggtgtg gcaaaactgt tggaaaaccgg tttggcggcg
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgcccgc
351 tgaagctctg gcgcggttga tagaacaggc gggcaacgcc gccgaaggcg
401 ggatttttgc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgaaaacgcc
501 gcagcttttt caagcgggtt tgctgcaccg cgcatgggtc gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgcgc tggaaaaact ggggtgtgct
601 ccgtactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcagcc tgctgctcaa tgccgtctga
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLBHVLG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
```

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR
 201 PLLIOGDARN LKLTOPDAY IVRLLLNAV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAGAC
 201 GGCATTTCCA CAGGTTCGGG TGTGGAAAAA CGCGCGACAG ACCCGCGCCG
 251 AAACCGTCCG CAACGGTGTG GCAAAACTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGCGG
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC GACGGTGGG
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)
 1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
 101 ETDNVLVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIG IFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFGADKPKQYVEIGSKTVLEHVLG IFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCLPSEAL					
	70	80	90	100	110	120
	130 140 150					
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	: : : :					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq
 1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTCAGAC
 201 GGCATTTCCA CAGGTTCGGG TGTGGAAAAA CGCGCGACAG ACCCGCGCCG
 251 AAACGTGTCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC
 351 TGAAGCTTTG ACGCGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC GACGGTGGG
 451 AACATTAGTG CAACCGTCGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC
 601 CCTTGCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGCTGTA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILEVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIIPV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m233.pep	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILEVHDAARCCLPSEAL					
a233	FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILEVHDAARCCLPSEAL					
	70	80	90	100	110	120
	130	140	150			
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLVQGDARNLKLTQPQDAYIVRLLLDVAX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgccgc catcgctttt gccgccgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgctcga
151 acattcgaca accgctccag cttccaaaaa ggcatcttct cgcacagtga
201 agaccgctcg ggcagccagg caaaaacccat cctggtaaca caccgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcccg caaagcgag aacctgaaag gcgcagatta
351 tgcgttacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctatc
501 cacacagggc gcgggcgaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRPNV LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSNRE IIGFGTSGY DATLNGKVL
201 LAIREAVDNL VQAVDNGANQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAI REAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

				10	20	30
m234.pep				GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
	140	150	160	170	180	190

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
g234	DLAIREAVDNLVQAVDNGAWQSNRX	
	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

				10	20
30					
m234.pep				GAGEYALSNREI	IGFGGTSGY
a234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSAQGA	GAGEYALSNREI	IGFGGTSGY
	50	60	70	80	90
					100

	40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX	
a234	DLAIREAVNSLVQAVDNGAWQPNRX	
	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

g235.pep

1	MKPLILGLAA	VLALSACQVR	KAPDLDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGMLAST	AAPISEAGYY	VFPAAVVEET	FKENGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITLVGYGTS	YQILDSVTVV	SAKARLVDSR	NGKELWSSGA
151	SIREGSMNSN	SGLLGALGVR	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSR
201	NGILKPRNFV	EEOPK*			

m235.seq

1	ATGAAACCTT	TGATTTTAGG	GCTTGC GCC	GTGTGGCGC	TGCTGCCTG
51	CCAAGTTCAA	AAAGCGCCG	ATTTTCGACTA	CAGTTCATTC	AAGGAAAGCA
101	AACCGGCTCT	AATTTTGGTG	GTTCGCCCGC	TGAACGAATC	GCCCCGATGC
151	ACCGGAACAT	GGGGTGTA CT	GGCTTCGACC	CGCGCGCGC	TTTCCGAAGC
201	CGGCTATTAC	GTCTTCCCG	CCGCAGTCGT	GGAGGAAACC	TTCAAACAAA
251	ACGGCTTGAC	CAATGCCGCC	GATATTCACG	CCGTCCGCC	GGAAAACTG
301	CATCAGATT	TCGGCAATGA	TGCGCTTGT	TACATTACGG	TTACCGAATA
351	CGGCACCTTCA	TATCAAAATT	TAGACAGCGT	GACGACCGTA	TCGCCCAAG
401	CACGGCTGGT	CGATTCCCGC	AACGGAAAAG	AGTTGTGGTC	GG3TTCGGCC
451	AGCATCCGCG	AAGGCAGCAA	CAACAGCAAC	AGCGGCTGT	TGGGGGCTTT
501	GGTCAGCGCA	GTGGTCAATC	AGATTGCCAA	CAGCCTGACC	GACCCGCGTT
551	ATCAGGTTTC	CAAAACCGCC	GCATACAACC	TGCTGTGACC	CTATTCTCAC
601	AACCGCATCT	TGAAGGTTCC	GAGATTGGTT	GAAGAGCAGC	CAAAATAA

m235 . pep

1	MKPLILGLAA	VLALSACQVQ	KAPDFDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGVLAST	AAPLSEAGYY	VFPAAVVEET	FKQNGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTVEYGS	YQILDVTVTV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVSA	VVNQIANSIT	DRGYQVSKTA	AYNLLSPYSH
201	NGILKGRPRFV	EEOPK*			

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/q235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPD	FDYTSFKESK	PASILVVPPLNES	FDVNGTWGVL	LAST	
g235	MKPLILGLAAVLALSACQVRKAPDL	DYTSFKESK	PASILVVPPLNES	FDVNGTWGML	AST	
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYVVFPA	AVVEETFKQNGLT	NAADIHAVRPEK	LHQIFGND	AVLYITVTEY	GTS
	:					
g235	AAPISEAGYVVFPA	AVVEETFKENGLT	NAADIHAVRPEK	LHQIFGND	AVLYITVTEY	GTS
	:					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDVSTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
g235      YQILDVSTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130    140    150    160    170    180

          190    200    210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190    200    210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTGGCGC TGTCTGCCTG
51  CCAAGTCAA AAAGCGCCG ATTCGACTA CACGTCATC AAGGAAAGCA
101 AACCGGCTTC AATTTGGTG GTTCGCGCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TGCGGTTTG TACATTACG TTACCGAATA
351 CGGCATTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGGCTGCT CGATTCCCGC AACGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTACGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGT S YQILDVSTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10    20    30    40    50    60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||
a235      MKPLILGLAAVLALSACQVQKAPDFDYSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10    20    30    40    50    60

          70    80    90    100   110   120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAHVRPEKLHQIFGNDAVLYITVTEYGT S
          |||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAHVRPEKLHQIFGNDAVLYITVTEYGT S
          70    80    90    100   110   120

          130   140   150   160   170   180
m235.pep  YQILDVSTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||
a235      YQILDVSTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130   140   150   160   170   180

          190   200   210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190   200   210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g235.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTTCGCATT TTTCGCGGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAAATTCG
251 GCTTCCGCCT GCAAggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTTACTGCTT CGCGCGCTTC GCGATTGCC GTCCATTTT
351 TCACCAgTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGGCGGGC GCGGTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTTTGCAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCACC ATATCCGCT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGCGCGTAG CTTTCGGTAA CCGTTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcgct gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGAGTTGC
951 CGATGGATT CGACATTTT CGGCCGTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TGC CGCTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQ IYIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNNV FHGVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQBAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRFQAO
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTGGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCAACAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCKTCTTCGC CGCCGCGGwT GayGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACaTG TCTTTTACGG CAAAGTGGAa kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACCTTTCG AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCG CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAAC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCTTC GCCGTGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRDGFVG AQRLDGGYR FAGFADCRPF FHQFGGFFV DGRELVPSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNXYFYGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFFHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LPIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

539

		10	20	30
m236.pep		LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
g236	FRHQQGKAQFFAQSIQIAGHFFRRGNFGFRLQGR	TSFVGAQRLDSGGYCFARFADCRPF		
	60	70	80	90
	100	110		
	40	50	60	70
m236.pep	FHQFGFGFFVDGRELVPMSBEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQGS			
g236	FHQFGFGFFVDGRELVPMSBEDAVFAAADVPRFFAGEAQNRCNQENQAARDVVQGLR			
	120	130	140	150
	160	170		
	100	110	120	130
m236.pep	AAACMAVCFGGVEAVFQDVEVERTQVFAERNXVFGKVEKITRIVIACTLLQLTQYH			
g236	AAAGAAVFGGVEAVFQDVEVERAQVFAERNNVFHGEVEGIARIVTACQTLQPPRQYQ			
	180	190	200	210
	220	230		
	160	170	180	190
m236.pep	GVAVDFHHIRLLHGFNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR			
g236	GVAVDFHHIRLLHGFNRIKVAQIGKQEAQGIADAAVAFGNAFEDFFGNRQFAAVIGGCR			
	240	250	260	270
	280	290		
	220	230	240	250
m236.pep	PQAQDVCAEFVINLLRCNDVADGFRHFFAFAVDNETMGQQLFIRRATHX			
g236	PQAQDVRAEFVIDFLRRDDVADGFRHFAVLNVHETVGGQQLFIRCASHG			
	300	310	320	330
	340			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

```

a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGACAG
51  CGGTTTCATG GCCTGCAACC GCGCCACAT CGCGSGTGTA GTGCCAGCAG
101 CGTTTCGATT TTTCACCATC ACTGGCTTTA GCGGCAACCG CAAGTTCGCT
151 GCCTACTTTC ACTTCTGCTT TAGACACCAG CAAAGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAATTTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGCGG GTTACCGCTT CGCGGGCTTC GCGGATGCGC GTCCATTTT
351 TCACCAAGTTC GGCTTCGGCT TTTTCGTTGA TGGTCGGGAA CTCGTGCCAA
401 GTATGGAATA GCACGCTGTC TTCTGCGCCG CCGCCGATGA TGTCCACGCG
451 TTCTTCGCGG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGCG GCGGCTGTCT
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTACGGCA AAGTGAAGG
651 CATAACGCGG ATAAAAATCA CCGGCAACGC GTTCTTGCGC CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCACAC ATATCGCCTT GTTGACGCGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTGAG GATTTCCTTG
851 GAAATCGCCA ATTCGCGGCT GTAATCGGTG GATGCGCGCC ACAGGCGCAG
901 GATGTCGCGC CCGAATCGT TATACACTTC TTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACCG CGCGCGACCC ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

```

a236.pep
1  MARFAFSADI LCTAFADGFM ACNRAHLAGV VPAAFAFFT I TGFSNGKFA
51  AYFHFCFRHQ QSKAQFFAQSI IQIAGHFFRR GNFGFGLQGR TDGFVGAQRL
101 DGGGYRFAGF ADCRPFFHQF GFGFFVDGRE LVPSMEKHAV FCAAADDVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAAG AAVGFGGIEA VFQDIEVERA
201 QVFRAERNHF FHGKVEGITR IKITGNAFLQ PPCQHOGIAV DFHHIRLLHG
251 IFNRIEVAQV GKQKAQGIAD TAVAFGYALE DFFGNRQFAA VIGGCRPQQA
301 DVRAELVIHF LRRDDVADGF RHFAPVLIHH ETMGQQLFVR RATH*

```

540

m236/a236 81.0% identity in 258 aa overlap

m236.pep					10	20	30
					LHGR	TDFV	GAQRLDGGGYRFAGFADCRPF
a236	FRHQ	SKAQFF	AQSIQI	AGHFFR	RGNF	GFGLQGR	TDFVGAQRLDGGGYRFAGFADCRPF
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
		FHQF	GFVF	VDGREL	VPSME	EDAVX	FAXDXDVRFFAGEAQNRCNQENQTACDVIQGS
a236		FHQF	GFVF	VDGREL	VPSME	KHAVF	CAAADDVPRFFAGEAQNRCNQENQAARDVVQGLR
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
		AAAC	MAVCF	GGVEA	VFQD	VEVERTQ	VFRAERNXVFYGVK
a236		AAAG	AAVFG	GGIEA	VFQD	IEVERA	QVFRFAERNHFFHGVK
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
		GVAV	DFHH	IRLLH	GIFN	RIKVAQ	VGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGR
a236		GIAV	DFHH	IRLLH	GIFN	RIEVAQ	VGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGR
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
		PQAQ	DVCAE	FVINL	LRCDV	ADGFRH	FFAFVDNETMGQQLFIRRATHX
a236		PQAQ	DVRAE	LVIHF	LRDDV	ADGFRH	FAPVLIHHE
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgctgggaca aggttgccg taatatcgca ctccccgccc cactgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccg
101 acaagctcgg tcatacgccg aggattgtcg ataaattcgt tatccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcggaataa tccaaaatat
201 gccggttgct gcatactgcc atattgttg gcgataagcc tttgtgccc
251 gcgccaagg gttcgggtgc aataataag gtgctgacg caatcgctt
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacg
351 catagaccac atttttacac tcgacgctgc ctcgggctg gtaaaccagc
401 caaccgtttt gatacgggtc gatgcgcgtc atcggggatt gtcgaaaaat
451 ctgcgcgcgc gcttcggcag cgcgcgtggc aacaccaac gtgtaattga
501 gcgatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctgtt caactcggtt ttatcccaa gttgataatg
601 actcgacccg taatgccgtt ggcggtgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgtgg cataaccgcg ctgccaatcg
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgcctg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagccg acctgtttt
801 caatttccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgcgaagcc gatacgtgcg gcttccaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaacccg
951 cgcgataat gcagggttcg gctttcagac ggcattggag tttcggataa
1001 acagtatgcg gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcagg cgaatcattg tgtttgctt atcgggtata ttttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcggttga

```

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEKQFAVRAE AVIIQNMAVV AYCHIVADKP FCARAQFGG NNGGADGNRL

```

541

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
 151 LRAGFGSGAG NTQVIERMK MPQGIELCA LVHIAVKLLF QLGFIPKLIM
 201 TRTVMLGVF MPLQLQFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTGCFQNDGF
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
 51 CGATTTTGAC ATCGGCAAGC TCGGAAAAA CTTTAAGCAT ATCTTGGCGG
 101 ACAAGCTCGG TCATA CGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAATAT
 201 GGCGTTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGGC
 251 GCCCCCAAGG GTTCGGTCCG AATAATAAAG GTGCTGACAG CAATCGCCTT
 301 GCGTTCCAAA GGCCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGGGGCGT GTAAACACAGC
 401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAT
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCCAA GTGTAAGTGA
 501 GCGGATGCAG GTGTCCGGAT AAGGGTCCGA ATTGTGCCCC TTGGTACATA
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
 701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
 801 CAATTTCCCC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
 901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
 1051 AAAATCAGGG CGAATCATTTG TGTTCGCTTT ATCAGGTGTA TTTTCGGACG
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep
 1 MRDKVGGNVA LPAPRIFDFD IGKLRKNFKH ILADKLGH TL RIVDKLVILT
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM
 201 TRTVMLGVF MPLQLQFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
 251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
 301 MSLLRQGQCS AQTQSAADD TGIGFQTALK FRINSMRINR TEIIRRQIFL
 351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE					
g237	MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TR RIVDKFVILTAEKQPAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNNGGADSNRLAFQRPEYRVQTCISIDSIDH					
g237	AVIIQNMAVVAYCHIVADKPF CARAQFGGNNKGADGNRLAFQRPEYRVQTCISIDGIDH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRF DARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					

[illegible]

```

a237.seq
1   ATGCGGGACA  AGGTTGGCGG  TAATGTCGCA  CTCGCCGCC  CACGAATATT
51  CGATTTTGAC  ATCGGCAAGC  TCGCGAATAA  CTTTAAGCAT  ATCTTGGCGG
101 AACAGCTCGG  TCATACGCGC  GGGATTGCTG  ATAAACTCGT  TATPCTTACC
151 GCCGAAAGC   AGTCTGCCGT  CCGCGCTGAG  GCGGTAATAA  TCCAAAATAA
201 GACGGTTGT'C GCATACGTGCC ATATTGTTGC  GGATAAGCCC  TTTTGCACGC
251 GCGCCCAAG   GCTCTGTGGC  AATAATAAAG  GTGCTGACAG  CAATCGCCTT
301 GCGCTCAAAA  GGCTTGAATA  TCGGATTCAA  ACCGGCATAA  GTATTGACGG
351 CGTACACCAG  ATTTTTCGAT  TCGACGCTGC  CTTCGGGGGT  GTAAACCAGC
401 CAACCGTTTT  GATAAGGTTT  AATGCGTATC  ATGGGAGAA  GCTCAAAAAT
451 CTTCTGACCA  GCTTCGGCAG  CGCGCGCGGC  GATGCCAAC  GTGTAATTGA
501 GCGGATGGAG  ATCCCGGAC  AAGGATCGA  ACTGTGCGCC  TTGGTACATA
551 TCGCTGTCAA  GCTGCTGCTT  CAGTTCAGTG  TTATCCAGA  GTTGATAATG
601 AGTTGCACCG  TAATATTTTT  GGGCGTGCTC  ATCAATCTGT  TGCAAATCTT
651 CCCAATGCTG  CGAACGGATG  GCAACCGTGG  CATAACCGCG  TCGCCAATCG
701 CAATCAATGG  CATCTTTGCG  GACCGGTTCC  TCACCAAGTT  CGACCGCTCG
751 CAAAGACTGT  TGCCAAAACC  ATTGCGCTTG  CTCAAACCG  ACCTGTTTTT
801 CAATTTCTCT  CATACCGCAG  GCGTAATCGC  TGAATAACCTG  CCGCCCACTG
851 CGTCCCAGCG  CGCCGAAACC  GATACGCGCG  GCTTCCAACA  CAACCGTTTC
901 ATGTCCTCTG  TCCGCCAAGG  GCAATGCAGT  GCACAAAACA  CTTCAATCCG
951 CGCCGATGAT  ACAGGTATCG  GTTTTCAGAC  GGCATTGAAG  TTTTCGGATA
1001 ACAGATATGAG  GATTAACCGA  TGTAAATAA  TAAGAAAGCA  GATATTCCTG
1051 AAAATCAGGG  CGAATCATTG  ACTTTGCTTT  ATCGGGTATA  TTTTCGGAGC
1101 GAATGATACA  GGCTGTGCGAG  CCATATCGTC  CAAACAGAAA  ATCGGTTGCA

```

a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVV	AYCHIVADKP	FCTRAQGGFC	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAAFGG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DAQRVIERME	MPGGGIELCA	LHVHIAVKLLL	QFSVIPPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLPKPLRL	LQTDLFFNFL	HTAGVIADNL	PATPSRRAET	DTRGFQHNRF
301	MSLLRGQCS	AQTQSAADD	TGIGFQTALK	FRINSMRINR	TEIIRRQIFL
351	KIRANHCVCF	IGYIFGRNDT	GCRAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	FDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE			
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	FDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE			
m237.pep	70	80	90	100	110	120
	AVIIQNMAVVAYCHIVTDKPF	CARPQGFGRNNKGADSNRLAFORPEYRVQTCISIDSID				
a237	70	80	90	100	110	120
	AVIIQNMVVAYCHIVADKPF	CTRAQGFGRNNKGADSNRLALQRLLEYRIQTGISIDGVHQ				
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMRFDARH	RGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP				
a237	130	140	150	160	170	180
	IFAFDAAFGRVNQPTVLI	RFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA				
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFI	PKLIMTRTVMLGVFMPLQLFPMRLTDGNRGITALPITIDGMEA				
a237	190	200	210	220	230	240
	LVHIAVKLLQFSV	IPELIMSCTVIFLGVLMPLQLFFPMRLTDGNRGITALPIAINGMEA				
m237.pep	250	260	270	280	290	300
	DAFVHQFDRQLRL	LQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF				
a237	250	260	270	280	290	300
	DAFVHQFDRQLRL	LQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF				
m237.pep	310	320	330	340	350	360
	MSLLRQGCSPAQT	TQSAADDTGIGFQTALKFRINSMRINRTEIIR	QIFLKIRANHCVC			
a237	310	320	330	340	350	360
	MSLLRQGCSPAQT	TQSAADDTGIGFQTALKFRINSMRINRTEIIR	QIFLKIRANHCVC			
m237.pep	370	380				
	IRCI	FRNDTGCRAISSXQKIGX				
a237	370	380				
	IGYI	FRNDTGCRAISSXQKIGX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

1	atgaatttgc	ctattcaaaa	attcatgatg	ctgttggcag	cggcaatatc
51	gatgctgcat	atccccatta	gtcatgcgaa	cggtttggat	gcccgtttgc
101	gcgatgatat	gcaggcaaaa	cactacgaac	cgggtggcaa	ataccatctg
151	tttggtaatg	ctcgcggcag	tgtaaaaaat	cgggtttgcg	ccgtccaaac
201	atttgatgca	actgcggtcg	gccccatact	gcctattaca	cacgaacgga
251	caggatttga	aggtgttata	ggctatgaaa	cccatttttc	aggacacgga
301	cacgaagtac	acagtccgtt	cgataatcat	gattcaaaaa	gcactttctga
351	tttcagcggc	ggcgtagacg	gcggttttac	cgtttaccaa	cttcacgga
401	cagggtcggg	aatacatccc	gcagacggat	atgacggggc	tcaaggcggc
451	ggttatccgg	aaccacaagg	ggcaagggat	atatacagct	accatatcaa
501	aggaacttca	acaaaaacaa	agataaacac	tgttccgcaa	gccccctttt
551	cagaccgctg	gctaaaaagaa	aatgccggtg	ccgcttcggg	ttttctcagc
601	cgtgcggatg	aagcaggaaa	actgatatgg	gaaaaacgacc	ccgataaaaa
651	ttggcgggct	aaccgtatgg	atgatattcg	cgcacatcgc	caagggtcgg
701	ttaatccttt	tttaacgggt	tttcaagggg	tagggattgg	ggcaattaca
751	gacagtgcgg	taagcccggg	cacagatata	gccgctcagc	agactctaca
801	aggtattaat	gatttaggaa	atttaagtcc	ggaagcacia	cttgcgcgcg

544

```

851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtacgagagg ccgaggttac ggtttgagcg ggtaaaaaag
1001 tagaacttaa ccgacccaaa tgggattggg ttaaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atggttaagt
1351 agagatggca ctgcacaata tcggccacca acagaaaaaa aatcacatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1  MNLP IQKFMM LLAA AISMLH IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKT KINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRA NRMDDIRGIV QGAVNPFITG FQGVGIGAIT
251 DSAVSPVTDt AAQOTLQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINs
301 ARQWADAHFN ITATAOTALA VAAAGTVWR GKVELNPTK WDWVKNTRYK
351 KPAARHMOTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYT IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1  ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51  GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGTGTTTATC GGTATGAAA CCCATTTTTC AGGGCAGCGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACTTCTGA
351 TTTCAAGCGG GGTGTAGACG GCGGTTTAC TGTTTACCAA CTTTCATCGA
401 CAGGGTCCGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCC CGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCCCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACAA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGGCG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCGCCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAAATCTT TACCAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAATCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTACAG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAATTTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1  MNLP IQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYPEGGKYHL
51  FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

```

151 DYPPPGGARD IYSYVKGTS TKTNTNIVPQ APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGINS
301 AKQWADAHPN ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRKQNFEPN SNWSSASFDS
401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY
451 LDSNGNAVKT GNLOGKQAXD YLQOQTHIRN LDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238 . pep	10	20	30	40	50	60
	MNLPIQKFMMFLAAAI	ISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK				
g238	MNLPIQKFMMLLAAAI	SMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN				
	10	20	30	40	50	60
m238 . pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPI	THERTGFEGVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG				
g238	RVCAVQTFDATAVGPILPI	THERTGFEGVIGYETHFSGHGHEVHSPFDNHDSDSKSTSDFSG				
	70	80	90	100	110	120
m238 . pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHP	EDGYDGPQGSDDYPPPGGARDIYSYVKGTS	TKTKTNIVPQ			
g238	GVDGGFTVYQLHRTGSEIHP	ADGYDGPQGGYPEPQGARDIYSYHIKGT	STKTKINTVPQ			
	130	140	150	160	170	180
m238 . pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFS	RADEAGKLIWESDPNKNWWANRMD	DVRGIVQGAVNPFLMG			
g238	APFSDRWLKENAGAASGFLS	RADEAGKLIWENDPKNWRANRMD	IRGIVQGAVNPFLTG			
	190	200	210	220	230	240
m238 . pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGKLSPEAQ	LAAASLLQDS	AFAVKDGINS		
g238	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGNLSPEAQ	LAAASLLQDS	AFAVKDGINS		
	250	260	270	280	290	300
m238 . pep	310	320	330	340	350	360
	AKQWADAHPNITATAQTALS	AAEAAGTVWRGKKVELNPTK	WDWVKNTGYKKPAARHMOTL			
g238	ARQWADAHPNITATAQTAL	AVAEAAGTVWRGKKVELNPTK	WDWVKNTGYKKPAARHMQTV			
	310	320	330	340	350	360
m238 . pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAE	KRKQNFENSNWSSAS	PDVHKTLPNAPGILSPDKVKT			
g238	DGEMAGGNRPPKSI	-TSEKANAATYPKLVNQLNEQNLN	IAAQDPRLSLAIHEGKKNFP			
	370	380	390	400	410	
m238 . pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYF	RIHDNSRKQYLD	SNGNAVKTGNLOGKQAKDY	LQOQTHIRN		
g238	IGTATYEEADRLGKI	WVGEGARQTS	GGGWLSRDGTRQYRP	PEKKSQFATTGIQANFET		
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

```
a238.seq (partial)
1 ATGAATTGCT CTATTCAAAA ATTCATGATG CTGTTTGAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGTTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTAAAAAAT CGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTTGA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTTAC CGTTTACCAA CTTTCATCGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAACTTCA AAAAAACAA AGAGTAATAT TGTTCCTTTC GCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGGTG CCGCTCTTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAA
651 TTGGTGGGCT AACCCTATGG ATGATATTTC CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTGCGG TAAAGACGG TATCAATTCC
901 GCCAGACAAT GGGCTGATGC CCATCCGAAT ATAAGTCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TTAATAATAC CGGCTATAAA
1051 ACACCTGCTG TTCGACCAT GCATACTTG GATGGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA
```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

```
a238.pep (partial)
1 MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHL
51 FGNARGSVKNRVYAVQTFDATABVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDKSTSDFSG
101 HEVHSPFDNHDSKSTSDFSGGVDGGFTVYQLHRTGSEIHPEDGYDGPQGS
151 DYPPPGGARDIYSYVKGTS TKTKSNIVPRAPFSDRWLKENAGASGFFS
201 RADEAGKLIWESDPNKNWWANRMDDIRGIVQGA VNPFLMGFQGVGIGAIT
251 DSAVSPVTDTAQAQTLQGINHLGKLSPEAQLAAASLLQDSAFVAVKDGINS
301 ARQWADAHPNITATAQTALVAEAATTVWGGRKVELNPTKWDWVKNTGYK
351 TPAVRTMHTLDGEMAGGNRPKKSITSNSKADASTQ
```

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHL	FGNARGSVKNRVYAVQTFDATABVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDKSTSDFSG				
a238	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHL	FGNARGSVKNRVYAVQTFDATABVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDKSTSDFSG				
	10	20	30	40	50	60
	70	80	90	100	110	120
m238.pep	RVYAVQTFDATABVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDKSTSDFSG					
a238	RVYAVQTFDATABVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHSDKSTSDFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVKGTS	TKTKSNIVPR			
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVKGTS	TKTKSNIVPR			
	130	140	150	160	170	180
	190	200	210	220	230	240
m238.pep	APFSDRWLKENAGASGFFS	RADEAGKLIWESDPNKNWWANRMD	DIRGIVQGA	VNPFLMG		
a238	APFSDRWLKENAGASGFFS	RADEAGKLIWESDPNKNWWANRMD	DIRGIVQGA	VNPFLMG		
	190	200	210	220	230	240
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTDTAQAQTLQGIN	DLGKLSPEAQLAAASLLQDS	AFVAVKDGINS		

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|||||
a238  FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAVVKDGIN
      250      260      270      280      290      300

      310      320      330      340      350      360
m238.pep AKQWADAHFNITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMQTL
      |||||
a238  ARQWADAHFNITATAQTALAVAEAATTVWGGKKVELNPTKWDWVKNTGYKTPAVRTMHTL
      310      320      330      340      350      360

      370      380      390      400      410      419
m238.pep DGEMAGGNKPIKSLP-NSAAEKRKQNEFEKFSNNWSSASFDSVHKTLTPNAPGILSPDKVK
      |||||
a238  DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttcacc ataaaggtat tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgata gcttcgtgat tcgccaacgc cgcctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctggttttgc tgcatacaca
201 cggaaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcggaccg
301 gcagtcgcgt ccgccacacg caaaactgcg ctccctcgcc tcgggttggc
351 ggcaatttcc gcttcacccg gctttaatgc cctgccacgc attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgcccagct cggcaggggc
451 tcgtgttgcg aatatTTTTT gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaacgccc gccctctttc agacggcaca
551 tgacctgcgc caataccgcc cctacttctt caagctcgcg gttataaaag
601 atcgcgattg cctggaaggt gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg tttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggacttcc cgcccggtgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLRII LLQGDFLFFR
51  LVQSCEVEPV LVLHHLNGKS GNAHRKQQKE IRFVHCRSDV FLCYYSGIGP
101 AVRSATRKTA LLALGLAIS ASPGFNALPT IFRGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWRL
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTray kGCCCgAAAC CGGCKGATGG AGGTTTGTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTCG TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAAATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCCAGCG CGGCAGGGGC
451 GCGTGTTCG AATATTTTTT GACAACTGTC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTAATTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CTTGGAAGGT GCGCGTCGCA GGATCCTGCC CCGCTCGCG
651 AGTACGGACG TTTGTGCCA CGATCTGCGC CAGCTTCCGG GTTGTATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CCGGCGGCTA
751 AACCGCTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

548

```

m239.pep
  1 MLHHKGXARN RXMEVLFFCR RPDRFVVROT RLLQPHLR I LLOGDFFLFFR
 51 LIQSCEIEPV LVLLHHNGKS GNAHRKQOKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGSSGKSA SLTAAQGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRTAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIRRL
251 NRSSP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 239 shows 93.7% identity over a 255 aa overlap with a predicted ORF (ORF 239.ng) from *N. gonorrhoeae*:

m239/g239

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVROT RLLQPHLR I LLOGDFFLFFRLIQSCEIEPV					
	:					
g239	MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLR I LLOGDFFLFFRLVQSCEIEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQOKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTA LLALGLAAIS					
g239	LVLLHHNGKSGNAHRKQOKEIRFVHCHSDVFLCYSGIGPAVRSATRKTA LLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
g239	ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
g239	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIRRLNRSSPX					
g239	ATMARTIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 897>:

```

a239.seq
  1 ATGCTCCACC ATAAAGGTAT TGCCCGAAAC CGGCGGATGG AGGTTTGTG
 51 TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTG GCGCATAATC CTGCTCCAAG GCGATTTTCT GTTTTTCGCG
151 CTTATCCAAA GCTGTGAAGT TGAGCCTGTA CTGGTTTTCG TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTCAATTG
251 TTCATGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCCG GCTTTAATGC CCTGCCCGCG ATTTTCAGGG
401 GCGGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC
451 CGGTGTGCG AATATTTTTT GACAACTGC TTCACAATGC GTCTTCCAA
501 CGAATGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CCTACTTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGATTG CCTGGAAGGT GCGCGTCGCA GGATCCTGCC CCGCTCGCG
651 AGTACGGACG TTTTGTGCCA CGATCTGCGC CAGCTTGGCG GTGTATCGA
701 TTGGACTTTC CGCCCGTTGC GCAACAATGG CGCGCGCAAT CTGGCGGCTA
751 AACCGTCTT CACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN RRMEVLFFCR RPDRFVVQR TRLQPHLR II LLQGDFLFFR
51  LIQSCEVEPV LVLLHHNGKS GNAHRKQKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKA L LALGLAAIS ASPGFNALPA IFRGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHKGXARNRXMEVLFFCRRPDRFVVQRTRLLQPHLR IILLQGDFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVQRTRLLQPHLR IILLQGDFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLHHNGKSGNAHRKQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMTGNTAPTSSSSRLIKMRTAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTGNTAPTSSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
	250					
m239.pep	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
51  ttgtgccgac gttggacgat tctgcataa tgccgcgcac atccaaagag
101 gggtaaacat gggtatcatc gcgcacggga gacggtccga tttataagg
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcggtt
251 acggcacggt tgcgccgctg ttcgctgtct gcccggccgg gtctgttggg
301 atcgtaggcg ggcgtatttg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttccg gcttttgct gatggatcc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcacaa caacttccgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagttcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacagggtg cccatcgggt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
51  LRIQPFVQIG FARIQCLRNH ERFDCTRFRD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVOLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNFR AVFAIQAVFK RKFQTFLTFA
```

550

201 VNIGKSDDVC QVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```

m240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```

m240.pep
1   MIEVIHFFGT ETRRQFACAD VGRFLHDAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFD CRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQND FRA VFAMQAVFKR KFQTLTFVAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAHIQRGVNMGIAHGRRSDFIRLRIQPFVQIG					
	: : : : : :					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAHIQRGVNMGIAHGRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
	60	70	80	90	100	110
m240.pep	FARIQCLRNHKRFD CRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGEDFPRAGIQXH					
	: : : : : :					
g240	FARIQCLRNHFRD CRTGFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGEDFPRAGIQNH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m240.pep	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR					
	: : : : : :					
g240	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRFCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
	180	190	200	210	220	
m240.pep	AVFAMQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAFX					
	: : : : : :					
g240	AVFAIQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```

a240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```

551

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGCATCCA
351 AAACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGGCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1 MIEVIHFFGT ETRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFDCTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVERGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAERVMFA*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
a240	VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1 ATGATAGAAG TCATACATT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGCATCCA
351 AACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAACGA CTTCGCGGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGGCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHPHE PASSTCAAKS

```



```

51  ANRRENSHNA OPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCTTC ATCGGATGCA TCGCGCACGC TTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCAC CAAAGGGAAT ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGCTCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDQD LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPSQ	RQSVVMTVR	TVDMTVCDL	IGCIAHAFNR
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVHHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFNR
g241	SFKADFHACQ	RMVAVHHRLA	VGNIGYTIDD	NIAGFRIVRF	KHHTDLDFNR	ERARIFNTDQ
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241	LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFI	QKLIVGIIHL
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241		IMQRNHGIFC	NSHICPFRNS	RLITGAFX		
		250	260			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACGCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```

a241.pep

```

m241.pep      .                               10          20          30
                                         RQSVVVM TVRAVDMTVCDFLIGCIAHAFNC
                                         |||||:::||:||:||:||:||:||:||:||:||
a241           QPTYLLHPSNKM PSEMEQT LFRRHQIP PSQRQS VVMTVR T VDMTVCDFLIGCIAHTFNR
              70             80             90            100           110           120

              40             50             60             70             80             90
m241.pep      SLKADFACQRMVA VHRLAVGNIGYTID DNIAGFRIVGFKHHADFD FNREHARIFD TDQ
              |||||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
a241           SLKADFACQRMVA VHRLTVGNIGYTID DNIAGFRIVGFKHHADFD FNREHARIFNTDQ
              130            140            150            160            170            180

              100            110            120            130            140            150
m241.pep      LRILLAERIVGRQRH IDRIAGILTVQ RL FHQREN AVVTAVQIR NRFFGFVQKLIVGI IHL
              |||||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
a241           LRILLAERIVGRKRH IDRIAGILTVQ RL FHQREN AVVTAVQIR NRFFGFVQKLIVGI IHL
              190            200            210            220            230            240

              160            170
m241.pep      IMQRNHGIFHD SHICPFRRNSRLITGA FX
              |||||:::||:||:||:||:||:||:||:||:||
a241           IMQRNHGILHDS HICPFRRNSRLITGA FX
              250            260

```

g241-1.seq

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMTVR
101 TVDMTVCDFL IGCIAHAFNR SFKADFHACQ RMVAVHHLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACTCG CGCTGCAAACT CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAAC AAAATGCCGT CTGAAACGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACACCGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMTVR
101 AVDMTVCDFL IGCIAHAFNC SLKADFHACQ RMVAVHHLA VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFDIDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMTVRAVDMTVCDFLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMTVRTVDMTVCDFLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVHHLAVGNIGYTIDDNIAAGFRIVGFKHHADFDNREHARIFDIDQ					
g241	SFKADFHACQRMVAVHHLAVGNIGYTIDDNIAAGFRIVRFKHHADFDNRRERARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACTCG CGCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCTC ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCCGT CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1 MPTRPTRA AK HPTPPTWLQT AYCPRPYP RP PSVQTHTPHE PASSTCAAKS
51 ANRRENFHNA QPTYLLHPSN KNPSEMEQTL FRRHQIPPS C RQSVVMTVR
101 TVDMTVCD FL IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFEGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRA	AKNPPTWL	QTA	YCPRPYP	RPPSVQTR	TPREPASSTCAAKS
a241	MPTRPTRA	AKNPPTWL	QTA	YCPRPYP	RPPSVQTH	TPHEPASSTCAAKS
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSN	KNPSEMEQTL	FRRHQIPPS	CRQSVVMTVR	AVDMTVCD	FLIGCIAHAFNC
a241	QPTYLLHPSN	KNPSEMEQTL	FRRHQIPPS	CRQSVVMTVR	TVDMTVCD	FLIGCIAHTFNR
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQ	RMVAVHHRL	AVGNIGYTIDD	NIAGFRIVG	FKHHADFD	FNREHARIFD
a241	SLKADFHACQ	RMVAVHHRL	TVGNIGYTIDD	NIAGFRIVG	FKHHADFD	FNREHARIFNTD
	190	200	210	220	230	240
m241-1.pep	LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFEGFV	QKLIVGIIHL
a241	LRILLAERIV	GRKRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFEGFV	QKLIVGIIHL
	250	260				
m241-1.pep	IMQRNHGIFH	DSHICPFRNS	RLITGAF			
a241	IMQRNHGILH	DSHICPFRNS	RLITGAF			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1 atgatcggcg aactgttgt tttgttcgtg atcgagcact tcaagcaacg
51 cgctggcggg atcgccccga aagtcgctgc ccaatttgct gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgcggggc atagagccga tataggtagc gcggtgcccg cggatttcgc
201 tttcgtcgcg cacgccgcc aaggccatac ggacatat ttcgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgc ccggagggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttggaacgg
351 cgaggatttc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtccggc tttggcgatg tctttgctga cgcgggattt
451 tttctccac ggcagtcgca gcagggtgct gatgtagttg cgtacgacgg

```

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```

501 tggattcggc agacatcggc ggcatacattt tgagtttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgctc ttcttcgccc aattccttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttgcggtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcggttgcg ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatecggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242 . pep

```

1  MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51  LAGHRADIGT AVPADFAFVA HAAQGHDTDF PPRCFDGFQA QRGFAHARRA
101 DQTONRTFEL VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPPADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242 . seq

```

1  ATGATCGGCA AACTTGTGTG TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51  CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTTGTC GATTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTCCG
201 TTTCGTGCGC CACGCCGCCC AAAGCCATGC GGACATATT TCCGCCCGTT
251 GCTTTGGCGA TGGATTCGCC CAAAGAGGTT TTGCCACGCG CCGGAGGGCC
301 GACCAGGCAC AGAATCGGCG CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAATCCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCC
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCITTTGCTG CGCGGGATT
451 TTCTTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATT TTAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGCTTT AATCTGTTCG TTCAGATAAT ATTCGCGCTG GEAATTTTCC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTC CAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242 . pep

```

1  MIGKLVVLFV IEHFQQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51  LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGFQA QRGFAHARRA
101 DQAQNRAFEF VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELE QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPPADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVVLFVIEHFQQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
	: : : : : : :					
g242	MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVS YACFCHILQNLGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQAQRGFAHARRADQAQNRAFEFVHTFLDGEVF					
	: :					
g242	AVPADFAFVAHAAQGHDTDFPPRCFGDGFQAQRGFAHARRADQTONRTFELVHTFLDGEVF					
	70	80	90	100	110	120

	130	140	150	160	170	180
m242.pep	QNPFDFDFFQAVVVGIQHQS	SGFGDVFADAGFFLPRQLE	QSV	DVVAYDGGFRRHRWHH	FE	LF
				:		
g242	QNPFDFDFFQAVVVGIQHQS	SGFGDVFADAGFFLPRQSE	QGV	DVVAYDGGFGRRHRHH	FEFF	
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGHTR	LF	DICFQGIQFAV	FVFFAQFFVYR	FNLFVQII	FALGFFHLAFDAS
		:				
g242	QFGQAFFFRFFGHTR	LFDAC	LQGIQFAV	FVFFAQFFVYR	FNLFVQII	FALGFFHLAFDAS
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVEFGFQ	LCQ	QEFHPFADFGN	FNLLALRQFQ	LQMRCDRIGX	
g242	AYAFFGLHNVEFGFQ	LCQ	QEFHPFADFGN	LNLLALRQFQ	LQMRCDRIGX	
	250	260	270	280		

```
a242.seq
1  ATGATACGGCGC AACTTGTGTGT TTTGCTCGGG ATCAAGCACT TCGAGCAACG
51  CGCTGGCGGAG ATCGCCCCGGC AAGTCGCTAN CCAATTGTGC GATTTCGTCG
101 AGCAGGAAAGA ATGGGTTTTTT TACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGGC ATGGAGCCGA TATAGGTGCG GCGGTGTCCC CGGATTTGCG
201 TTTCTGTCGCG CACGCCGCCCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTTCGCC CAAGAGGTTT TTGCCACAGC CTGGAGGGCC
301 GACCAGGACG AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTGGACGG
351 CGAGGTATTC CAAATCC3T TCTTTGACTT TTTCCAGGCC GTAGTG6TCG
401 GTATCCAGCA CCAATCCG3T TTTGGCGATG TCTTTGCTGA CCGCGGATTT
451 TTTCTTCCAC GGCAGTTCSA GCAGGGTGTC GATGATAGTT GCTACGACGG
501 TGGATTCCGC AGACATCGGC GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCGCCTTTT TGATATCTCG
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCTTTGT
651 GTATCGTTT ATCTGTTTCG TTCAGATAAT ATTTCGCGTG GAGATTTTCC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAA7GTC
751 GAGTTCCGAT TCCAGCTGTG CCAGCAGGAA TTCCATCGT TTGCCGATTT
801 CGGGAATTTT CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGTTAG
```

a242.pep

1	MIGELVVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQQWF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCEGDGFA	QRGFAHAWRA
101	DQAQNRAFEF	VHTFLDGEVF	QNPFDFDFQA	VVVGIQHQSG	FGDVFEADAGF
151	FLPRQFEQGV	DVVAYDGGGF	RHRRHHFELF	QFGQAFFFRF	FGHTRLFDIC
201	<u>FGQIQFAVF</u>	<u>FFAQFFVYF</u>	<u>NLFVQIIFAL</u>	<u>GFHFLAFDAS</u>	<u>AYAFGLHNHV</u>
251	EGFGQLCQVE	PHFPADFNGF	QNLLALRQFO	LMQRCDRIG+	

	10	20	30	40	50	60
m242.pep	MIGKLVLVLF	GIHFEQRAGGI	ASEVVTQFVDF	VEQEQQGVF	HAGFCHILQ	NLTGHRADIGA
a242	MIGELVVL	LGIKHF	EQRAGGIA	PEVAXQFVDF	VEQEQQWVF	YAGFCHILQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQ	SHADIFPPRC	FGDGF	FAQRGFAHARRADQAQ	NRAFEV	FVHTFLDGEVF
a242	AVSPDFAFVAHAAQ	SHADIFPPRC	FGDGF	FAQRGFAHAWRADQAQ	NRAFEV	FVHTFLDGEVF
	70	80	90	100	110	120
	130	140	150	160	170	180
m242.pep	QNPFFDFFQAVVVG	IGIQHSGSG	GDVFADAGFF	LPRQLEQSV	DDVAYDGGF	RRHRWHHFE

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```

a242      QNPFDFFOAVVVGIIQHQSFGVDVFADAGFFLPRQFEQGVDDVAYDGGGFRHRRHHFELF
           130      140      150      160      170      180

           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           |||||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRNLVQIIFALGFFHLAFDAS
           190      200      210      220      230      240

           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHPEADFGNFQNLALRQFQLQMRCDRIGX
           |||||||
a242      AYAFFGLHNVEFGFQLCQQEFHPEADFGNFQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATcc tgCCGATGAG CTTTTTGTIT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IORFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGyGGT TTTTACCGGA ATCCACACG GGGGCGAaYA GGTCTTCCTC
201 TTCCTGCAAA CCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTIT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IOXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

           10      20      30      40      50      60
m243.pep  MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      MVIVWLPELPPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIORFLTESKT
           10      20      30      40      50      60

           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

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70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGC GA GATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGTTC
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRTSTISS TVTLPMSEFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRTSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRTSTISSTVTLPMSEFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
51  tcgacgcgtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggag
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct tatcgccgc tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaaagt catctgcaca cccattttca
351 ggcacatgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttcac ggcaaaactc tgccggcgga acttggtgct
451 atcggaatt tcctgctggt ggcggcgagg caggttttgc tcgtttgcca
501 aagcgcgag ttgttcgtct ttcaactgag cttccagctc ggcaatccgc
551 gcctgcaaat cctcataaag cggctcggcg gcagcctgtt cctgtacacc
601 gtcgcgattt cctactgtct cgaagggttc caccgcctcc acattttcaa
651 ccgcttcttc actgctttgc tgcgtgtct gttcgtcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcggcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTONALOEIN QIIPOTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHLRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTRFQRIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRQLILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSGYYPKSKR
251 TFSRNFKQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq

m244 . pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEIN  QIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFQLQVOS  HLHAHFQRIE  IAAIQKRHF  QIILDROHFH  GKLLSGELVR
151  TRNFLVAAA  QVLLVCQSA  LVFQLRQFH  NPRLQILSR  LCGSLFLHTV
201  RISYCFDGFH  RLLHFCNRF  VLLRLCFANI  VSLKTNWKS  SSYPYRKIRT
251  ESRNFEXOR  ISNSFSNPLP  KKKYRR*

```

Homology with a predicted ORF from *N. gonorrhoeae*

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTQNALOEINQIIPQTSPSGFLLRHNRHSRAQHVAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTSPSGFLPCHRNHSRAQHTVQGIGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	: : : : : :					
g244	LHHTNHGIGFLLTGHRHLRMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m244 . pep	IAALIQRKRFQIILDRQHFGHKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
	:					
g244	ITALIQRKRFQIILDRQHFGHKLLSGELVRIGNFLVAAAQVLLVCQAQLFVFQLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244 . pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTLLLLCLFAHIVSLKTNWKS					
	: :					
g244	GNPRLQILISRLGGSLFLYTVRISYCLDGFHRLHIFNRFFTLLLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRX					
	: : :					
g244	KSGYYPSKIRTFSRNFKORQEI SHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGGCG TCGGACAGCG TATAACCCTT CTTATCACG CCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATGCGCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAA CTCTATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCGCTTCTC ACTGTTTTC TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAACAACAA TTGGAAATCA AAATCCAGTT ATTACCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGAC GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQEI	QIIPQTPSGFLLRHRNHSRAQHAVGQRITL				
a244	MPSEARQAGSDGIAALLRSVYTONALQEI	QIIPQTPSGFLLCHRNHSRAQHAVGQRITL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIAR	FRVDFDLRSIKCFLQLVQSHLHAHFQRIE				
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIAR	FRIDFLDLRSIKCFLQLVQSHLHAHFQRIE				
	70	80	90	100	110	120
	130	140	150	160	170	179
m244.pep	IAALIQRHFQIILDRQHFHGKLLSGELVR	IRNFLVAAAQVLLVCQSA-LLVFQLRFQL				
a244	IAALIQRHFQIILDRQHFHGKLLSGELVR	IRNFLVAAAQVLLVCQSAQLLVFQLRFQL				
	130	140	150	160	170	180
	180	190	200	210	220	230
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGF	HRLHIFNRFFTVLLCLFAHIVSLKTNWKS				
a244	GNPRLQILISRLCGSLFLHTVRISYCLDGF	HRLHIFNRFFTVLLCLFAHIVSLKTNWKS				
	190	200	210	220	230	240
	240	250	260	270		
m244.pep	KSSYYPRKIRTFSRNFXQXORISNSFSNPL	PKKXYRRX				
a244	KSSYYPRKIRTFSRNFXQXORISNSFSNPL	PKKXYRRX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgcgcctg aagcccgcc gccgggttca gacggcattg ccgctttact
```

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```

51  tcgatcggtt  tatacgcaaa  acgcgcttca  ggaaataaat  cagattattc
101  cccagacgcc  ttcaggcttc  cttccgtgcc  accgtaacca  tagccgggcg
151  caacacacgg  tcggacaggg  tataaccctt  cttcatcaca  ccaaccacgg
201  tattgggttc  ctgctcactg  gccaccgcct  gcacgcctg  atggatatcc
251  ggatcgagct  tatcgcccg  tttaggattg  atttcttga  tttgcgtggc
301  atcaaacgcc  ttctgcaact  cattcaaat  catctgcaca  cccattttca
351  gcgcacgaa  attaccgctc  tgatccaaaa  gcgcatttc  cagataatcc
401  ttgaccggca  acatttccac  ggcaaaactt  tgcgcggcga  acttgtgcgt
451  atcggaatt  tcctgctggt  ggccggcgcg  caggttttgc  tcgtttgcca
501  aagcgcgcat  ttgttcgtct  ttcaactcgc  cttccagctc  ggcaatccgc
551  gcctgcgaat  cctcataagc  cggctcggcg  gcagcctgtt  cctgtacacc
601  gtccgcattt  cctactgtct  cgacggtttc  caccgcctcc  acattttcaa
651  ccgctttctc  actgttttgc  tgctgtgtct  gttcgctcat  atcgatatcc
701  tcaaaacaaa  ttgaaatca  aaatccggtt  attaccggag  caagataagg
751  acattttcaa  gaaacttcaa  gcaaaggcag  gaaatttcac  atccgcgcgc
801  gaatacccta  ccgcaaaaac  catataaacg  gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS  DGIAALLRSV  YTQNALQEI  NIIPQTPSGF  LPCHRNHRSR
51  QHTVGQGITL  LHHTNHGIGF  LLTGHRHLRL  MDIRIELIAR  FRIDFLDLRG
101  IKRLQLIQS  HLHTHFQRIE  ITALIQKRHF  QIILDRQHFF  GKLLSGELVR
151  IGNFLLVAAA  QVLLVCQSAQ  LVFVQLRFQL  GNPRLQILIS  RLGGSFLFLYT
201  VRISYCLDGF  HRLHIFNRF  TVLLCLFAH  IVSLKTNWKS  KSGYYPKIR
251  TFSRNFKRQ  EISHPPNTL  PQKPYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGCTCG  AAGCCCGACA  GCGGGGTTC  GACGGCATTG  CCGCTTTACT
51  TCGATCGGTT  TATACGCAAA  ACGCGCTTCA  GGAAATAAAT  CAGATTATTC
101  CCCAGACGCC  TTCAGGCTTC  CTTCTGCGCC  ACCGTAACCA  TAGCCGGGCG
151  CAACACGCGG  TCGGACAGCG  TATAACCCCT  CTTATCACA  CCCACCACGG
201  TATTCGGCTC  CTGTTGCTT  GCCACCGCCT  GCATCGCCTG  ATGGATATTC
251  GGATCGAGCT  TATCGCCCGC  TTTAGGGTTG  ATTTCTTGA  TTTGCGTAGC
301  ATCAAATGCT  TTCTGCAACT  CGTTCAAAGT  CATCTGCACG  CCCATTTTCA
351  GCGCATCGAA  ATTGCCGCTC  TGATCCAAAA  GCGCCATTTC  CAGATAATCC
401  TTGACCGGCA  GCATTTCCAC  GGCAAACTTC  TGTCGGCGCA  ACTTGTGCGT
451  ATCCGCAATT  TyCTGCTGGT  GCGCGCGCGC  CAGGTTTTGC  TCGTTTGCCA
501  AAGCGCGCTG  CTCGTCTTTC  AACTGCGTTT  CCAGCTCGGC  AATCCGCGCC
551  TGCAATCCT  CATAAGCCGG  CTCGTGCGCA  GCCTGTTCCT  GCACACCGTC
601  CGCATTTTCT  ACTGTTTCTGA  CGGTTTCCAC  CGCTCCACA  TTTCAACCG
651  CTTCTTCACT  GTTTGCTGC  TGTGCTGTT  CGTCATATC  GTATCCCTTA
701  AAACAAATTG  GAAATCAAAA  TCCAGTTATT  ACCGCGCA  GATAAGGACA
751  TTTTCAAGAA  ACTTCAAKCA  AAACAGAGA  ATTTCAAATT  CATTTTCAAA
801  TCCCTACCG  AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS  DGIAALLRSV  YTQNALQEI  NIIPQTPSGF  LLRHRNHSRA
51  QHAVGQRITL  LHHTHHGIRL  LFACHRLHRL  MDIRIELIAR  FRVDFDLRS
101  IKCFLQLVQS  HLHAHFQRIE  IAALIQKRHF  QIILDRQHFF  GKLLSGELVR
151  IRNFLLVAAA  QVLLVCQSAL  LVFQLRFQLG  NPRLQILIS  LCGSLFLHTV
201  RISYCFDGF  RLHIFNREFT  VLLCLFAHI  VSLKTNWKS  SSYPYRKIRT
251  FSRNFXQQR  ISNSFSNPLP  KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEI NIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEI NIIPQTPSGFLPCHRNHSRAQHTVGQGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m244-1.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIIRNFIIVAAAQVLLVCQSAALLVFQLRFLQ					
g244-1	ITALIQRHFQIILDRQHFHGKLLSGELVRIIRNFIIVAAAQVLLVCQSAQLFVFQLRFLQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTVLLLCFLAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTVLLLCFLAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTC GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTATCAGC UCCACCACGG
201 TATTGGGTTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCGCG TTTAGGATTG ATTCCTTGA TTGCGTAGC
301 ATCAAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCGC CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCGC CTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCAATT CCTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCCTTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTAACAACAA TTGGAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGCGAG AGAATTTCAA ATTCATTTTC
801 AAATCCCTCA CCGAAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFQLQVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFIIVAAA QVLLVCQSAQ LLVFQLRFLQ GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTSGFLLCHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIIRNFIIVAAAQVLLVCQSA-LLVFQLRFLQ					
a244-1	IAALIQKRHFQIILDRQHFHGKLLSGELVRIIRNFIIVAAAQVLLVCQSAQLLVFQLRFLQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m244-1.pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFTVLLLCFLAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVIRISYCLDGFHRLHIFNRFFTVLLLCFLAHIVSLKTNWKS					
	180	190	200	210	220	230
	190	200	210	220	230	240

g246.seq

1	atgtacgggc	ggaacggtag	tactcaagcg	gccgttgccct	tcgttttcga
51	ccagacacag	cgtgcccggt	tcggcaacgg	cgaagtttac	gccgctcaag
101	ccgacatcgg	cagtgcgtga	aatatcgcgc	agggctttgc	gggcgaatcc
151	ggctcagttg	tccacgtcgt	ctgtaagcgg	tgtgcgcagg	ttttgttgga
201	acgtctcgct	gacctgttct	ttggttttat	gatatgcggg	catcacgata
251	tgggtcggta	tttcgcctgc	catttggacg	ataaactcgc	ccaagtcgct
301	ttccacggcc	ttaatgcctt	ttgcttcaag	ataatggttc	agctcgattt
351	cttcgctgac	catggatttg	cctttgacca	tcagcttgcc	gtttttggct
401	gtgatgatgt	cgtggataat	ttggcaggct	tcggcagggg	tttcgcacca
451	gtgtactttc	acgcccaact	tagtcagggt	ttcttccaa	tgctccagca
501	gcgcgggtaa				

g246.pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFPAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDFPAD	HGFAPDHQLA	VFGCDDVDVN	LAGFGRGFRP
151	VYFHAQLSQV	FFQLLQQRG*			

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCATCAAAAC
101 GCACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTACGCGC GTACCCAGGT TTTGTGTGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTGCCTGCC ATTTGGACGA TGAACTCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGcYTTT TGCTTCAAGA TAATGrTTCA GCTCGATTTT
351 CTCGCTGACC ATCGATTTCG CTTTGACCAT CAGCTTGCCG TTTTGGCTG
401 TGATGATGTC GTGGATAATT TGGCAGGCTT CGGTGGGGT TTTCTGCCG...
```

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQIQ	RTCFSGNGKVY	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFGFVDSR	HHDMGRFFAC	HLDDLEAQVA
101	FYRFNAFCFK	IMXQDLFLAD	HREAFDHOLA	VFGCDDVVDN	LAGEGRGFCP...

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVHFQ	TQRTCF	SNKGVI	YATQTDIG	SAVNIAQC	FTGEAGQLVYIVCQR
	: :	: :	: :	: :	: :	: :
g246	MYGRNGSTQA	AAVAFV	PDQTOR	ARFNGE	VYAAQADIG	SAVNIAQGF
	: :	: :	: :	: :	: :	: :
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANL	FFGFVDSR	HRHDMGR	FFACHLD	DELAQVAF	YRFNAPCFKIMXQLDPLAD
	: :	: :	: :	: :	: :	: :
g246	CAEVLVEQFADL	FFGFMD	CGHDMGR	FFACHLD	DKLAQVAF	HLNAPCFKIMVOLDPLAD
	: :	: :	: :	: :	: :	: :



565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1   ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTTGCCT TCGTTTTCCT
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGTCTGT AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCACTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGG
201 ACAGTTCGCT AACCTGTTCT TTGGTTTAT GGATTGCGGG CATCACGATA
251 TGGGTCGGTT TTTCACCTGC CATTGGGACG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATT
351 CCTCGCTGAC CATCGATTG CCTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1   MHGRNGGTQA TVAEVFHQQTQ RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HHDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDVD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:	:	:	:	:	:
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCHLDELAQVAFHFRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1   atgaaacgta aaatgctaaa cgtaccaaag ggcggttatg atggtatgaa
51  ggggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccggaa attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaatgttc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaactcaa
301 tctaaccctt caaaaccggt tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattgata acaactgat tcccgttgcg gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggttttccaa
451 tacggtatcg atgatcttga tgcgagtgcg gagactgttg tagtcagcag
501 ctgttccaaa atagcaaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatc

```

566

```

601 acccgtcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttgttcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tgcacaaatc caaaaatgct gttacgcctg
851 ccggggtgga ggttttattg gatagcggcc ttaatgccaa gattgcccgt
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIIVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTO
101 SNLAKPGAQK ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFQ
151 YGIDDLASA ETVVSSCSK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KKVKRMDVRY
251 IYVSGCPEDE DAGKEKFRY TNKFDKSNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTACC ATTATGAAT TTTTGGTTGC GGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCATA
251 TGTCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAT
301 TCTCCTTTT CTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTDQQN
101 SPFSLKRNGI DKLIPIAESS NINYONFFQV GSALIFOYGI DVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKGKW GNPQL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ					
	: : : : : :					
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIIVVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONSPFSLKRN					
	: : : : :					
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAAPGAQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYONFFQVGSALIFOYGIDVNAATATTVVSSCAAISKPGKQIPT					
	: : : : : :					

g247 GMDKQLIPVAESIDIKYPGFIQRLNALVFQYIGIDDLDAETAETVVVSSCSKIAPGKKIST
130 140 150 160 170 180

m247.pep LEDAKKELKIPDQDKENGNITARQRHVVNAYAVGRIAD-EESLFRFQLDDKGKWGNPQL
|::||: |:| ::|| ||||::|::| |||||::|::| |::| ||||| ||||| |||||
g247 LQEAKSALQITNDDK-QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKWGNPQLL
190 200 210 220 230

g247 VKKVKRMDVRYIYVSGCPEDEDAGKEEFRTYNKFDSKNNAVTPAGVEVLDDLSDGLNAKIA
240 250 260 270 280 290

```
a247.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAATTATG  ATGGTATGAA
51  GGGTTTTACC  ATTATTGAAT  TTTTGGTTGC  GGGCATGCTC  AGTATGATTG
101 TCTGTATGGC  GTGTCGGATC  AGTTACTTCA  CATCCCGGAA  ATTAATGAT
151 GCGGCAAACG  AGCGTCTTTC  CGCGCAACAG  GATTGCGGA  ATGCGGCAAC
201 ATTGATTGTC  CGCGATGCAA  GAATGGCAGG  GGGCTTCGTT  TGTTCCAATA
251 TGTCGGAGCA  TACTAAAAAT  GATATTATTG  TTGATCCAAG  TAAGCAAACT
301 CACATGCTCC  CTGTAAAAAC  CGGTGCCAAA  CAAGAAATC  CCGTTTTTTC
351 TTTAGAGTGG  GCTAATACTA  ATAATACTAA  TAATAATACA  GCTAATTTGA
401 TTCCTATTGC  TGAATCCACA  GATATTAAAT  ATCCGGGTTT  TGCCCAGGCT
451 CGTCCGGCAT  TGATTTTCCA  ACTCGGCATC  GATGATCTTG  ATGCGAGTGC
501 TGAGACTGTT  GTAGTCAGCA  GCTGTTCCAA  AATAGCAAAA  CCGGGTAAGA
551 AAATATCTAC  CTTGCAAGAA  GCAAGAGAGT  CATTACAGAT  TACTAATGAT
601 GATAAACAAA  ATGGAAATAT  CACCCGTCAA  AGGCATGTGG  TCAATGCCTA
651 TGCGGTGCGC  AGGATTGCCG  GTGAGGAAGG  TTTGTTCCGC  TTCCAATTGG
701 ATGATAAGGG  CAAGTGGGTT  AATCTCTCAG  TGCTCGTGAA  AAAGATTAGA
751 CATATGAAAG  TGCGGTATAT  CATGTGTTCC  GACTGTCTGT  AAGATGACGA
801 TGCCGGCAAA  GAGGAAAAAT  TCAAATATAC  GGGTACATTG  GACAGCTCCA
851 CAAATGCTGT  TACCGCCGCG  GGGGTGGAGG  TTTTATTTAG  TANCGGTACT
901 GATACCAAGA  TTGCGCGCTT  TTCAGACAAAT  CATATTATTG  CTTACCGTAT
951 GCATGCGACA  ATACGCGGGG  GAAATGATG  CGCAACACGA  ACACTTTGA
```

```
a247.pep
  1  MRRKMLNVPK  GNYDGMKGFT  IIEFLVAGML  SMIVLMAVGS  SYFTSRKLN
51  AANERLSAQQ  DLRNAATLIV  RDARMAGGFG  CFNMSEHTXN  DIIVDPQSQT
101 QHVPVKPGAK  QENPLKSLW  ATNTNTNNT  AKLPIAEST  DIKYPGFAQA
151 RPALIFYQGI  DDLDAEATV  VVSSCSKIAK  PGKKISTLQE  AKSALQITND
201 DKQNGNITRQ  RHVVNAYAVG  RIAGEEGLFR  FQLDDKGKVG  NPQILVKKIR
251 HMKVRYIYVS  DCPEDDDAGK  EEKFYGTGTF  DSSNAVTPA  GVEVLLSXGT
301 DTKIAASDDN  HICAYRIDAT  IRGNVNCAR  TL*
```

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIIEFLVAGLLSMIVLMAVGSSYFTSRKLNDAAANERLAAQQ					
a247	: : : : : : : :					
	10	20	30	40	50	60
	MRRKMLNVPKGNYDGMKGFTIIIEFLVAGMLSMIVLMAVGSSYFTSRKLNDAAANERLSAQQ					
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQQNSPFSLK-					
a247	: : : : : : : : :					
	70	80	90	100	110	120
	DLRNAATLIVRDARMAGGFGCFNMSEHTKNDIIVDPSKQTOHPVPKPGAKQENPLFSLEW					
	110	120	130	140	150	160
m247.pep	-----RNGIDKLIPIAESSNINYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISK					
a247	: : :					
	ANTNNTNNNTAKLIPIAESTDIKYPGFAQARPALIFQYGIDDLDASETVVVSSCSKIAK					
	130	140	150	160	170	180

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	170	180	190	200	210	220
m247 . pep	PGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVNAYAVGRIADEESLFRFQIDDKGKW					
a247	PGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVNAYAVGRIAGEEGLFRFQLDDKGKW					
	190	200	210	220	230	
m247 . pep	GNPQL					
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEKFKYTGTFSSTNAVTPAGVEVLLSXG					
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1 CCCGGTGCCA AACAAAGAAA TCCCCTTTT TCCTTAAAAA GGAGCGGCAT
51 GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG AAGAGGCAA GTGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGT ATGGATGTGC GGTATATTTA TGTTCGGGT
451 TGTCTGAAG ATGAAGATGC CGGCAAGAG GAAAATTCA GATATACGAA
501 TAAATTCGAC AAATCCAAA ATGCTGTAC GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TCGGACAATA CGCGGGGAA ATGTATGCGC
651 AACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1 PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYGIID
51 LDASAETVVV SSCSKIAKPG KKISTLQEAK SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDNS
201 IYAYRINATI RGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1 ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTTGCTC AGTATGATTG
101 TCCTGATGGC GGTGCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAACAG AGCGTCTTGC CGCGCAACAG GATTTCGGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTCGAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAA*
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAAATT TTTCAGGTT GGTAGCGCAT
401 TGATTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGGCACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAGAGT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTT CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCCGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAATGTC
801 TGTTACGCCG GCCGGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1 MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTDQQN
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAIK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEGLF RFOLDKKGW GNPOLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TOTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

      70      80      90     100     110     120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVI PDTTQQNSPFLKRNIGDK-LIPIAESSNI
      | : | : | | | | : | | | | | : |
g247-1      PGAKQENPFLSLKRSMDKQLIPVAESIDI
              10      20      30

      130     140     150     160     170     180
m247-1.pep  NYQNFFQVGSALIFQYIGIDVNSTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDODK
      : | : | : | | | | | : | : | | : | | | : | | : | : |
g247-1      KYPGFIQRLNALVFQYIGIDDLASAETVVVSSCSKIAKPGKKISTLQEAQSALQITNDDK
              40      50      60      70      80      90

      190     200     210     220     230     240
m247-1.pep  EONGNIAQRHVVNAYAVGRIAD-EEGLFRFQDDKKGWGNPQLLVKKVRHMKVRYIYVS
      | | | | : | | | | | : | : | | | | | | | | : | | | | |
g247-1      -QNCNITRQKHVVNAYAVGRFGNNEESLFRFQDDKKGWGNPQLLVKKVRMDVRYIYVS
              100     110     120     130     140

      250     260     270     280     290     300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
      | | | | : | | | | : | : | | | | | | | | : | | | | |
g247-1      GCPEDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDGLNAKIAASSDNSIYAYRINAT
      150     160     170     180     190     200

      310
m247-1.pep  IRGGNVCANRTLX
      | | | | | | | |
g247-1      IRGGNVCANRTLX
      210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

```

a247-1.seq (partial)
1  AATAATACAG CTAAATTGAT TCCTATIGCT GAATCCACAG ATATTAAATA
51 TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TCGGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCTCAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAA AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCTTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCCGCCG GGGTSGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATATG TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

```

a247-1.pep (partial)..
1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51 IAKPGKKIST LQEAQSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQDDKKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

              10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | | : | : | : |
m247-1      GFGCFNMSEHPATDVI PDTTQQNSPFLKRNIGDKLIPIAESSNINYNQNFFQVGSALIFQ
              80      90     100     110     120     130

      40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAQSALQITNDDK-QNGNITRQRFVVNA
      | | | | : | | | | : | | | : | | : | : | | | | |
m247-1      YGIDDVNSTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIAQRHVVNNA
      140     150     160     170     180     190

      90      100     110     120     130     140     149
a247-1.pep  YAVGRIAGEEGLFRFQDDKKGWGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
      | | | | | | | | | | | | | | | | | | | | | | | |

```

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```

m247-1      YAVGRIADEEGLFRFQDDKKGKNGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggttttgcg
201 ggagggcgaa tttcaggttt tggatttgga atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaagggt tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgcgg caggcgtcag caaaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSEEA FGNIVVQKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIEYLVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTKCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCtT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAaC TTCAGGTTTt GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACTGTG GAAAAGGTCT GTstGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCACCGG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCac.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAAACGGA
451 GAAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFs ENCgKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS cPANSTDLcI DKGXKEYKKG TRSVTKMPRY IIEYLVGXNG
151 ENVYRVTAkA WgKNANTVvV LQSYVSNNDE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
              | | | | | | | | | | | | | | | | | | | | | | | |

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :|||||: :||| |||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFGNIVVQGKP
           70      80      90      100     110     120

           110     120     130     140     150
m248.pep  TVEAVKRSCPA---NSTDLCLDKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTA
           :|||||||  |||||:| ||:|: :|:||||||| ||:|||||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGXNGQNVYRVTA
           130     140     150     160     170     180

           160     170     180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           ||||| ||||| ||||| :|||
g248      KAWGKNANTVVVLQSYVGNINDEX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGXNGENV YRVTAKAWGK NANTVVVLQS YVSNINDEX*

```

m248/a248 89.4% identity in 180 aa overlap

```

           10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAQSYNTEQRISXNESDRKLAXS
           |||:||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVVTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGKGLXAAVNVRTNNDNEEAFDNIVVQKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGKGLCTAVNVRTNNDNEEAFDNIVVQKPT
           70      80      90      100     110     120

           110     120     130     140     150     160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGXNGENVYRVTAKAWGK
           ||||| ||:| |||:| |||||:|:||||||| ||||| |||||
a248      VEAVKRSCTAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGXNGENVYRVTAKAWGK
           130     140     150     160     170     180

           170     180
m248.pep  NANTVVVLQSYVSNINDEX

```

572

|||||
a248 NANTVVVLQSYVSNINDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq
1 ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51 GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAATTT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTAG CGAAACTGT GGAAGGTC TGTGTGCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep
1 MRKQNTLTGI PTSQGQGFALFIVLMVMIV VAEFLVTTAAQ SYNTEQRISA
51 NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCDKK GMEYKKGTRS
151 VSKMPRIIIE YLGVKNGENV YRVTAANGK NANTVVVLQS YVSNDE*

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQ	RGFALFIVLMVMIV	VAEFLVTTAAQ	SYNTEQRISANES	DRKLALS	
g248	MRKQNTLTGIPTSDGQ	RGFALFIVLMVMIV	VAEFLVTTAAQ	SYNTEQRISANES	DRKLALS	
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGELOVLD	LEYDTDSKVTFSENC	GKGLCAAVNVRTNND	NEEAFDNIVVQKPT		
g248	LAEALREGEFQVLD	LEYAADS	SKVTFSENCEKGLCT	AVNVRTNNGSSEAF	GNIVVQKPT	
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----	NSTDLCDKKGMEYK	KGTRSVSKMPRII	EYLG	VKNGENVYRVTA	
g248	AVEAVKRSCPAKSGN	STDLCIDNKGMEYK	GAGVSKMPRII	EYLG	VKNGQNVYRVTA	
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQ	SYVSNINDEX				
g248	KAWGKNANTVVVLQ	SYVGNINDEX				
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQ	RGFALFIVLMVMIV	VAEFLVTTAAQ	SYNTEQRISANES	DRKLALS	
a248	MRKQNTLTGIPTSDGQ	RGFALFIVLMVMIV	VAEFLVTTAAQ	SYNTEQRISANES	DRKLALS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGELOVLD	LEYDTDSKVTFSENC	GKGLCAAVNVRTNND	NEEAFDNIVVQKPT		
a248	LAEALREGELOVLD	LEYDTDSKVTFSENC	GKGLCTAVNVRTNND	NEEAFDNIVVQKPT		
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDL	CDKKGMEYKKGTR	SVSKMPRII	EYLG	VKNGENVYRVTA	KAWGK
a248	VEAVKRSCPAKSTGL	CIDNKGMEYKKG	TSVSKMPRII	EYLG	VKNGENVYRVTA	KAWGK
	130	140	150	160	170	180

```
g249.seq
1  atgaagaata atgattgctt ggcctgaaa aatccccagt cgggataggc
51  gttgatagaa gtcttggtcg ctatgctctg tctgcacatc ggtattttgg
101 cattgtgcga cgtacagctt gtcagcgtcg cttccgtca ggaagcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatgtt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgctgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgcgggatgc ggtagctatt cattacgcgc
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcgggtct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcgga
601 ggtcgtgaat ga
```

g249.pep

1	MKNNDCLRRLK	NPQSGMALIE	<u>VLVAMLVLTII</u>	<u>GILALLSVQL</u>	RTVASVREAE
51	TQTVISQITQ	NLMEGNLMNP	TIDLDSNKKI	YSLYMGKQTL	SAVDGEFMIL
101	AEKSKAQLAE	EQLKRFSHBL	KNALPDVAIV	HYAVCKDSSG	DAPTLSDSGA
151	FSSNCDNKAN	GDTLIKVLWV	NDSAGDSDIS	RTNLEVSGDN	IVYTYQARVG
201	FSS*				

```
m249.seq
1  ATGAAGAATA  ATGATTGCTT  CCGCCTGAAA  GATTCCCAGT  CCGGTATGGC
51  GCTGATAGAA  GTCTTGGTGT  CTATGCTCGT  TCTGACCATC  GGTATTTTGG
101 CACTATTGTC  TGTACAGTTG  CGGACAGTCN  NNNNNNNNNN  NNNNNNNNNN
151 NNNNNNNNNN  NNNNNNNNNN  NNNNNNNNNN  NNNTTGATGG  AGGGAATGTT
201 GATGAATCCG  ACCATTGATT  CGGACAGCAA  CAAGAAAAAC  TATAATCTTT
251 ACATGGGAAA  CCATACACTA  TCAGCTGTGG  ATGCGGATT  TGCAGTTGAT
301 GCCATGAAAA  CTAAGGGGCA  ATTGGCAGAG  GCACAATTGA  AGAGATTTAG
351 TTATGAGCTG  AAAAAATGCT  TGCCGGATGC  GGCAGCCAAC  CATTACGCCG
401 TCTGCAAGGA  TTCGTCGGGT  AACGCGCCGA  CATTGTCCGG  CAATGCTTTT
451 TCTTCAAATT  GCGACAATAA  GGCAACGGG  GATACTTTAA  TTAAAGTATT
501 GTGGGTAAAT  GATTCCGCAG  GGGATTCCGA  TATTCCCCT  ACGAATCTTG
551 AGGTGAGCGG  CGACAATATC  GTATATACTT  ATCAGGCAAG  GGTCCGAGGT
601 CGGGAATGA
```

```
m249.pep
  1  MKQNDCFRLK  DSQSGMALIE  VLVAMLVLTI  GILALLSVQL  RTVXXXXXXXX
51  XXXXXXXXXX  XLMEGMLMNP  TIDSDSNKKN  YNLYMGNHTL  SAVDGDFAID
101 AMKTGKQLAE  AQLKRFSYEL  KNALPDAAAI  HYAVCKDSSG  NAPTLSGNAP
151 SSNCDNKANG  DTLIKVLWVN  DSAGSDSISR  TNLEVSGDNI  VYTYQARVGG
201  RE*
```

m249.pep MKNNDCFR LKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
| | | | : | : | | | | | | | | | | | | | | | : | | : : :

576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAGSAFPTAPSSCTPLPDAIKDRLGCWAEQVKNLEPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTL-
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYIICRSSK-----PGDCDG--KGSMLERLAWRGKQGACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLKDSQSGMALIEVLV	VAMLVLTIGILALLSVQLRT	VASVREAETQTIVSQITQ		
a249	MKNND	CFRLKDPQSGMALIEVLV	VAMLVLTIGILALLSVQLRT	VASVREAETQTIVSQITQ		
	10	20	30	40	50	60
	70	80	90	100	110	119
m249-1.pep	NLMEGMLMNPTIDSDSNKKNYNLYMGNH	-T	LSAVDGDFAIDAMKTKGQLAE	AQLKRFSYE		
a249	NLMEGMLMNPTIDSDSNKKNYNLYMGNH	HALSVVDGDFQVDAIKTKTQLAE	AQLKRFSYE			
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKNALPDAAAIHYAVCKDSSGNAPTLS	-G	NAFSSNCDNKANGDTLIKVLWV	ND	SAGDS	DI
a249	LKNALPDAAAIHYAVCKDSSGVAPTLS	AGSTFSSNCDGSANGDTLIKVLWV	ND	SAGDS	DI	
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRTNLEVSGDNIVYTYQARVGGREX					
a249	ARTNLETNGNNIVYTYQARVGGREX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1   atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgetgattg ggettttgcc ttgggcattg atactcggta
101 tgcaggcgcg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgccatat cctgatggg ggcggcgctt gccacgcaca tgaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1   MHTTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1   ATGCACACCT TCCCCGATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCSGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAAATACCGC
301 TGAATAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1   MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

m250/q250

	10	20	30	40	50	59
m250.pep	MHTPSPHNEFIRGIKESSPMLIGLLPWALIIGMQGGQKGSWLEMLLMTSMNFAGGSEF					
	:					
g250	MHTTASPRDEFIRGIKESSPMLIGLLPWALIIGMQGGQKGMGRLEMLLMTGMNFAGGSEF					
	10	20	30	40	50	60
	60	70	80	90	100	110
m250.pep	ATVNLWAEPLPILLIATVTFMINSRHIIMGGGACPAPEPNTAEKSRRARTVFYVX					
	:					
g250	ATVNLWAEPLPILLIATITFMINSRHIIMGGGACHAHERNTAEKSRRARAFYV					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 979>:

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCTGATGGGG	G.CGGCACTT	CCCCCGCACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACGTGT	TTTTATGTGT	GA

This corresponds to the amino acid sequence <SEQ ID 980; ORF 250.a>:

a250.pep

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT
51 GMNFAGGSEF ATVN LWAEPL PILLIATVTF MINSRHILMG XGTC PAPERN
101 TAEKS RARTV FYV*

m250/a250 94.6% identity in 111 aa overlap

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMOGGQKGMSWLEMLLMTSMNFAGGSEF
          |
||:||||||||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMOGGQKGMSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60
m250.pep          60          70          80          90          100          110
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAAPERNTAEKSRARTVFYVX
||||||||||||||||||||||:|||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAAPERNTAEKSRARTVFYVX
          70          80          90          100          110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 981>:

q251.seq

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgggg ttgatttttt
51  tgcgcttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggaagctc gaacccaaac qtcqtaacc

```

578

```

151 gaggttgacg ctgaggttgt ggcggatttt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at caccgggtcg
251 gattttagt aggaagacgg cttgtcggca ctcggggcgc aatatttgtc
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgccca agtgtcttta
401 tcggcattgg tatagacata tccaaaccg tagcggcttt tgggtgctg
451 ctgctcgtaa aacacgcccg taccgtattc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgtgtgatt tgcggccgcc cgcgtatttg
551 ccgtagcctc tcatcgatcc gtatttttta tttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgcg
651 tgcgttcgag tatgcgcgcg atgtagtgcg gtttgttttc aaaacgaaaa
701 cccgggcgga acagccacga ccggttttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAV LRGFRORIGA VGMLIIIIILM AEVGTKT VVT
51 EVDAQVADF GGIEGFFECL LQEPVAFPVN HAVGFVVGRR LVGTRAAIFV
101 RTVGGTVRL KMIQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFVVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECRNRHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGCCTG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTACCGTGTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTT CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCC GTTGGGGCTG ATTTTTTTCG CGTTGTTTTC AGGGGGCGTG
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 TGGCATAAAT CCAAAGCGGT CAAACCCGAG ATTACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTCG ATGCCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTGTCCGA ACCGTCCGCA GAACAGTCCG
501 CTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGTC GTAAGAGAGG
551 CGGCATAAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAC AACCCGTAC
651 CGTATCCGC GCCCACCAGC GCACCGTTT CGCCGTTGGT AACAGTCCG
701 CCGTATTTGT GGTGCCCCGC GTATTGCGG TTACCGGGCA AAGAACCAGC
751 CTGTTTTTTC TTTGCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGAAA GTTTGTTGCG TGTGTTGAG TATGCCGCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCGGGCGGGA ACAGCCACGA
901 CCGGCTTTCG TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDARRAV RISIVAQAAD
51 LPRNDISPAY GDPIGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIILMA
101 EIRAKAVKPE IHAQVADFG GIEGFFECL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFVRL VVKHARTVFR AHQRTVFAVG KQSAVFVVAR VFAVTGQRT
251 LFFICIKNRL GQECRNRHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40          50          60          70          80          90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPIGAGFTAVGADFFAVVLGRVRRIGAVG
          ||||  |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g251      MPDPGILFAAVGVDFFAVVLRGFRORIGA
          10          20          30

```



```

a251      ADPIGLVLAAVGVGGF----RGRFRRIGAVGMLIIIIILMAEIRVKAVKTEIHAQVVADEFG
              70              80              90              100             110

              130             140             150             160             170             180
m251.pep  GIEGFFECLRQEPVAFPVNHAIGFVIGKRLVGTRAAIFVRTVGRTVRLCLKMIIQTDALPV
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      GIEGFFECLRQEPVAFPVNHAIGFVVGKRLVGTRAAIFVRTVGRTVRLCLKMIVQTDALPV
              120             130             140             150             160             170

              190             200             210             220             230             240
m251.pep  VREAGIIRPSVFIFIGIDIFQTVAAGFVRLVVKHARTVFRAHCRTVFVAVGKQSAVFVVAR
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VREAGIIRPSVFIFIGIDIFQTVAAGFVRLVVKHARTVFRAHCRTVFVAVGKQTAVFVVAR
              180             190             200             210             220             230

              250             260             270             280             290             300
m251.pep  VFAVTGQRTLFFICIKNRLGQECNRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR
            ||||:|:|:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a251      VFVAVSYRS-VFSIFIKNRLGQECNRNRIARVESLLRVFEYAADVVPFVKTKTRAEQPR
              240             250             260             270             280             290

m251.pep  PAFVX
            |||
a251      SAFVX
            300

```

g253 . seq

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253.pcp

1	MIDRDRMLRD	TLERVVRSF	WLWVVASMM	FTAGFSGTYL	LMDNQGLNFF
51	<u>LVL</u> AGVLGMN	TLMLAVLAT	LFLRVKVGRF	FSSPATWFRG	KGPVNQAVLR
101	LYADQWQPS	VRNKIGATAH	SLWLCTLLGM	LVSULLLLLV	ROYTFNWEST
151	LGSNAASVRA	PEMLAWLPK	LGFPVPDARA	VIEGRLNGNI	ADARAWSGLL
201	VLSIVCYGIL	VRLAWVCK	ILLKTSENGL	DLEKTTYQAV	IRRWNQKITD
251	ADTRRETUSA	VSPKIVLND	PKWALMLETE	WODGOWFEGR	LAEWLDPKV

582

	190	200	210	220	230	240
m253 . pep	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILPRL	LAWVVKILL	KTSENGLDLEKPYQAV
g253	VIEGR	LNGNIADAR	AWSGLLVGS	IVCYGILPRL	LAWVVKILL	KTSENGLDLEKTYQAV
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 . pep	IRRWN	QKITDADTR	RETVSAVSP	KIILNDAPK	WVMLETEW	QDGEWFEGRLAQEWLDKGV
g253	IRRWN	QKITDADTR	RETVSAVSP	KIVLNDAPK	WVMLETEW	QDGEWFEGRLAQEWLDKGV
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 . pep	ATNREQ	VAALETEL	KOKPAQLL	IGVRAQTV	PDRGVL	RQIVRLSEAAQGGAVVQLLAEQGL
g253	AANREQ	VAALETEL	KQKPAQLL	IGVRAQTV	PDRGVL	RQIVRLSEAAQGGAVVQLLAEQGL
	310	320	330	340	350	360
	370	380	390			
m253 . pep	SDDL	SEKLEHWR	NALAE	CGAAWLEP	DRAAQE	GR
g253	SDDL	SEKLEHWR	NALTE	CGAAWLEP	DRAAQE	GR
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 . seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTT	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCTTT
	151	TGGTTTGG	CGGCGTETT	GGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TGTTCTCTGC	GCGTGAAAGT	GGGCGGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTTCGGGGC	AAAGACCCTG	TCAATCAGGC	GGTGTGCGCG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTCGCAC	AGCTTGTTGG	TCTGCACGCT	GCTCGGAATG	CTGGTGTGCG
	401	TATTGTGTCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCAGC
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCCTGCGAAA	CTGGGTTTTT	CCGTGCGCTG	TGCGCGGCGC	GTCATCGAAG
	551	GTGCTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGCTC	GGGCGTCTG
	601	GTCGGCAGTA	TCGCCTGCTA	CGGCATCCTG	CCGCGCCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCAGT
	751	GCGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGG	AATGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGC	CGCGC	CCAACTGTG
	1001	GCGTGTGCG	GCAGATCGTC	CGACTTTCGG	AAGCGCGCA	GGGCGCGCG
	1051	GTGGTGCAGC	TTTTGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 . pep	1	MIDRNRMLRE	TLERVRAGSF	WLWVAAATFA	FFTGF	SVTYL	LMDNQGLNFF
	51	LVLAVLGMN	TLMLAVNLAM	LFLRVKVGRF	FSSPATWFRG	KDPVNAVLR	
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSLLLLLV	RQYTFNWEST	
	151	LLGDSSSVRL	VEMLAWLPAK	LGFPVPDARA	VIEGR	LNGNI	ADARAWSGLL
	201	VGSIACYGIL	PRLLA	WVCK	ILLKTSENGL	DLEKPYQAV	IRRWNKITD
	251	ADTRRET	TVSA	VSPKIVL	NDA	PKWAVMLETE	WQDGEWFEGRLAQEWLDKGV
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGVL	RQIV	RLSEAAQGGGA
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRLKTNDR	
	401	*					

m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGF	SVTYLLMDNQGLNFFLVLAGVLGMN				
a253	MIDRNRMLRETLERVAGSFWLWVVAATFAFFTGF	SVTYLLMDNQGLNFFLVLAGVLGMN				
	10	20	30	40	50	60
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGRRFFSSPATWFERGKDPVNQAVLR	LYADEWRQPSVRWKIGATSH				
a253	TLMLAVWLAMFLRVKVGRRFFSSPATWFERGKDPVNQAVLR	LYADEWRQPSVRWKIGATSH				
	70	80	90	100	110	120
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVLRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVCKILLKTSENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVCKILLKTSENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	250	260	270	280	290	300
	IRRWNKIDADTRRETTSVAVSPKIIILNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253	IRRWNKIDADTRRETTSVAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	250	260	270	280	290	300
m253.pep	310	320	330	340	350	360
	ATNREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGA	VQQLAEQGL				
a253	AANREQVAALETELKQKPAQLLIGVRAQTVPDRGVLRQIVRLSEAAQGGA	VQQLAEQGL				
	310	320	330	340	350	360
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcgggtttgat
51  tctggcggcg gcagggtttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactggttt ctttgagaaa cgggccgggc
301 tggacggtat ttctactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggctctgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcgagcag gcggtatgct
501 gtacagcgtc gccatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aaccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```


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51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYIVMGW MVLAVMKSLT
 151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
 201 VSVYGYVI*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT
 51 GTACCACGGA ATTGCAGCCG GAAAACAGAA AAGCATTTTG AAAAAACCG
 101 ACCACTGCAT GATTATATGT CTGATTGCCG GAAGCTACAC ACCGTTTGCA
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
 201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
 301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
 351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTACTGCT
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTT
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGACG GTTACGTAAT
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYI VLIAGSYTPFA
 51 LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLS IYIYVVMGWM
 101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEK IRHGHGIWHLF
 151 VLGGSITQFV SVYGYVI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHG	IAAGKLKSI
g254	HLSGLILAAAGL	MMLLKTIGHG	DGYRIFSV	VSVYGISLLL	LYLSSSLYHG	IAAGKLKSI
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG	WTVFSLSWLL	AAAGIAQELT
g254		KKTDHCMYI	VLIAGSYTPF	ALVSLRNGPG	WTVFSLSWLL	AAAGIAQELT
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IYIYVVMGWM	VLAVMKSLTA	SLPSAGLAWL	AAGGMLYSVG	GIYWFVNDEK
g254		IAIYIVMGWM	VLAVMKSLTA	SLPPAGLAWL	AAGGMLYSVG	GIYWFVNDEK
	140	150	160	170	180	190
m254.pep		160				
		VLGGSITQFV	SVYGYVIX			
g254		VLGGSITQFV	SVYGYVIX			
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGAT
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAACCC ATAGGACACG
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
 151 CTGCTCTATT TGAGTTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACCT
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

a254.pap

m254/a254 97.6% identity in 167 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

Computer analysis of this amino acid sequence gave the following results:

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m255 . pep	VVGQ	EALRGQ	FFVAVFAA	ALRYAVKTCAD	FHAFDGVDAH	HRVGD
	:					
g255	MVGQ	EALRGQ	FFVAVFAA	ALRYAVKTCAD	FHAFDGVDAH	HRVGD
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m255 . pep	GC	FDMQLRAD	GIQGFA	HAVHIVFQL	GNL	AMVGGK
g255	GG	FDMQLRAD	GIQGFA	HAVHIVFQL	GNL	AMVGGK
	70	80	90	100	110	120
	130	140	150	160	170	180
m255 . pep	FRAE	FFQ	PPF	FGNGSG	SNAGGG	TGGAPAAA
	:					
g255	FRAE	FFQ	PPF	FGNGSG	SNAGGG	TGGAPAAA
	:					

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	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1  GTGGTTGGAC  AGGAAGCCTT  GCGGGGTGAG  TTCGTCGCCG  TGTTGCGCTGC
51  CGCGTTGCGT  TACGCTGTCA  AAACCTGCGC  CGATTTCAC  GCCTTTGACG
101 GCGTTGATGC  CCATCATGGC  GTAGGCGATT  TCGGCATCGA  GGCGGTCGAA
151 TACGGGTTGC  CCCAAGCCGA  CGGGGACGTT  GGCGGCTTCA  ATATGCAGCT
201 TCGCGCCGAC  GGAATCCAAG  GATTTGCGCA  CGCTGTCCAT  ATAGTTTTC
251 AGCTCGGCAA  TTTGGCTATG  GTTGGCGGCA  AAAAAAGGAT  TTTGGGAAAT
301 GTGTTGCGAG  CCTTCAAACC  GGATTTCTTT  TCGCCGACT  TGGGTAACGT
351 AGGCGGTGAT  TTCCGTGCCG  AATTTTCTT  TCAACCATT  TTTGGCAACG
401 GCTCCGGCGG  CAACGCGGGC  GCGGTTTCG  CGGGCGGAAC  TCCTGCCGCC
451 GCCCCGGTAG  TCGCGCGTGC  CGTATTTGTG  CCAATAGGTA  TAGTCGGCGT
501 GGCCGGGGCG  GAAGCTGGTG  GCGATGTTGC  CGTAGTCTTT  GCTGCGCTGG
551 TCGGTATTGC  GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1  VVGQEALRGE  FVAVFAAALR  YAVKTCADFH  AFDGVDAHGG  VGDFGIEAVE
51  YGFAQADGDV  GGFNMQLRAD  GIQGFHAVH  IVFQLGNLAM  VGGKKRILGN
101 VFAAFKPDPF  FADLGNVGGD  FRAEFFQPF  FGNGSGGNAG  GSFAGGTPAA
151 APVVARAVFV  PIGIVGVAGA  EAGGDVAVVF  AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVKNRFAQADRD					
a255	VVGQEALRGEFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDGFGIEAVEYGFADGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
a255	GGFNMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDPFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
a255	FRAEFFQPFNGSGSNAGGGFAGGTPAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
m255.pep	FRAEFFQPFNGSGSNAGGGFTGGAPAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
a255	FRAEFFQPFNGSGSNAGGGFAGGTPAAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1  atgctcgcgg  tacgcaatcg  gggttggcac  ggcgcagtcg  tccatttccg
51  cagctgcggc  ggcgtagcga  acaccgcccc  ggtgttctac  cacttgggtg
101 ataccgcga  aatcgccctt  gctttggaca  cgctcaccgc  gcggtaccgt
151 gaaatatacg  ccgtcggcgt  atcgctgggc  ggcaacgcgc  cggcaaaata
201 ttggggcgaa  cagggcaaaa  aggcattgcc  gcacgcctcg  gccgcgctat
251 ccgcccccg  tgatgcagag  gcggcaggca  gccgcttcga  cagcggcatc
301 acgcggctgc  tctacacgcg  ctacttcctc  cgcacactga  taccctaaagc

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```

351 acgttcgctc caagggttttc agacggcatt tgccgcaggg tgcaaaacac
401 tgggagagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451 cggcagcact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501 tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551 ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601 caacctgcac acggcgggca cgccggcttt gtcagcagca ccggcggcag
651 gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttagacgt
701 tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1 MLAVNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
 51 EIYAVGVSIG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNANDP FLPPEALPRA DEASEAVTLF
201 QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1 ATGCTTGCGG TACGCGATCG GGGTTGGCAC GGCCTAGTCG TCCATTTCGG
 51 CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101 ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTGCTCT
251 CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301 ACGCGGCTGC TCTACACGCG CTACTTCCTC CGCACCTGA TACCCAAAGC
351 AAAATCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCTGTTC
601 CAGCCGCGAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1 MLAVRDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFARYR
 51 EIYAVGVSIG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRRFDSGI
101 TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLLNANDP FLPPEALPRA DEVSEAVTLF
201 QPAYGGHVG FVSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

m256/g256

```

          10      20      30      40      50      60
m256.pep  MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSIG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256      MLAVNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSIG
          10      20      30      40      50      60

          70      80      90     100     110     120
m256.pep  GNALAKYLGEQGKKALPQAAVISAPVDAEAAGRRFDSGITRLLYTRYFLRTLIPKAKSL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256      GNAPAKYLGEQGKKALPHASAAVSAPVDAEAAGSRFDSGITRLLYTRYFLRTLIPKARSL
          70      80      90     100     110     120

          130     140     150     160     170     180
m256.pep  QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCPKLLKHVAKPLLLLNANDP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256      QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHHDYYRQTSCPKLLKHVAKPLLLLNANDP

```

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	130	140	150	160	170	180
m256.pep	190	200	210	220	230	240
	FLPPEALPRADEVSEAVTLFQPAYGGHVGFSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```
a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GGCCTAGTCG TCCATTTCCG
51  CAGCTGCGGC GGCCTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACCGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCGC GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTACCCGCAC CGCTGCACGG CTTTGGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGGCA GACGAAGTGT CCGAAGCCGT TACCCTGTTT
601 CAGCCGACAC ACGGTGGTCA TGTGCGCTTT GTCGGCAGCA CCGGCGGCAG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```
a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIIYAVGVSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSGI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*
```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVHFRSCGGIANTAPVFYX	HLGDTAEIAFTLDTFAARYREIYAVGVSLG				
a256	MLAVRDRGWN	GVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG				
	10	20	30	40	50	60
m256.pep	GNALAKYLGEQGKALPQAAAVISAPVDAEA	AAGRRFDSGITRLLYTRYFLRTLIPKAKSL				
a256	GNALAKYLGEQGENALPQAAAVISAPVDAEA	AAGNRFDSGITRLLYTRYFLRTLIPKARSL				
	70	80	90	100	110	120
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFAD	RHDYYRQTSCKPLLKHVAKP	LLNNAVNDP			
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFAD	RHDYYRQTSCKPLLKHVAKP	LLNNAVNDP			
	130	140	150	160	170	180
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVG	FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX				
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVG	FVSTGGRLHLQWLPQTVLSYFDSFRTNRRX				
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```
g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAT TCCTGCAACA CCGGCACCC GCATACCGCC
```

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```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAACCCG CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGGAAGTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCAGAGTCG TCCATTTCGG CAGCTCGCGC
301 GGCCTAGCGA ACACCGCCCC GGTGTCTTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTACCCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCGCCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGAGGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTGCGCGC CGGAAGCCCT
801 GCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CGGCGGCGAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTAT TTTGACAGCT TCCGCACAAA
951 CAGCGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLOHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGAFD RHDYRQTSK PLLKHVAKP
251 LLLNNAANDP FLPPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGGRHLH
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CAGGCCCTTT TTCCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCCACGCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGAGGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCAGGCG GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCGC
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTCTCTCCGC ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTCA
651 CGACCGCTTC ACCGCACCCG TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCTTGCAAA CGGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CGCGCGCAGC GAAGTATCCG AAGCCGTTAC CTTGTTCAG CCGGCATAIG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCTATTTC GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGAFD RHDYRQTSCK PLLKHVAKEL
251 LLLNAVNDPF LPEALPRAD EVSEAVILFQ PAYGGHVGFEV SSTGGRHLHL
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

	10	20	30	40	50	59
m256-1.pep	MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP					
g256-1	MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP					
	10	20	30	40	50	60
	60	70	80	90	100	119
m256-1.pep	LVVLFHGLEGSSSRSHYAVELMLAVDRGWHGVVVHFRSCGGIANTAPVYFHLGDTAEIAF					

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```

g256-1      |||||:|||||:|||||:|||||:|||||:|||||:
            LVVLFHGLEGSSRSYAVELMLAVRNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
            70      80      90      100     110     120

m256-1.pep  120      130      140      150      160      170      179
            TLDTF AARYREIYAVGVSLGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAGRRFDSGI
            :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      ALDTLTARYREIYAVGVSLGGNAPAKYLGEQGGKALPHASAAVSAPVDAEAAGSRFDSGI
            130      140      150      160      170      180

m256-1.pep  180      190      200      210      220      230      239
            TRLLYTRYFLRTLIPKAKSLQGFTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      TRLLYTRYFLRTLIPKARS LQGFTAFAGCKTLGEFDDRFTAPLHGFADRHDIYRQTSC
            190      200      210      220      230      240

m256-1.pep  240      250      260      270      280      290      299
            KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRLHL
            :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      KPLLKHVAKPLLLNNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHL
            250      260      270      280      290      300

m256-1.pep  300      310      319
            QWLPQTVLSYFDSFRNRRX
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g256-1      QWLPQTVLSYFDSFRNRRX
            310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCTTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCCGCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTGCGCCGA TSCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGGCGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGGC
301 GTAGCGAACA CCGCCCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACGCGCTGG CAAAATATTT GGGCGAACAG
451 GCGGAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAGAGGCG CGAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG AACTGATAC CCAAAGCAGC GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTTC ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAA CGACCCCTTC CTGCCGCCCG AAGCGCTGCC
801 CCGCGCAGAG GAAGTGTCCG AAGCCGTTAC CCTGTTCCAG CCGACACAGC
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARS LQ
201 GFQTAFAAGC KTLGEFDDR FAPLHGFADR HDYYRQTSC PLKLVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHGVFV GSTGGRHLHL
301 WLPQTVLSYF DSFRNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

a256-1.pep  10      20      30      40      50      60
            MILTPPDTPFFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1      MILTPPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
            10      20      30      40      50      60

a256-1.pep  70      80      90      100     110     120
            VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVVHFRSCGGVANTAPVFYHLGDTAEIAFT
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m256-1      VVLFHGLEGSSRSYAVELMLAVDRGWNGVVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```


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	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFDSGIT					
m256-1	130	140	150	160	170	180
	LDTFAARYREIYAVGVSLGGNALAKYLGEQCKKALPQAAAVISAPVDAEAAGRRFDSGIT					
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHQYRQTSCK					
m256-1	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHQYRQTSCK					
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGSTGGRLHLQ					
m256-1	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	310					
	WLPQTVLSYFDSFRTNRRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

```

g257.seq
1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gttttctctg
151 aaaggtgtcg cgctgggttc cggcgcgagg ctgcgctctg tcggcggtgga
201 cgacagacag gcggcggttt tggtaataa gggtttggcg gaagtggcgc
251 gtttggaata aatgttcagc ctttacgtg aagacagcct gatcagccgt
301 ctgaaccgag acggttatct gacttcgctt ccggcggttt ttttgaact
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

```

g257.pep
1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKVLA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIFT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

```

m257.seq
1  ATGGGCAGGC ATTTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGgAc. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTTGG
151 AAAGGTGTCT CACTGGGTTC CCGTGCGGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAATA ATTGTTTCTG CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCGG TCGGCGGATT TTTTGAAC
351 GKTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

```

m257.pep
1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKVLA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLXLXSL AAIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng)

from *N. gonorrhoeae*:

m257/g257

10 20 30 40 50 60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAD
          |||||:||||:||||: ||||| ||| |:|:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:|||||:|||||:|||||:|||||:|||||: ||||| ||
g257      LRLFGVDDRQAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTCGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAATAAGAT GAAAAACGCA ATGAAAATGT GTTTTCTGG
151 AAAGGTGTCG CACTGGGTTT CCGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGGCGGATT TTTTGGAAC
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVAAVAAG AAVSFLPNP AADDEKRNKD EKRNVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKV LA EVARLEKMF S LYREDSLIS
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAX
          ||||| :|||||: |||||
|||
a257      MGRHFGRRRFLTVAAVAAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
          10      20      30      40      50
60
          70      80      90      100     110
120
m257.pep  LRLFGVDDRRADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLELXSL
          |||||:|||||:|||||:|||||:|||||: |||||
||
a257      LRLFGVDDRRADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |:|
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1 atgcgccgct tcctaccgat cgcagccata tgcgccgctc tcttctgtga
51 cggattgacg gcggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctctgttcagc gcaatgctgc tgcgtgtgtt gtccgccgtt
151 ttggcacgtt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgcgc
251 tactgcccg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccggcagc aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ygcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccc caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccga aagaacattg ggaacagatt
601 cagcagaccg gtccggttcg gagtttgaa agcataggcg gcgtattgta
651 cgcgcaggga tgggtgtcgg caggtacgca caacgggcgc gattacgcgc
701 tgttcttcgg ccagccgatt ccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc tttttctg taacctgct gattgcctcg ctgctgtcga
851 tttttcttgc gctggtaatg gcaactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgtttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgcgccgtat tgcgcaacga cgagtccgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcca ggaagccgcc cgtcactacc tcgagtgcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctaccctc ctctcttgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctctc ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51 LARYVILLLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIIAS LLSIFLALVM ALYFARRFEV
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVDLG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGOGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGGTTTCAGC GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCACGTT ATGTCAATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GGCGGCAGAC AACGCCCTCG
401 GCAACGCCGT CCCCGTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAATAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGCGCAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCTGCTG GATTGCCTCG CTGCTGTGCA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCTGTCGA
901 CCCGTCTAT CGCTTGCCGA GGGGCGGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCGTGTG TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAAACsTT CAACAAAGCG GCGGAACAGA TTYTGGGGAT GCCGCTTACC
1201 CCCcTGTTGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAAgT GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCGCCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGCGGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS ANLLLVLSAV
51  LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSINL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQSSLL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAANGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

```

m258/g258

      10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVAFSAML LVL SAVLARYVILLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSSLADYFWWIVSFSAM LVL SAVLARYVILLK
          10      20      30      40      50      60

      70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSINL
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSINL
          70      80      90     100     110     120

      130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
          130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SINPHQFDQPLPDKEHWEQIQOTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
          190     200     210     220     230     240

```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARFVE					
	:: : :					
g258	PENVAQDAVLIEKARAKYAELSSYSKKGLQTFFLVTLIASLLSIFLALVMALYFARFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEAGAKAVAQGDFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
	:					
g258	PILSLAEAGAKAVAQGDFSQTRPVLNRNDEFGRLTKLFNHMTEQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAAEQILGMLPTPLWGSSRHGWHGVSAQQSLL					
	: : :					
g258	RHYLECVLDGLTTGVVVSYP LSCCR TAVFSTCHSSPLSYFX					
	370	380	390	400		

```

a258.seq
1 ATGCGCCGTT TTTCCACGAT CGCAGCCATA TGCGCCGTGC TCTGTGTGTA
51 CGGACTGACG GCGGCAACCG GCAAGCACCAG TTCGTGTGGC GATTATTTCT
101 GGTGGATTGT TGCCTTTCAG CCAATGCTGC TTGCTGGTGT TCCGCCGCTT
151 TTGGCACGTT ATGTTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTCCGAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCGG CGTGTTTCTG TTCGGCGTTC CCGCACAGTT TATCAACGGC
301 ACGATTAAAT CGTGGTTTCG CAACGATAAC CACGAGCGCG TTGAACGGAG
351 CCTCAATTGG AGCAAGTCCG CATTGAATCT GCGGCGAGAC AACGCCCTTG
401 GCAACGCCAT CCCCGTGCAG ATAGACCTCA TCGGCGCGCG TTCCTTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCGCCGACGC GTTTTGCCTA
501 GCTTGCCCTG TACAATGCCG AACCGGCCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAaaaaaatc
601 CAACAGCGCG GTTCGCTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGCG TGGCTGTCCG CAGGTACGCA CAACGGGCGC GATTACGCTT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGCGG TGGCAGAGGA TCGCGTCTTA
751 ATCGAAAAAG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAaaaaagg
801 TTTGCAGACC TTTTCTCTG CAACCTGCT GATTGCCTCG CTGCTGTGTA
851 TTTTCTTGCT ACTGTGTCAT GCACTGTATT TCGCCCGCCG TTTCTGCGAA
901 CCCGTCTCAT CGCTTGCCGA GGGGCGCAAG GCGGTGGCGC AAGGCGATT
951 CAGCCAGACG CGCCCCGTGT TCGGCAACGA CGAGTTCGGA CGCTTGACCA
1001 AGTTGTTCAA CCATGATGAC GAGCAGCTTT CCA*TCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCGCGCGCGA GGAAGCCGCC AGACATTATC TCGAATTGCT
1101 GTTGGAGGGE GTGACCACGG CGCTGGTGTG GTTTGACGAA CAAAGCTGTC
1151 TGAAACCTT CAACAAAGCG GCGGAACAGA TTTTGGGGAT GCCGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGCGCGACGA
1251 GTCCCTGCTT GCCGAAGTGT TTCCCGCCAT CGGCGCGCGC CAAAGTACGG
1301 ACAAACCGTT CCATGTGAAA TATGCCGCGT CGGACGATGC CAGAACTCTG
1351 CTGGGCAAGG CAACCGTCTT GCCCGAAGAC AACGGCAACG GCGTGGTAAT
1401 GGTGATTGAC GACATCACC G TTTTGATACA CGCGCAAAAA GAAGCCCGCT
1451 GGGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTACCG
1501 CCCATCCAGC TTTCTGCCGA ACGCTGGCG GTGAAATTGG CGGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCAGC ACCATCATCA
1601 AACAAAGTGG GGCATTAAAA GAAATGGTCG AGGCAATTCC CATTACGCG
1651 CGTTCCTCTT CGCTCAAAAT GGAATAACAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG CGATTGTACG AAGCTGGTCT GTGCGCGTTT GCGGCGAGAC
1751 TTGCCGCGCA ACCGCTGATG ATGGCGGCGG ATACGACCCG CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATGCCGCC GAAGCGCGCG AGAAGACCTG
1851 TGTGCCCGAA GTCAGGGTAA AATCGGAAGC GGGGCGAGGAC GGACGGATTG
1901 TCTTGACAGT TTGCGACAAC GGCAGGAGGT TCGCGAGGGA AATGCTGCAC
1951 AATGCCTTTC AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGGC CGCATCAGCC
2051 TGAGCAATCA GGATGCGGGC GCGCGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATCGGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK  DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FCVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAANGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TIIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMQ
601 VLHNIFKNAA EAAEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```

      10      20      30      40      50      60
m258.pep  MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLK
          |||
a258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAV LARYVILLK
      10      20      30      40      50      60

      70      80      90     100     110     120
m258.pep  DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
a258      DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
      70      80      90     100     110     120

      130     140     150     160     170     180
m258.pep  SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
a258      SKSALNLAADNALGNAIPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
      130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep  SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||
a258      SINPHKLDQFPFGKARWEKIQQAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
      190     200     210     220     230     240

      250     260     270     280     290     300
m258.pep  PKGVAEDAVLIEKARAKYAE LSYSKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
          |||
a258      PKGVAEDAVLIEKARAKYAE LSYSKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE
      250     260     270     280     290     300

      310     320     330     340     350     360
m258.pep  PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRREEAA
          |||
a258      PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRREEAA
      310     320     330     340     350     360

      370     380     390     400     410     420
m258.pep  RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
          |||
a258      RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
      370     380     390     400     410     420

      430     440     450     460     470     480
m258.pep  AEFVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
          |||
a258      AEFVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
```

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIRKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAEEAAEEADVPEVRVKSEAGQDGRIVLTVC DNGKGF GREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

```

g259.seq
1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaatctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatacacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgtc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccg acgacgaaga cgcgcgcacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctg
451 ggcgaaacct atggcgcgct gttcgccgat attttcgagt tgcgcgcggc
501 tttggaaagg cgcgcgttca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgtcaat caggcgttga gggaaatctc gaaaacgcgc gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

```

g259.pep
1  MMHSAVSQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

```

m259.seq (partial)
1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGCGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTCGCCTCG
451 GGCgAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGMGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA .AACATCT TCGGmGATGC CTGCCGTTG GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

```

m259.pep (partial)
1  MMHSAVSQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```

599

151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSALEGRAFGLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTDASGETYGRVFADIFELSALEERRAFGLKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRRTQSGVAGDFKNIR					
g259	AEYKXHLRRCCLPFGNGVGVGRRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTC TTTGCCGTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTTCGTG TCGCGCGGTT CAAAGGCTAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAAGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCGCCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCCGCCGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAA.CATCT TCGGCGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCGCTCAAT CAGGCGTTGC AGGAGATTTC AAAAACATCG GAAAAGTCCA
651 A

```

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASV
151 GETYGRVFAD IFELSALEG RAFKGLKLT AEYKXHLRRC LPFGNGVGVG
201 RAQSGVAGDF KNIGKVQ

```

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					

600

	10	20	30	40	50	60
m259.pep	70	80	90	100	110	120
	SARSKAKAEKIFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
a259	SARSKAKAEKIFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
m259.pep	130	140	150	160	170	180
	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSALEGRAFGMLKLT					
a259	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSALEGRAFGMLKLT					
	130	140	150	160	170	180
m259.pep	190	200	210			
	AEYKXHLRRCLPFGNGVGVGRVTSQSGVAGDFKNIR					
a259	AEYKXHLRRCLPFGNGVGVGRAQSGVAGDFKNIGKVQ					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGTCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTCGTG  TCGGTGCGTT  CAAAGGCTAA
201 GGCAGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATAACCC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATGCTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAGGC  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCACG  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTCGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GGCAGAACCT  ATGGGCGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SVRSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQML
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVFAD  IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC  ACGCTTCTGT  CCAAAGCCGT  TTCGCACCGA  TACTTTATGT
51  TTTGATTTTC  TTTGCCGGTT  TTTTGACCGC  GCAAATCTGG  TTCAATCAGA
101 AAGCCTATAC  TGAAGAGCTG  CCTCCGCTTC  TGTCCGCATT  GTCCGCCGTC
151 GCGCTGGTGT  GGCTGGCGTG  GCGGTCGTG  TCGGCGCGTT  CAAAGGCCAA
201 GGCAGAAAAG  TTCTACCGCG  AAAAAATGAT  ACAGAACGAA  AGCATAACCC
251 CCGTCCTGCA  CGCTTCTTTG  CAACACTTGG  AACACAAGCC  GCAATACTC
301 GCCCTGCTGG  TCAAAAACCA  CGGCAAGGG  ATGGCGGAAC  AGGTCAGGTT
351 CAAGGCGGAA  GTGCTGCCCG  ACGACGAAGA  CGCGCGCACG  ATTGCCGCCG
401 AGTTGGCAAA  AATGGATATG  TTCGCATTGG  GGACGGACGC  GGTGCGCTCG
451 GGCAGAACCT  ATGGACGCGT  GTTCGCCGAT  ATTTTCGAGT  TGTCGGCGGC
501 TTTGGAAGGG  CGCGCGTTCA  AAGGAATGTT  GAACTGACG  GCGGAATATA
551 AAACATCTT  CGGCGATGCC  TGCCGTTCCG  AAACGGCGTT  GGAGTTGGGC
601 GCACTCAATC  AGGCGTTGCA  GGAGATTTC  AAAACATCGG  AAAAGTCCAA
651 ACGGATATTT  TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMHASVQSR  FAPILYVLIF  FAGFLTAQIW  FNQKAYTEEL  PPLLSALSAV
51  ALVWLAWAFV  SARSKAKAEK  FYREKMIQNE  SIHPVLHASL  QHLEHKPQIL
101 ALLVKNHGKG  MAEQVRFKAE  VLPDDEDART  IAAELAKMDM  FALGTDVAS
151 GETYGRVFAD  IFELSAALEG  RAFKGMLKLT  AEYKNIFGDA  CRSETALELG
201 ALNQAALQEIS  KTSEKSRIF  Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAACTCGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GCGTGGCGTG GCGTTCGTG TCGCGCGGTT CAAAGGCTAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGCGCC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AACCGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC A AACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQBEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHGKGMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQILALLVKNHGKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFKGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQLQBEISKTSKSKRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQLQBEISKTSKSKRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1  atgggtgcgg gtgtagtatt cgttgctctt cagccgttct tcagcctgtt
51  tcgagcggtg ttcgagggcg gagtcggtat agtcgagggg gcgcacgatg
101 ccgctgaatg cgacttcttg tccgaggaat ttaccgctat ccggatcggg
151 gatgttttta ttgattcggg aggtcagata acggcccggg tctttcaggc
201 ctttggtgta aaccctggcg cctttggtgt acagcagcct gccttccggg
251 cccgagagca ggcgcggcgc ggcagcggtt tctttgcggg aaacgatttg
301 cgggtgctgc ataaagacgc ggtagaagtt gacatcgatg gcgggaatac
351 cgtatccgga cacttcctta tccggactga ttttgacgac ggggatgccg
401 tctgtctgtt ccaagccgag gcgcgggtcg ccgccaacgt agcgcaacac
451 caatacctgg cccggataaa tcaggtcggg attgtggatt tgatcccggt
501 tcgcgccccca caggggggga ccattgccac gggctgtaca ggtatttgcc
551 cgaataatccc cacaggggtg cgcctgttt ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1  MGAGVVFVVF QPFFSLFRAL FEGGVGIVEG AHDAAECDL SEEFTRIRIG
51  DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVLHKDAVEV DIDGNTVSG HFLIRTFDD GDAVCLFQAE ARFAANVAQH
151 QYLARINQVG IVDLIPVRAP QGGTIATGCT GICPKYPTGC RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGCTCTT CGGCCGTCTT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGwCA sCGCGGyGC GGCAGCGGTT TCTTTCGGG AAACGATTG
301 CGGATGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCGATAAA TCAGGTCGGG ATTGTGATT TGATCCCGT
501 TCGCGTyCCA CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1  MGAGMVVFVVF RPFSSSLFRAL FEDRVGIVEG AHDAAECDL PEEFTRIRIG
51  DVFIDSVGQV AARLFQAFGV NPGAFGVQQP AFRARXXARX GSGFFAGNDL
101 RMPHKDAVEV DIDGNTVSG HFLIRTFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVRINQVG IVDLIPVRVP Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFFSSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGQV					
	: :					
g260	MGAGVVFVVFQPFSSSLFRALFEGGVGIVEGAHDAAECDLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAPFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGNTVSG					
	: : : :					
g260	TARFFQAFGVNPGAFGVQQPAPFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTFDDGDAVCLFQAEARFAVNVAQHQYLVRINQVGIVDLIPVRVPQ					
g260	HFLIRTFDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CCACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGTT TCTTGCGGG AAACGATTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCEATG CCGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTG CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGTGT GCCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep
1 MGAGMVFVVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL
101 RVPHKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVFVVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG DVFIDSVGQV					
a260	MGAGMVFVVF RPFSSLFRAL FEDRVGIVEG AHDAAECDLF PEEFTRIRIG DVFIDSVGQV					
	10	20	30	40	50	60
m260.pep	AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL RVPHKDAVEV DIDGGNTVSG					
a260	AARLFQAFGV NPGAQVQGP AFRAREQARR GSGFFAGNDL RVPHKDAVEV DIDGGNTVSG					
	70	80	90	100	110	120
m260.pep	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLVRINQVG IVDLIPVRVPQ					
a260	HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH QYLVRINQVG IVDLIPVRVP QAAXIATGCT					
	130	140	150	160	170	180
m260.pep	GICPKCPTGCRPVX					
a260	GICPKCPTGCRPVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq
1 atggagcttg ggcataatcgt attccttctg ctttgcgcgc cttcagacgg
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgcgg atgtagtcca acacgcccac ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtag atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcagt gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgccc ccatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggttcc
451 gatggcggcg gtttcgatgg cggcgggttc gtccatcagg gcgttgtagc
501 taacttgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat gcggttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgcccgtag gtttgattg

g261.pcp

1	MELGHIVFLV	LCARSDDLFT	FQIFRQPAFA	QDARAFAAA	ADDTLVAGVG
51	LFADVVOHAH	FVRQRPRLRL	GQVHQRRVDL	KIVVHRQIKG	NVHGDFDEHAA
101	DVGIIARKIGF	AHARDDVPDT	LPFGKNGGVK	QEKRVTPVHK	GIGNAVVGGF
151	DDGGFDGGGF	VHQGVVRNLP	HQAIEYGLT	DTQILRDLPLC	AFQLDGMALP
201	VSEGGDLDFV	APVGLDCLNQ	HAGRILITARE	DDQGLFV*	

m261.seq

1	ATGGAGCTTG	GGCATATCGT	ATTCTTATG	GTTTGC GCGT	GTTCAGACGG
51	CCTTTTFACT	TTCCAGATAT	TCGCCAGACC	cGcGTTTCGG	CAGATACAG
101	CTCGGGCATT	CGCGgCAGCC	GCCGACGATG	CCGTTATAGC	AGGTGTGGGT
151	TTGTCGCGG	ATATAGTCCA	GCCAGCCCAT	TTGCTTCGCC	AACGCCACG
201	TTTGCGCCCT	GGTCAGATAC	ATCAGCGCGC	TGTGGATTGG	AAAATCATAG
251	TCCATCGCCA	AATTAAAGGT	AACGTTTCATC	GATTTGACAA	ACACGTCGCG
301	GCAGTCGGGA	TAGCCGGEAG	AGTCGGTTTC	GCACACGCCC	GCGATGATGT
351	GCCGTATCCC	CTGCCCTTTG	CGGTAAATCG	CGGCATAGAG	CAGGAAAAGC
401	gCGTTGCGGC	CGTCTACAAA	GCGTATTCGA	ACGCCGTTTT	CGCAGTTTC
451	GATGCGCGCG	GTGTCGTCCA	TCAGGGCATT	GTGCGTATC	TGCCGCATCA
501	GgCTcAAGTC	GAGTACGGTT	TGTTTGACGC	CCAAATCCTG	CGCAATCCAG
551	CGGGCAGCTT	CCAGCTCGAC	GGCATGGCGT	TGCCCGTATT	GGAAAGTAAT
601	GGCTTTGGACG	TTTTCGCGCC	CGTAGGTTTG	GATTGCCTGA	ATCAGC3AGG
651	TGGTcGAATC	CTGACCGCCC	GAAGAAATGA	CCAAGGCTTG	TGGGTTTGA

m261.pcp

1	MELGHIVFLM	VCACSDGLFT	FQIFRQPAFA	QDTARAFAAA	ADDAVIAGVG
51	LLADIVQHAH	FVRQRPRLRL	GQIHQRRVDL	KIIVHRQIKG	NVHRFDKHVA
101	AVGIAGEVGF	AHARDVVPYP	LPFGVNRGIE	QEKRAVAAYK	GIRNAVFGSF
151	DGGGVVHQGI	VRNLPHQAQI	ELYGLFDAQIL	RNPAGTFOLD	GMALPVLESN
201	GLDVDPAPVGL	DCLNOAGGRI	LTARKDDOGL	LV*	

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m261/q261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQD	TARAF	AAAADDAVIAGVGLLADIVQHAH			
		:			:	:
g261	MELGHIVFLVLCARSDGLFTFQIFRQPAFAQD	TARAF	AAAADDTLVAGVGLFADVVQHAH			
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHR	FDK	HVA	AVGIAGEVGF	FAHARD	DVPYP
		:	:	:	:	:
g261	FVRQRPRLRLGQVHQRRVDLKIIVHRQIKGNVHG	FEH	AAAVGIARKIGFAHARD	DVP	PD	T
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRVAAVYKGI	RNAVFGS	FDGGGV----	VHQQGIVRNLP	HQAQVEYGLF	
		:	:		:	:
g261	LPFGKNGGVKQEKRVTPVHKIG	RNAVVG	FGDGGG	FVHQGVVRNLP	HQAQIEYGLT	
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPA	GTFLQ	DGMALPV	LESNGLDV	FAPVGLDCLN	QAGGRILTARKDDQGLLVX
	:	:	:	:	:	:
g261	DTQILRDPLCA	FTFLQ	DGMALPV	SEGDGLDV	FAPVGLDCLN	QAGGRILTAREDDQGFVLX
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCAAG
201 TTTGCGCCTT GGTCAATAC ATCAGCGGCG TGTGGATTTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTC GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA SGTATTGCGA ACGCCGTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGTCAAGTC GAGTACGGTT TGTTCGACG CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGCGCT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC GTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHGFDPKHT
101 AVGIAGEVGF AHARDVPYP LPFGVNRGIE QEKRAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA	AVGIAGEVGF	AHARDVPYP			
a261	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVT	AVGIAGEVGF	AHARDVPYP			
	70	80	90	100	110	120
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	130	140	150	160	170	180
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGFLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgcga cagcctgacc gcccgcgaa gtcgaagtgat
201 ccggatcatc gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccg ctttggcggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctcgaagcgg gctacaaccg gcagcaggca
```

606

451 gtcgaagtcg taatggggcgt agccttggca actttgtgca actacgccaa
501 caacctcgcc caaaccgaaa tcaaccccaa attgcagycg tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263.pep
1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
51 GKLNAAANSLT AGEVEVIRII AVRTNQCSFC VAGHTKLATL KLLSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDEELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANNLA QTEINPKLQA YA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)
1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151 GGCGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)
1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101 CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151 GGCGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC
201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

				10	20	30
m263.pep				AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
				:		
g263	QCSFCVAGHTKLATLKKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD					
	80	90	100	110	120	130
		40	50	60	70	
m263.pep	ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVMNLGQTEINPELQAYAX					
	: :					
g263	ELNAFLAAGYNRQQAVEVVMGVALATLCNYANNLAQTEINPKLQAYAX					
	140	150	160	170	180	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq
1 ATGGCACGTT TAACCGTACA CACCCTCGAA ACCGCCCCCG AAGCCGCCAA
51 AGCGCGCGTC GAGGCGGTAC TTCAAAACAA CGGCTTTATC CCAACCTTA
101 TCGGCGTATT ATCAAACGCC CCCGAAGCCT TGGCGTTTAA CCAAGAAGTC
151 GGCAAGCTCA ACGCCGCCAA CAGCCTGACC GCCGGCGAAG TCGAAGTAAT
201 CCAGATTATT GCCGCCCGCA CCAACCAATG CGGCTTCTGC GTGGCAGGGC
251 ACACCAAACG CGCAACCCTG AAAAAACTCC TTTCCGAACA ATCCGTCAA
301 GCCGCGCGCG CTTTGGCGGC AGGCGAATTT GACGATGCTA AACTCGGCGC
351 GCTCGCCGCC TTTACCCAAG CCGTAATGGC AAAAAAAGGC GCGGTATCCG
401 ACGAGGAACG CAAAGCATTT TTTGATGCGG GCTACAACCA GCAGCAGGCA
451 GTCGAAGTCG TGATGGGCGT AGCCTTGCCA ACTTTGTGCA ACTACGTCAA
501 CAACCTCGGA CAAACCGAAA TCAACCCCGA ATTGCAGGCT TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep
1 MARLTVHTLE TAPEAAKARV EAVLQNNNGFI PNLIGVLSNA PEALAFYQEV
51 GKLNAAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA*

607

m263.pep
 AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
 a263
 QCGFCVAGHTKLATLKKLLSEQSVKAARALAAGEFDDAKLGALAAFTQAVMAKKGAVSDE
 80 90 100 110 120 130
 40 50 60 70
 m263.pep
 ELKAFFDAGYNQQQAVEVVMGX~~XL~~ATLCNVVNNLGQTEINPELQAYAX
 a263
 ELKAFFDAGYNQQQAVEVVMGVALATLCNVVNNLGQTEINPELQAYAX
 140 150 160 170 180

```
g264.seq
1      ttgactttaa cccgaaaaac ccttttctc ctcaccgcg cgttcggcac
51     acactccctt cagacggcat ccgccgacgc agtgggtcaa ccggaaaaaac
101    tgacagcctc cgccaaccgc agctacaaag tcgcgaatt cacgcaaac
151    gggcaacgcct cgtgggtacg cggcaggttt caccgggcca aaacttcggg
201    cggagaccgc tacgatatga acgcctttac cgcgcgccac aaaacctgc
251    ccatccccag ccatgtgcgc gtaaccaaca caaaaaacgg caaagcgtc
301    atcgtcgcg tcaacgacgc cggccccctc caccggcaac ccatcatcga
351    cgtatccaaa gcgcgcgcgc aaaaattggy ctttgtcagc caagggacgg
401    cacacgtcaa aatcgaacaa atcgtccgg gccaatccgc accggttcgc
451    gaaaacaaag acatctttat cgacttgaaa tctttcgyta cggaaacaga
501    agcacaagcc tatctgaacc aagccgcccc aaatttcgcc gcttcgctat
551    caagcccgaa cctctcggtt gaaaaacgcc gttcagaata cgttgtcaaa
601    atggggccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggc
651    acqcqgtatg qttccqqcqg tactgaacct cqqttqqa
```

g264 pep

1	<u>LT</u> LTTRKTLFL	<u>L</u> TAAFGTHSL	<u>Q</u> TASADAVVK	PEKLHASANR	SYKVAEFTQT
51	GNASWYGGRF	HGRKTSGGDR	YDMNAFTA AH	KTLPPIPSHVR	VTNTKNGKSV
101	IVRVNDRGPF	HGNRIIDVSK	AAQKLGFVS	QGTAVHKIEQ	IVPGQSAPVA
151	ENKDFIDFLK	SFGTEHEAQA	YLNQAQNFSA	ASSSSPNLSV	EKRREYEVVK
201	MKPFASOERA	AEAEAOAAGM	VRVRLTSG*		

```
m264.seq
1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCGGCAC
51  ACACCTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC GCCCAACCGC AGTACACAAG TCGCCGGAAA ACGCTACAGC
151 CGCAAAAAAC AAGTCGCGGA ATTACGCAA ACGGCAACG CTCGTGGTGA
201 CGGCGGCAGG TTTCACGGGC GCAAAACTTC CGGCGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAATTT GGGCTTTGTC AACAAGGGA CGGCACAGT CAAAACTCGA
451 CAAATCGTCC CGGGCCAATC GCACCGGTT CGCGAAAAA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACA GCCTATCTGA
551 ACCAAGCCGC CAAAACCTTC GCCGTTTCGT CATCGGGTAC GAACCTCTCG
601 GTTGA AAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTACCTC
651 CGAGGAACGC GCGCCGAAG CCGAAGCTCA GGC GCGCGGT ATGGTTCGGG
701 CGGTATTGAC CGCCCGCTGA
```

m264 .pep

1	<u>LT</u> LT <u>TR</u> KT <u>LF</u> LT <u>FL</u> <u>LT</u> AAFG <u>TH</u> SL QTASADAVVK AEKLHASANR SYKVAGKRYT
51	PKNQVAEFTQ TGNASWYGGF FHGRKTSGGF RYDMNAFTAA HKTLPFPSVY
101	RVTNTKNGKS VIVRVNDRGFL FSHGNRIIDVS KAAAQKLGFV NQGTAVHKIE
151	QIVPGQSAVP AENKDFIDFL KSFGEAEHAQ AYLNQAAQNF AVSSSGTNLS
201	VEKRRYEYVV KMGPTFSOER AAEEAEAOARG MVRVALTAG*

608

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHGRKTSGGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSPGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENKDI FIDLKSPGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAEQA RGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAEQA RGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

```

1   TTGACTTTAA CCGAAAAAC CCTTTTCCTC CTCACCGCCG CATTCCGGCAT
51  ACATTCTTTT CAGACGGCAT CCGCCGACGC AGTGGTCAGG GCAGAAAAAC
101 TGCACGCCCTC CGCCAACCGC AGCTACAAAG TCGCCGGAAA ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGCGGGCAGG TTTCACGGGC GCAAACTTC CGGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCCGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCGCACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACC GTT GCCGAAAACA AAGACATCTT
501 CATCGACTTG AAATCTTTTG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CAAAACCTG GCTTCATCGG CATCAAACCC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTTGCTC
651 GCAGGAACGC GCCGCCGAGG CCGAAGCTCA GCGCGCGGGT ATGGTTCGGG
701 CGGTATTAAAC CGCCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

```

1   LTLTRKTLFL LTAAFGIHSF QTASADAVVR AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGR FHGRKTS GGE RYDMNAFTA HKTLPISYV
101 RVNTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAAQKLG FV NQGT AHVKIE
151 QIVPGQSAPV AENKDI FIDL KSPGTEHEAQ AYLNQAAQNL ASSASNPNLS
201 VEKRRYEYVV KMGPFASQER AAEAEQA RGMVRAVLTAG*

```

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	50
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKAELHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	50

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	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENKDIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGCGCTG ATGATTTTGT CTTGTTTGT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTGTATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTGGGCTTC GCGGCGCGT TCCTGCGAGG TAAACGGTCC
351 CATTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNVRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGA EMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGA EMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFVNVRGLENVDINKVSNNRQPAVNTARTI PRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTI PRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

```
a265.seq
1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

```
a265.pep
1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQF AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*
```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AAFSAWARLMIL	SCLLCWCAACP	WSSSPCPSWW	ASAGAEMLSA	VAAAEV
a265	MSVILPPTRANA	AAFSAWARLMIL	SCLLCWCAACP	WSSSPCPSWW	ASAGAEMPISA	VAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI	XFAFVNRGL	ENVNDINKV	SNRQPAVNT	ARTIPRAXAS	ASAARSCEV
a265	KRRRLKFI	---FAPAKYL	XXCLKDVKA	GHQPAVNT	ARTIPRAXAS	ASAARSCEA
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

```
g266.seq
1   agttcagacg gcatacgccg cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgttcggcgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgatc gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgcc acatcctcga atcccgctgc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttcc
301 cgtgtttcgt gcggcgggat tttgggcaca cgcgcaacag ggaataa
```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

```
g266.pep
1   MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT TRLFVAAALKR
51  KHFGHHLIEL AAGFALTASL AYILESRAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

```
m266.seq
1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CGGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTTG CGTTTCCATG TTTTGTGTGG CGGTATTTTT GGCACACGCG
351 CAACAGGGA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      MQFRRHRRRQCPNRKPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      LIELAAGFALTAVLAYILES RAGAVHNDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90      100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTG CTGCTTGCCT
101  TGATTTTTC CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATT CCGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTT CTTGCTTACAT CCTCGAATCC CGTGCGGGAG
251  CCGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC GTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  ||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90      100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

1	atgcaagtcg	ccttttttct	cgccgtggta	ttcaaaaata	tgggtttcca
51	caatcgcatt	ggtcgggcag	gcctcttcgc	agaaaccgca	gaagatgcac
101	ttggctcagg	cgatgctcga	acgcttggtg	cggcgggtgc	cgtcttcgcg
151	tctctccgat	tcgatgttga	tgcgcattgc	cgcacacc	cgtctgcaca
201	atttacacgc	gatgcagcgt	tctctctcgt	tcggaaaacg	gcgttgcgcg
251	tcgacagccg	ggaaacgcac	ggattgcgcg	gttttctctt	cgggaaaaata
301	aatgtgtctt	ttgcgggcaa	aaaagttttt	gagcgttacg	cccatgcctt
351	tcaccagttc	qccaaqcaca	aaqatgttta	ctaa	

g267.pep

m267.seq

m267.pcp

m267/g267

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TCGCAGATTG	GGGGCAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GCGTTGCGCG
251	TGCACAGCCG	GGAAACGCAC	GGATTGCGCG	GTTTCTCTT	CGGGAAAAATA
301	AATCGTGTCT	TTAGCGGGCAA	AAAAGTTTTT	GAGCGTTACG	CCCATACTCT
351	TTACCAATTC	GCCAAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTCFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLF	FAETAEDALGQVDVV	TLGAARTV	FTFFRFDVNRHC	
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFA	FFRFDVDRHC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLEFAVRI	PPLRVQTAETHGLRRFL	FGEINCVFAGEKV	FERYAHTFYQF		
a267	GANGFTQFTRDAFLAVWIT	ALRVQTAETHGLRRFL	FGKINRVFAGKKV	FERYAHTFYQF		
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tgggtcaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccgcgca
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaaacgcc cgactttttt gaaccttact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttgacaaa agcgaaacaa
601 aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801 ctgcgagaaa acatggaaaa gcggtatgga caagatctgt gccaaacatg
851 cgaaagccga aggtgaaacg ccaaaccgga taaaagtcag tgagttggcg
901 tgtaaacgag cagaaaccca agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tgggtcaggga agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTEKTD
101 SSKLKCEAAL KLDVPDDVVD YAVANQSIG NSHKKTPDF EPYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAEEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAE3ET FNGIKVSELA
301 CKTAETEARL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAACCG TCACAGAAAA CATGGAAGAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401 AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1  ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAARVS EWEERYKLSR
51  XQFEQFWKGL POTVQNKLOP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

```

m268/g268

m268.pep                               10      20
                               MALIKEPLDKVKQRNEELEAAE-----
                               |||||:||||:||||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKORNEKLEAAETAQEARE
          160      170      180      190      200      210

m268.pep      30      40      50      60      70      80
--EAAAQEALGREQEAARVSEWEERYKLSRSQFEQFWKGLPQTVQNKLOPSQKTWKSMD
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g268      AEEAAAQEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMD
          220      230      240      250      260      270

m268.pep      90      100     110     120     130     140
KICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g268      KICANNAKAEGKTPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1  ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTGCGCG
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAGAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1  MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTVQNKLOA SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

m268.pep      10      20      30      40      50      60
MALIKEPLDKVKQRNEELEAAEAAAQEALGREQEAARVSEWEERYKLSRXQFEQFWKGL
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a268      MALIKEPLDKAKQRNEELEAAEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

	10	20	30	40	50	60
m268.pep	70	80	90	100	110	120
	PQTVQNKLQPSQK	TWKSGMDKICANNAKAEGKTPNGIKFSELACKTA	KTAEARLEELHN	NRK		
a268	PQTVQNKLQASQK	TWKSGMDKICANNAKAEGETPNGIKFSELACKTA	ETAEARLEELHN	NRK		
	70	80	90	100	110	120
m268.pep	130	140				
	KALIDEMKREADXK	ELSKRLX				
a268	KALLDEMARFADK	ELPKRLX				
	130	140				

m268-1.seq

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.ppt

m268-1/q268 82.3% identity in 164 aa overlap

				10	20	30
m268-1.pep				VQSR	DGLHKFKHKICS	AAMALIKEPLDKVKQRNE
				:	: : :	
g268	KEGAY	YVKTIS	YSVQPT	DDKSKI	FAEL	SOAHDI
	150	160	170	180	190	200
	40		50	60	70	80
m268-1.pep	ELEA	RE-----	EAA	QEA	LGRE	QEAARV
	:					
g268	KLEA	AEATA	QEA	REAE	EAA	QEA
	210	220	230	240	250	260
	90	100	110	120	130	140
m268-1.pep	KLQAS	QKTWK	SGMD	KICAN	NAKA	BEGKTP
g268	KLQAS	QKTWK	SGMD	KICAN	NAKA	BEGT
	270	280	290	300	310	320
	150	159				
m268-1.pep	MARE	ADKKEL	SKRL	X		
	:					
g268	MVRE	EDKKEL	PKRL	X		
	330					

a268-1.seq

1	GTGCAATCCC	GATATGATGG	TTTGCATAAA	TTTAAACATA	TATGTTCCGC
51	AGCTATGGCA	CTGATTAAAG	AGCCGTTGGA	CAAGACGAA	CAAAAGCAAG
101	AAGAACTTGA	AGCGGACGAA	GAAGCGCGCG	CCAGGAGAGC	ATTGGGTCCG
151	GAGCAGGAAG	TCGACCCGGT	ATCCGCAATGG	GAAAGAACCT	ACAAGCTGTC
201	CGCGACGGAG	TTCGAGCACT	TCCTGAAGTG	ATTGCTCTAC	ACCGTACAGA
251	ATAAGCTGCA	AGCCTCACAG	AAAACATGGA	AAAGCGGGAT	GGATAAAATC
301	TGTGGCAACA	ATGCGAAAGC	TGAAGGTTGA	ACGCCAACCG	GCATAAAATC
351	CAGCGAAGCT	GCATGCAAAA	CGCGCGAAAC	CGAGCAACGC	TTGGGAAGAG

616

401 TGCACAACCG TAAAAAGCC CTTCTGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep
 1 VQSRDGLHK FKHCISAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR
 51 EQEVDVRSEW EERYKLSRSE FEQFWKGLPQ TVONKLOASQ KTWKSGMDKI
 101 CANNAAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LLEDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCISAAMALIKEPLDKAKQRNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCISAAMALIKEPLDKVQKQRNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEKTPNGIKFSEL					
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKALLDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq
 1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc
 51 cagcccttgg atttgggcgg tgggtgtggg gtggtcgcgg tcggcttttt
 101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc ggcgttgccg
 151 gtttcgccgt gggactttat ccggaacacg gcttcgccca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
 251 cgcccggtgc cattttgctg tccaatcgcg gggtaaaaa accggtgtcg
 301 tttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep
 1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq
 1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTGT
 101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT
 151 TCGCGGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTGCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTGCTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep
 1 MVWRVNCAAT AVLIFSSSPW IWAAVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng)

from *N. gonorrhoeae*:

```

m269.pep    MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT    59
|||||
g269        MVWRVNCAATAALIFSSSPWIWAVVWWSRSASFCKPCASLDASSAPALAVSPWDFIRNT    60

m269.pep    ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS    119
|||||
g269        ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSPKSPSVQVDTSAALLCLSLRS    120

m269.pep    SX    121
||
g269        SX    122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1   ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51  CAGCCCTTGG ATTTGGGCGG CCGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCCTGT CCAGCGCGCC GGCCTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGCGCG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTGTGCG
301 TTAAATTTT  CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1   MVWRVNCAAT AVLIFSSSPW IWAAVVWWAR SALSWRFCAS VPASSAPALT
51  VSPWDFIQNT ASPKVSAAALM HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

m269.pep    10    20    30    40    50    59
MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
|||||
a269        10    20    30    40    50    60
MVWRVNCAATAVLIFSSSPWIWAAVWWSRSALSWRFCASVPASSAPALTVSPWDFIQNT

m269.pep    60    70    80    90    100   110   119
ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSPKFSSVQVDTSAALLCLSLRS
|||||
a269        70    80    90    100   110   120
ASPKVSAAALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSPKFSSVQVDTSAALLCLSLWS

m269.pep    120
||
a269        SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1   atgaataaaa accgcaaatt actgcttgcc gactgctgc tgactgcctt
51  tgccgccttc aagctcggtt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgac gctgcccggc
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cagcgccccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcatt cgctgcccgc tctgtgtcga
351 aggcaggcgc gattttacgg cgacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270.pep
 1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca . CAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCTGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTT
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng)

from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLL	AFAAVKLVLLQWWQA	XQPQAVAAQC	DLTEGCTLPD	GSRVRAAAVS	
g270	MNKNRKLLLAALLL	AFAAFKLVLLQWWQA	XQPQAVAAQC	DLTEGCTLPD	GSRVRAAAVS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDIYIEHAPAGTEQVS	ISFSMKNMMDMGFNRYMFERQ	PSGTWQAVRI	RLPICVEGRR		
g270	TKKPFDIYIEHAPAGTEQVS	ISFSMKNMMDMGFNRYMFERQ	PSGTWQAARI	RLPVCVEGRR		
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCTGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTT
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLIAFAAVKLVLLQWQAXQPQAVAAQC	DLTEGCTLPDGS	SRVRAA	AVS	
a270	MNKNRKL	LLAALLIAFAAVKLVLLQWQAXQPQAVAAQC	DLTEGCTLPDGS	SRVRAA	AVS	
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPF	DIYIEHAPAGTEQVSISFSMKNM	DMGFNRYMFERQPSGTWQAVRIRLPICVEGRR			
a270	TKKPF	DIYIEHAPAGTEQVSISFSMKNM	DMGFNRYMFERQPSGTWQAVRIRLPICVEGRR			
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGSRTFQTAFTAEX					
a270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

1	atgttcagtt	cgcggatggc	gaggatttgg	gcgacggggg	taacgttgtg
51	tatgggtcagt	ccgtgtcccg	cgttgacgac	caagcccaaa	tcgcccgcga
101	aatgcgcgcc	gttttgatg	cgctcgaaact	gcctgatttg	ttcggcgtgg
151	ctttgtgctg	cggcatatgc	gccggtgtgc	agctcgacaa	cgggcgcgcc
201	gacatcacgg	gcggcttggg	tttgctgtgc	gtcggcatcg	ataaacaagg
251	acacgcgtat	gcccgcgtcg	gtcaggattt	tggcgaattc	ggcgattttt
301	tcctgttgcg	ccaatacgtc	caaaccgcct	tcggtcgtga	tttcctgcgc
351	tttttcaggc	acgatgcaca	cgtcttccgg	catcacttta	agcgcgtttt
401	cgagcatttc	ttccgtcaac	gccatttcaa	ggttcaggcg	cgtgcggatg
451	gcgtttttga	cggcaaatac	atccgcgtct	ttgatgtggc	ggcggctctc
501	gcgcaggtgc	atggtaatca	ggtctgcacc	gtgcgtttcg	gcaaccagtg
551	ccgcctccac	ggggtcggga	taa		

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

1	MFSSRMARIW	ATGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LCASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILANSAIF
101	SCCANTSKPP	SVVISCRFSG	TMHTSSGITL	SAFSSISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIRSAPCVS	ATSAASTGLG*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

1	AwGTTcAGTT	CGCGGATGGC	GAGGATTtGG	GCGATGGGGG	TAACGTtGTG
51	TATGGTcAGT	CCGTGTCCGG	CGTTGACGAC	CAAGCCCAAA	TCGCCGgCGA
101	AATGCGCGCC	GTTTTGGATG	CGCTCGAACT	GCCTGATTtG	TTCCGGCGTGG
151	CTGCGCGCGT	CGCATACGCG	GCCTGTGTGC	AGCTCGACAA	CGGGCGCGCC
201	GACATCACGG	GCGGCTTGGG	TTTGCCTGTG	GTCGGCATCG	ATAAACAAAG
251	ACACGCGTAT	GCCTGCGTCG	GTCAGGATtT	TGGTGAACCC	GGCGATtTTT
301	TCCTGTtTGC	CCAATACGTC	CAAACCGCCT	TCGGTCGTGA	TTTCCTGACG
351	TTTTTCAGGC	ACGATGCACA	CGTCTTCCGG	CATCACTtTC	AAAGCGtTTT
401	CCAACATtTC	TTCCGTCAAC	GCCATtTCAA	GGTTCAGGCG	CGTGCGGATG
451	GCGTtTTTGA	CGGCAAAACG	GTCCGCGTCT	TTGATGTGGC	GGCGGTCTTC
501	GCGCAGGTGC	ATGGTAATCA	AATCCGCACC	GTGCGTtTCG	GCAACCAAGT
551	CCGCCTCCAC	GGGCTGGGA	TAA		

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

1	XFSSRMARIW	AMGVTLCMVS	PCPALTTKPK	SPAKCAPFWM	RSNCLICSAW
51	LRASAYAPVC	SSTTGAPTSR	AAWICLSSAS	INKDTRMPAS	VRILVNPAIF
101	SCCANTSKPP	SVVISXRFSG	TMHTSSGITF	KAFSNISSVN	AISRFRVRM
151	AFLTANTSAS	LMWRRSSRRC	MVIKSAPCVS	ATSAASTGLG *	

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPSPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTS KPSPSVVISXRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271 . pep	TMHTSSGITLFAFSSISSVNAISRFRVRMAFLTANTASLMWRRSSRRCMVIRSAPCVS					
g271	TMHTSSGITLFAFSSISSVNAISRFRVRMAFLTANTASLMWRRSSRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271 . pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271 . seq

```

1  ATGTTCA GTT CGCGGATGGC GAGGATTTGG GCGATGGGGG TAACGTTGTG
51  TATGGTCA GTT CCGTGTCGGG CGTTGACGAC CAAGCCCAAA TCGCTGGCAA
101 AATGCGCGCC GTTTTGGATG CGCTCGA ACT GCCTGATT TG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGGG TTGCCTGTC GTCGGCATCG ATAAACAAGG
251 ACACGCGTAT GCCGCGCTCG GTCAGGATT TGGTGAATTC GGCAATTTTG
301 TCTTGTTGCG CCAATACGTC CAAGCCGCCT TCGGTCGTGA TTTCCTGACG
351 TTTTCCGGC ACGATGCACA CGTCTTCCGG CATCACTTTA AGCGCGTTTT
401 CGAGCATTTT TTCCGTCAAC GCCATTTCAA GGTTCAGGCG CGTGCGGATG
451 GCGTTTTTGA CAGCAAACAC GTCCGCGTCT TTGATGTGGC GGCGGTCTTC
501 GCGCAGGTGC ATGGAATCA GGTGGCACC GTGCGTTTCG GCAACCAAGT
551 CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271 . pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTS SKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271 . pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271 . pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTS KPSPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTS KPSPSVVISXRFSG					

621

	70	80	90	100	110	120	
	130	140	150	160	170	180	
m271.pep	TMHTSSG	ITFKAFS	NISSVNA	ISRFRVR	MAFLTAN	TASASL	MWRRSS
a271	TMHTSSG	ITLAFSS	ISSVNA	ISRFRVR	MAFLTAN	TASASL	MWRRSS
	130	140	150	160	170	180	
	190						
m271.pep	ATSAAST	GLGX					
a271	ATSAAST	GLGX					
	190						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

```

g272.seq
1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggttcc gacctgtttg tgacgaccca ttteccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatggaaa tcgccttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtcca atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgct caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgccgcc
351 ggccttgaag gatgttcgcg tgaacaaacg cgggctgggt attttgtcgc
401 gcggcaccgg ctccgggcaa tcgacttcgc tcgcctcgct taccgactac
451 cgcaatgaaa attcggttcg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcacatc taccagcgcg gaggtcggcg
551 tggacacgga aaactggatg gcggcggttg aaaatacgct gcgtcaggcg
601 ccggatgtga tccttatcgc cgaatccgcg gaccgtgaaa caatggacta
651 cgccatcgcc ttgcccgaac cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcaccgca tcatcaactt cttcccgcag
751 gagcggcgcg aacaattgct gacggatttg tcgctcaacc ttcaggcggt
801 tatttcgcaa cgctcgttc cgcgagacgg cggcaaggcg aggggtgagg
851 cagtcgaggt gctgctcaat tcgcccctga ttccggaggt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttcgct
1051 ttggcggtag agttgcgcag ccgcagggca caaagttccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

```

g272.pep
1  MTAKEELFAW LRHMKNKGS DLFVTTHFPF AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RAITSKIPKF ESLNLPALK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMMT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

```

m272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTTC TGACAACCCA TTTCCTCGCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCCTGAC GGCgGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GCGGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 AGTCTTGAAG GATGTCGCGC TGAaaaaaAC GGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCAGCGC GAGGTGCGCG

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```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAAATTGCT GACGATTTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCAAA CGCCTCGTTC CGCGAGACGG CGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTCGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAAATCCG ATTCCGCACA CGATTTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAAAGTTyCA GCCCGGATTT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1 MTAKEELFAW LRHMxQNKGs DLFVTTTFPP AMKLDGKI TR ITDEPLTAEK
51 CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAI IQRGATALVF
101 RTITSKIPKF ESLNLPPVLK DVALKKRGLV IFVGGTGSgK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCII TQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLyQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

	10	20	30	40	50	60
m272.pep	MTAKEELFAWLRHMxQNKGsDLFVTTTFPPAMKLDGKI TRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMKNKGsDLFVTTTFPPAMKLDGKI TRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
g272	AKQAEFSSTNECNFAISLPDTSRFRVNAI IQRGATALVFRITSKIPFESLNLPPVLK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
g272	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCII TQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIR DRETMDYAIAFAETGHLcMATLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
g272	LDRIINFFPEERREQLLTDL SLNLQAFISQRLVPRDGGKGRVA AVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
g272	GNIHEIKEVMKKSTTLGMQTFDQHLyQLYE KGDISLQEALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

                370
m272.pep      QSXSPDLXLLX
                || :||| |||
g272          QSSDPDLELLX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GCGCGAAAAA
151 TGTATGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAECAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGACCCGG CTCGGGCAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACCTGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCIGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTCGGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTC TCGCTCAACC TTCAGGCATT
801 TATTTGCAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTACAAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCCACCAAC ACCTTTACCA ATTGTATGAA AAAGCGGAGA
1001 TTTCCTTGCA GGATGCCTTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTIGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH ENKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETHGLCMA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMOF FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

                10      20      30      40      50      60
m272.pep      MTAKEELFAWLRHMKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
                ||||| :|||||
a272           MTAKEELFAWLRHMKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEKCM EIAFSIMS
                10      20      30      40      50      60

                70      80      90      100     110     120
m272.pep      AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVERTITSKIFKESLNLPVLK
                ||||| :|||||
a272           AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIFKESLNLPVLK
                70      80      90      100     110     120

                130     140     150     160     170     180
m272.pep      DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
                ||||| :|||||
a272           DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
                130     140     150     160     170     180

```


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	190	200	210	220	230	240
m272 . pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
	250	260	270	280	290	300
m272 . pep	LDRIINFPEERREQLLDLSLNLAQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFPEERREQLLDLSLNLAQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m272 . pep	GNIHEIKEVMKKSTTLGNQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGNQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
	370					
m272 . pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273 . seq
1  atgagtccttc aggcggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacgc ttttcctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcgcca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacgggttaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnacc gcgcccgcgc tatgtgccga aatattattt
401 gtcgctcacc tgcaaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgctcg ctttttgttt ttcaagcagt
501 ttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273 . pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRARWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCCR VPLKSRREFK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273 . seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTCTCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTTATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAAATG CAAAATTGT TTGCGGCGGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTCTCCGAC GCGCGCCCT GTGTGCCGA GTTATTGTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATACGGCGT TTACCTGCCT TTGTGTWTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273 . pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCCR VPLKSGRPEG CSRRALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

625

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTFFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFEAGTFFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFEG					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273.pep	CSRRALCALCAGVICRSPAKSPRTRFAEFPHCLVSYGVYLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273.seq

```

1  ATGAGTCTTC AGGCGGTATT TGTATACCCC CCAAGCCGTA CCGCACAAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCATAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCCGT CAGGATATAG GCGTATTCCA GACCGGAAC
151 CCATTACCGG TTTTCCTGCC GCTTTTGTG GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT AATGTTTATT
251 GTTGTTCCTT AACGGTTAAA AACC CGCCCG TCCGTGCAAC CGTTTAAAG
301 AGGCGGTAAA TCACAAAGTT TGTGGCGGA CGTGCTCTCT TACAATCAGG
351 GCGGTTTAAAG GGGCATGATG CACTGCCCGG TGTGCCGGAT ATTATTTGTC
401 GCTCACCTGC AAAATTGCCA AGAACGCGCT TTGCGGGATT TCCACATTGC
451 CCACTTGTTT CATACGCGT TTGCCTGCTT TTTGTTTTTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273.pep

```

1  MSLQAVFVYP PSRTAQYNEN QENGGAHKQ GQSGKHADRR QDIGVFQGTG
51  PFTVFLPLFV AFEIKDDAGK QGRSRARH*H NVHCCSLTVK NPPVRATVFK
101 RR*ITKFVGG RALLQSGRFK GHDALPRVPD IICRSPAKLP RTRFAGFPHC
151 PLVSYGVCLL FVQAVFSYA *

```

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGGSGKHADRCQDIGVFKAGTFFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGGSGKHADRRQDIGVFQGTFFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273.pep	GCSRRALCALCAGVICRSPAKSPRTRFAEFPHCLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIIICRSPAKLPTRTFAGFPHCLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTITTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGCGG ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTTCGATTG
451 ACCCCGATGG ACAAACCTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFG GEPDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTITTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAAATAT CGACATCCAG CTTTCATCGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTGCGG GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTTCGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFG GEPDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQGNVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
g274.pep	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
g274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQGNVDLTPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GGCAGATTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTTG
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESXX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESXX					
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESXX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESXX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1  atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggacgaga tgatgcgggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgctcaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaaatgg cgcgggcat
201 ggcgacgcgt tgccgctgtc cgcggataaa gttgctgccc ttgatccga
251 tggcgtggtg cagtccgagc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggtttgga ggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaaaca ggggtgctgc aaacaggaaat acgtcttggg
401 agacgagggc gaattgggag cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcggg
501 cagaagggtg acgacgggtg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctctg atgtcgaggt tgaagttgtc gagggtttg
601 atgccgtctg aacgggtatt gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgaga gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcggcga ggaacatcgt ctgcataagg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgcgatggtt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

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```

1  MILPPSMTMM RSADSTVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

```

m276.seq
1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCCGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GCGGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGA GGGCGAACAG GACTTCGGCT TCGCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTGCTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCACT CGAGTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCT ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGTGCGA GCGTGCCCTT GTCCTGTTTC GCGGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATTG GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

```

m276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSILMSAM
151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng)

from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRW WATMMPVRFS IRRSSACWTRRS DLSNALVASSNNNIGAS					
	:					
g276	MILPSSITMMRSADSTVVRW WATMMPVRFS IRRSSACWTRRS DLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLP FDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDKLLP FDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGRRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLCMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPLCMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

```

1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTCAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGCG AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTGTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGGTGCGA GCGTGCCTTT GTCCTGTTG GCGGGGTGT
701 CGAGAAATGC ACATACGCG TCGGCGGCGA GGAACATCG CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

```

1  MILPSSITMM RSAPSMVVR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRKLMPSTR CGASVPLSCS GGVSNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRKLMPSTRCGASVPLSCSGGVSNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

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250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtacg ggcgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaacccac gcaccgaggg tggggtttcc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgagc
301 ggagtcgaga tagaggtctt ggatattggc gggggcgggg ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tggggttgtc gccgtagcgg
401 ccgtcttttg ggcggcggtt ggggttgagc taggcggcaa accaagggtc
451 gggggccgagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttg atgacgggtg agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttgttggaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG YFHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVL DIGGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
151 GAERAQAGG MGCAGTDFHV EGLDDGA AFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT AAAGTGGGT ACTTCCATGC
351 CGTTGAGCCA GACTTCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCAGTCGT CTTCGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGAGCGG
501 GCTTGAGGCG GACTTGGAA TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGTT GGATAGCGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG IAVFEVVGGLL
51  DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG YFHAVEP DFPAQTPRAE GGVFPVVDK ADVVDFGIDA
151 QFAQRVEIEV LDIGGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N.gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

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```

                                     :||||| :|||:|||||:||||:||||
m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAVGDGVAVERFCPNEVVDFYTLQVH
           30      40      50      60      70      80

           40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAFEPDFPAQTPRTEGGVFPVVFDDKADV
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEPDFPAQTPRAEGGVFPVVFDDKADV
           90      100     110     120     130     140

           100     110     120     130     140     150
g277.pep   DFGIDAQFAQGVIEVLDIGGGFEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPR
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      DFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQAVGVVAVAVFGAAAGLDVGGKPR
           150     160     170     180     190     200

           160     170     180     190     200
g277.pep   GAERAQAGGMGCAGTDFHVEGLDDGAAFVCEPGLQFEDDLLEGKHGLL
           ||| |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||
m277      GAECAQAGGMGCAGTDFHVEGLDDGAAFVCEPGLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1   ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTCGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCAGTTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTT
701 TCTGCCAGA ATGTTTGCAG TTTGAAGATG ATTGTGTTGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1   MPRFEDKLVG RQEGGVVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFLVHVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDD ADVVHFGVDA
151 QFAQGVIEIV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCEPCLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

           10      20      30      40      50      60
m277.pep   MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVHVAV
           |||||:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      MPRFEDKLVGRQEGGVVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLDFVLVHVAV
           10      20      30      40      50      60

           70      80      90      100     110     120
m277.pep   GDGVAVERFCPNEVVDFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAFEP
           : :|:|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120

           130     140     150     160     170     180

```


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```

m277.pep  DFPAQTPRAEGGVFPVVFDDKADVVDFGI DAQFAQRVEIEVL DIGGSGLEGDL ELVIVLQA
a277      DFPAQTPRAEGGVFPVVFDDKADVVHFGVDAQFAQGV EIEVL DIGGSGLEGDL ELVIVLQA
          130      140      150      160      170      180

m277.pep  VGVVAVAAVFGAAAGLDVGGKPR LGAECAQAGGGMGCAGTDFHVEGLDDGAA FVCPECLQ
a277      VGVVAVATVFGAAAGLDVGGKPR LGAECAQTGGGMGCAGTDFHVEGLDDGAA FVCPECLQ
          190      200      210      220      230      240

m277.pep  FEDDLLEGKHGLX
a277      FEDDLLEGKHGLX
          250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1  ttgctgtgcaa tcacgcccg tgcgattttt tgcacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaat acggccggta
151 caggtaaccg tgtcgcttc tttaatatgt tgcgtactcg ccaacactac
201 ggcaccgacg gagtcgcgct ccaggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca cttgcattg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSAFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1  TTGCGCGCAA TCACGCCCGG TCGATT TTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTGCGCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGCGCAGCG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSAFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFD FDRDFQLAVET LIQHLHLQAD
201 LFGVQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

633

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVV	LIGPLPSIGRPNASTTRPTNSRPTGTSKIRPVQVT	VSPSLIC			
m278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	VSPSLIC			
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVLTSAFT	
m278	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVLTSAFT	
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGLS	CMKTLIRHSRVQSTOFALYRQIQNLITHFNF				
m278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQSTOFALYRQIQNLITHFNF	YAANQLRFDF			
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

```

1  TTGCGCGCAA TCACGCCCCG TGCGATTTT TCGATAGGG CCGTCAAAGT
51  TGTATTAATC GGGCCTTTCG CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCCTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTCGCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTTGTCC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

```

1  LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLIC SCSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	VSPSLIC			
a278	LRAITPGAIFSIGAVKVV	LIGPLPSIGRPNASTTRPTSSRPTGTSKIRPVQVT	VSPSLIC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNNTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVRTSAFT	
a278	SCSPNTTAPT	ESRSRFIAKPKVLP	GNSSISPCIASDKP	WMRTIPSVTEIT	VPRVRTSAFT	
	70	80	90	100	110	120

634

	130	140	150	160	170	180
m278 .pep	DRFSILALIKSLISAGLS	CMKTLIRHSRVQGTQF	FALYRQIQNLITHFN	FYAANQLR	EDF	
a278	DRFSILALIKSLISAGLS	CMKTLIRHSRVQGTQF	FALYRQIQNLITHFN	FYAANQLR	EDF	
	130	140	150	160	170	180
	190	200	210	220		
m278 .pep	DRDFQLAVETLIQHLHQL	ADLFVQGRI	TVNDGR	FDMVEX		
a278	DRDFQLAVETLIQHLHQL	ADLFVQGRI	TVNDGR	FDMVEX		
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279 .seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagttttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gtgcctgca atcacgactt gtccgggcga
201 gttgaagtgt acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcacat tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaa ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279 .pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAALPA ITTCPELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279 .seq

```

1  ATAACGCGGA TTGCGGCTG CTGATTTC ACGGTTTCA GGGCTTCGGC
51  AAGTTTGTGCG GCGGCGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCAGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCGGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279 .pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAALPA ITTCPELKL TASTTSLWAA SAQMALTSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N.gonorrhoeae*:

	10	20	30	40	50	60
m279 .pep	ITRICGLISTVFRASASLSAAGFIRLQWE	CTDTGSGRARLAPASLAAAMARPTAALPA				
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWE	CTDTGSGRARLAPASLAAAMVRPTAALPA				
	10	20	30	40	50	60
	70	80	90	100	110	120

m279 . pep
ITICPGELKLTASTTSLWAASQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA
|| ||||||| | : ||||| : |||||||
g279
ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA
70 80 90 100 110 120

130 140 150
m279 . pep
SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX
||| || ||||||| ||||||| : |||
g279
SAKSNSAATSAVYSPRLCPATAAGVLPTTSKX
130 140 150

a279.seq

```
1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNNA GGGCTTCGGC
51 GAGTTTGTCTG GCGGCGGGTT TCATGAGGCT GCAATGGGAA GGTACNGACA
101 CNGGCAGCGG CAGGGCGCGT TTGGCGCCGG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCTGCA ATCACGATT GTCCGGCGCA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGCGGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG
```

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCPGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAIAIAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPAAT</u>	<u>SAVYSPXLCF</u>	<u>ATAAGVLPPA</u>
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRRARLAPASLAAAMARPTAAALPA					
	:	:	:	:	:	:
a279	MTXICGCLISTVXRRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASQAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRSTLTA					
	:	:	:	:	:	:
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTFCGTADCISSARXRSTLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
	:	:	:	:	:	:
a279	SAKSNAPAATSAVYSPXLCPATAAGVLPPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Ouakvi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgcgga
151 gccaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagcaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccaaa acgtcgctga aaccctgata aaggccgata ccgaaggcaa
501 agttttattat caacaacgct tgggcaacta ccaaatagcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaaat cgtccctcgc cgccaaacgc
601 aaagtctctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 caaacaagat cgccgcatc atccgcaaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtt accgcacgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101  TKGIQPLKAE EEGGHHHDHH HDHDHDHEGH HHDHGEYDPH VWNDPVLMDS
151  YAQNVAETLI KADPEGKVYY QRLGNYQMQ LKKLHSDAQA AFNAVPAKR
201  KVLGTGHDAPS YGMNRYNLSF IAPQGVSSSE EPSAKQVAAI IRQIKREGIK
251  AVFTENIKDT RMVDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301  ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACCTCAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGCTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCCTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CTTTTCTTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACGCGCCCG
851 CAGACACCTA CATCGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101  TKGIQPLKAE EEGGHHHDHD HDHEGHHHDH GEYDPHVWND PVLMSAYAQN
151  VAKALIKADP EGKVVYQORL GNYQMLKKL HSDAQAAFNA VPAKRKRLT

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAAIIRQI KREGIKAVFT
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN
 301 AMKQ*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSFILGDAKQIGGERVSIQSLVGANQDTHAYHM					
	: : : : : : : : : : : : : : : : : :					
g280	MKHLKLTIAALLATAATAAPLPVVTFSFILGDAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDII-					
	: : : : : : : : : : : : : : : : : :					
g280	TSGDIKKIRSAKLVLLNGLGLEAADIQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDHH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYVYQORLGNVYQMQ					
	: : : : : : : : : : : : : : : : : :					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAETLIKADPEGKVYVYQORLGNVYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	: : : : : : : : : : : : : : : : : :					
g280	LKKLHSDAQAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	: : : : : : : : : : : : : : : : : :					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACAC CCTTATCGCC GCATTGCTGA CCACTGCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGCGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CCGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGGCGAATA TGACCCCCAC GTCTGGAACG ACCCCGTCCT TATGTCGCGC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAAATGCAG CTCAAAAAAC
551 TGCACAGTGA CGCACAAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCCCTTTCC TATATGGGCA AACGTTACCA
651 TATCGAATTC ATCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC

```

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep
 1 MKHPKLTLLIA ALLTTAATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA
 101 TKGIQPLKAE JEEGGHHHDHD HDHDHDHEGH HDHDHGEYDPH VWNDPVLMSA
 151 YAQNVAEALI KADPEGKVYY QORLGNYQMQ LKKLHSDAQA AFNAVPAAKR
 201 KVLTHDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAAI IRQIKREGIK
 251 AVFTENIKDT RMDVRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNIK
 301 ALTNAMKQ*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTLLIAALLTASATAAPLPVVTSFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
a280						
	10	20	30	40	50	60
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE EGGHHHDHD					
a280						
	70	80	90	100	110	120
	130	140	150	160	170	
m280.pep	HDH----EGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
a280						
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA AFNAVPAAKRKVLTGHDAFSYMGKRYHIEF IAPQGSSEA EPSAKQVAAI					
a280						
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIK AVFTENIKDTRMDVRIAKETGVNVSGLKLYSDALGNAPADTYIGMYRHNIK					
a280						
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
a280						
	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq
 1 atgcactacg ccctcgcatc cgtctctgc ctgtccctca gcgcgcacc
 51 cgctcgcgta ttccctcgta tgcgcgcat gagcctgata ggcgacgcat
 101 tgagccacgc cgtcctgccc ggtgccgccc tcggctacat gtttgccggc
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgccc gtatgctgat
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa
 451 agcatagacc cccttttctt caagtccgct aacggcaaa gcgggctttg

639

```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgcatt
601 accgccggtt tatgggcaag aaatatgggg acgctcattc tgttgctcgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt ccctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgca gctcctttat
751 cttttttccg tcatactcgg caaagaaggc ggcatcttgc ccaaatggtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

```

g281.pep
  1 MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
  51 LSLPAMGVGG FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL
 101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
 151 SIDPLFLKSV NGKGGLWHVI FLVLVVMNLV SGFQALGILM SVGIMMLPAI
 201 TARLWARNMG TLILLSVLI LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
 251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

```

m281.seq (partial)
  1 ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
  51 CGTCGGCGTA TTCTCGTCTA TCGCGCGTAT GAGCCTGATA GGCGACGCAT
 101 TGAGCCACGC CGTCCTGCCC GGTGCCGCGG TCGGCTACAT GTTTGCCGGC
 151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGAG GCATGCTGAT
 201 GGCACCTGTT GCCGGACTCG TCAGCCGCTT CACCACCTG AAAGAAGATG
 251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCTCT
 301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
 351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
 401 GCCTCACGCT CATTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
 451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GGCGGCAAAG GCGGGCTTTG
 501 GCACGTCTCT TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
 551 AAGCCCTCGG CACATCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
 601 ACCGCCCGCC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
 651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
 701 TCGAAATTC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCTTTTAT
 751 CTCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

```

m281.pep (partial)
  1 MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
  51 LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
 101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTITL AVIYRPLVLE
 151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
 201 TARLWAKHMG ALILLSVLI LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
 251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng)

from *N. gonorrhoeae*:

m281/g281

```

          10      20      30      40      50      60
m281.pep  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGLGG
          | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g281       MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG LSLPAMGVGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m281.pep  VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL VSKNGSSVDL LHLLFGSVLA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g281       FAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVIL ISKNGSSVDL LHLLFGSVLA
          70      80      90     100     110     120

          130     140     150     160     170     180
m281.pep  VDIPALQLIA AVSSLTITL AVIYRPLVLE SIDPLFLKSV GKGGLWHVL FLVLVVMNLV

```


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g281	VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLILVVMNLV	130	140	150	160	170	180
m281.pep	SGFOALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLISYHIEIPSGP	190	200	210	220	230	240
g281	SGFOALGILMSVGIMMLPAITARLWARMGTLILLSVLIALFCGLIGLLISYHIEIPSGP	190	200	210	220	230	240
m281.pep	AIILCCSVLYLFSVILGKEGGILT	250	260				
g281	AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

a281.seq	1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
	51	CGTCGGCGTA	TTCCTCGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
	101	TGAGCCACGC	CGTCTGCCCC	GGTGCCGCCG	TCGGCTACAT	GTTTGCCGGC
	151	TTAAGCCTGC	CCGCCATGGG	TTTGGGCGGC	GTAGCCGCAG	GTATGCTGAT
	201	GGCACTGCTT	GCCGACTCG	TCAGCCGCTT	CACCACCCTG	AAAGAAGATG
	251	CCAACCTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	TGTAGTCCTC
	301	GTCAGCAAAA	ACGGCAGCAG	CCTCGATTTC	CTCCACCTCC	TTTTCGGCTC
	351	CGTACTTGCC	GTCGATATTC	CTGCCCTGCA	ACTCATCGCC	GCCGTATCCA
	401	CCCTCACACT	GCTTACCCTT	GCCGTCATCT	ACCGCCCGCT	CGTACTCGAA
	451	AGCATCGACC	CCCTGTTTCT	CAAATCTGTC	GGCGGCAAAG	GCGGGCTTTG
	501	GCACGTCCTC	TTTCTCGTCC	TGGTCGTCAT	GAACCTCGTA	TCCGGCTTTC
	551	AAGCCCTCGG	CACACTCATG	TCCGTCGGAC	TTATGATGCT	GCCAGCCATT
	601	ACCGCCCGCC	TATGGGCGAA	GCACATGGGC	GCACTCATCC	TCCTATCCGT
	651	TCTGACAGCC	CTGCTGTGCG	GCTTGAGCGG	ACTGCTCATT	TCCTACCACA
	701	TCGAAATTCC	TTCCGGTCCC	GCCATCATCC	TCTGTTGCAG	CGTCCTTTAT
	751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GGCATTCTGA	CCAAATGGCT
	801	CAAAAACCAC	CGCCACCACA	CCACCTGA		

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

a281.pep	1	MRYALASVFC	LSLSAAPVGV	FLVMRRMSLI	GDALSHAVLP	GAAVGYMFAG
	51	LSPAMGLGG	VAAGMLMALL	AGLVSRTTL	KEDANFAAFY	LSSLAIGVVL
	101	VSKNGSSVDL	LHLLFGSVLA	VDIPALQLIA	AVSTLTLLTL	AVIYRPLVLE
	151	SIDPLFLKSV	GGKGLWHVL	FLVLVVMNLV	SGFOALGTLM	SVGLMMLPAI
	201	TARLWAKHMG	ALILLSVLTA	LLCGLSGLLI	SYHIEIPSGP	AIILCCSVLY
	251	LFSVILGKEG	GILTKWLKNH	RHHTT*		

m281/a281 99.2% identity in 264 aa overlap

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLP	GAAGVGYMFAGLSLPAMGLGG				
a281	MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLP	GAAGVGYMFAGLSLPAMGLGG				
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVVLV	VSKNGSSVDLLHLLFGSVLA				
a281	VAAGMLMALLAGLVSRTTLKEDANFAAFYLSSLAIGVVLV	VSKNGSSVDLLHLLFGSVLA				
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTLLTAVIYRPLVLESIDPLFLKSV	GGKGLWHVLFVLVVMNLV				
a281	VDIPALQLIAAVSTLTLLTAVIYRPLVLESIDPLFLKSV	GGKGLWHVLFVLVVMNLV				

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIIILCCSVLYLFSVILGKEGGILT					
a281	AIIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata gccggtgcgc tattgaaggt
201 tttgggcata agcgtcgggt cgtttcaggt cggcggcggg attttgggtc
251 tgcctgacgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggagatt gccgtcgtgc ccacgcgat accgatcacc atcggtccgg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatcgcgcgc tgattatcgc ggccggtttg gtggtcagtg cgatttgta
501 tgccatttta atcgttgccg ggaaggtcag ccgctgctg gccgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc gccggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccgcg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYS
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLAAVS
201 VEIIVSGLKT IFFQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCCTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGCTTTG GTGGTCAGTG CGATTGTGTA
501 TGCCATTTTA ATCGTTGCCG GGAAGETCAG CCGCTGCTG GCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLAAVS
201 VEIIVSGLKT IFFQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	: : : : : : : : : : : :					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	: : : : : : : : : : : :					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	: : : : : : : : : : : :					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSIALIIAAGLVVSAICYAILIVAGKVSRLI					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	: : : : : : : : : : : :					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

```

1   ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGACCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGCGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGT CGTTTCAGGT CCGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CCGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTTAAACCGT ATCATGGGTA TGATGCTGGC GCGGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG AATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

```

1   MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAARTYD
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	: : : : : : : : : : : :					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGIVSGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGIVSGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282.pep	GATGLTILNRINGMMLAAVSVEIIVSGLKTIFPQLAGX					
a282	GATGLTILNRINGMMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1  atgaactttg ctttatccgt catcacattt accctcgcct ctttctcgcc
51  cgtcccgccg gccggaaccg ccgtctttac ttggaaagac ggcgggcgga
101 acagctattc ggatgtgccg aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccc gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaaatcc tgccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1  MNFALSVITF TLASFLEVPVP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPKPAVDN NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNAVNKY CR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1  ATGAACCTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCTTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAACCTGCG GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGCG ACAGGAAAAC AATCCCAGCA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAGA AGAAACTGCG CGGATTCAA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1  MNFALSVIML TLASFLEVPVP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRLTQTKP AVKPAQADAG KRTDGAAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLEVPVPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP					
g283	MNFALSVITFTLASFLEVPVPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRLTQTKP					
	10	20	30	40	50	60

	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
	: : : : :					
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNGQLEEEKKIIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNVAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNVAVNKYCRX					
	120	130	140			

a283.seq

```
1 ATGAAC TTTG CTTTATCCGT CATTATGTTG ACCTCGCCT CTTTCCTGCC
51 CGTCCCGCCT GCCGAGACCG CCGTCTTTAC TTGGAAGGAC GGC GGCGGCA
101 ACAGCTATT C GGATGTACCG AACACGCTT C ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG CGCGTCAAC CGCCCAAGC
201 TCACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGG AGAACAPAA AGAAACCTG CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAAATTCAA ATGCAAAATAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGACGTAAAC AAATACTGCC GTTAA
```

a283.pep

1	MNFALSVIML	TLASFLVPP	AGAAVFTWKD	GGGSYSQDVP	KQLHPDQSQI
51	LNLRTQTKP	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEKKRIAE
101	TERONKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNAVN	KYCR*

	10	20	30	40	50	60
m283.pep	MNFALSVMILTLASFLVPFPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVMILTLASFLVPFPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAGQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
a283	AVKPAQADAGKRTDGAAGQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	130	140				

g284.seq.

```
1  atgccgtctg aaactcgaaa tcggtttcag acggcattgg tttacgcggc
51  aggttggggc ttagcgggtct ttgtaacggc attcgtcttt gccctgcaaaa
101 gagtcgccgg ctttgcggtt gccctttgaag ccttcgccgg tttttttgaa
151 actgtctttc ttaaagcctt cttctttgaa accttcgccg cgcggtttgc
201 cgccgaagcc ttctttgccc ggtttatgat cgccgcgcgc gccgcgggat
251 ttcttatcgc ccacgcgcgc ttgaccttc ggcttgccgc ctgcggattt
301 cggtttgcgg gccggtccca tgccttcgat ggtcagttcg gccagtttgc
351 cgttaatgta tttttcgatt ttgtggacct tgacgtattc gttcacttcg
401 gcaaacgtaa tcgcaatacc cgtgcggcct gcgcggccgg tgcgcgcgat
451 cgcgttgacg tagttctccg cctgtttccg caggtcgtag tttatgacct
```

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```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaatcc gtcagcgtgc ggttgcgcca
601 gccctgcggc atatcgccgt gcaggcagtt ggcgcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttgg-gga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgagg atgtggcga gcaggcggtt
751 tttgtggcgc atatcgtcgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttg
851 cgcgcagatt tgccgactgc gccgtcccaa gtggcggaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51  TVFLKAFFLE TFAARFAAEA FFARFMIAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD GQFGQFAVNV FFDFVDFDVF VHFGKRNRT RAACAAGAPD
151 AVDVVFLFR QVVYDVNGNG RYVNTACGNV GGNONFAAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDVG IAQDVVEQAV
251 FVAHIVAVQQ LLEDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGCTCG AACTCGAAA TCGGTTTCAG ACGGCATTGG TTTATGCGGC
51  AGGTTGGGGC TTAGCGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCCTTT GCCTTTGAAG CCTTCGCCGG TTTTTTGA
151 ACCGTCTCTC TTAAAGCCTT CTTTCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTATTGAT CGCCGCCGCA ACCGCCGGAT
251 TTACGATCGC CCCAGCCGCC TTTGCCTTTC GGCTTGCCGC CTGCGGATTT
301 GCGTTTGGCG GTCGGTTCCA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTCCGCCCT GCGCGGCCGG TCGGCCCGAT
451 GCGGTGGACG TAGTCTTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGGTAATGGT CGTACGTCG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AARATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGCCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TCGCGCGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTCATGG CTTTGGTGGA CGTGAAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCCGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTTCTTCG ATTTTGCCTT
801 GATCGTCAC GCGTTCGACT TCGATGATT CAGGCTCTT GGTCACTTTC
851 CGCGCCAGTT TGCCGACGCG GCCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGGCCTTG CTTCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAAATCAG CACTTCCAAA
1001 CGTTCAAAT CACTTTTGCC GCTTTGCATC AGGTCCATCA GACGGCCCGG
1051 CGTGGCGACA ATCAGATCGA CCGGTTTGCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCCGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGGCATAAG CCAGCGCGTT TTTCTCGACT TGAGCCGCCA GTTCGCGGGT
1201 CGGGGTCAAC ACCAAAGCAC GCGGCTTTT GCCCGGTTT TCGCTGCGTT
1251 TGTCAGTTT TTGCAAAGTC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51  TVSLKAFFLE TFAARFAAEA FFARFMIAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSVNV FFDFVDFDVF VHFGKRNRT RAACAAGAPD
151 AVDVVFLFR QVVVDVNGNG RYVDTACGNI GGNONFAAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFGG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LLEDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQATAR
351 RGDNQIDREA QGTGLVAERR AADDADGAEP THIFGIRQRV FLDSLRSQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284.pep	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFQ TALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAPTAGFTIAPAAFAFRLAACGFAGRFHAFDQGQFQFSVNV					
g284	TFAARFAAEAFFARFMIAPAGFPPIAPAAFAFRLAACGFAGRLHAFDQGQFQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDV FVHFGKRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVDTACGNI					
g284	FFDFVDFDV FVHFGKRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRGYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRRFGGRENHTLVDDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFFDFRVFQFARQFADRAVPSGGEQXS					
g284	IAQDVVEQAVFVAHIVAVQQLFFDFALAVHAFDFFDFRVFQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQTFKINFAALHQVHQQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTATTATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTCG  GGCAGTTTTC
351 GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGGCGGAAA  CCTTTTTCGT
651 ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GGTCTGCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCAAGTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCT  TCCGCGGTGG  CTTGACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001 CGGGCGAAAT  CGACTTTGCC  GCTTGCATC  AAGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTGGTAGC
1101 CGAACGATGC  ACCACGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCGGCCA  ATTCGCGGGT
1201 CGGCGTCAAC  ACCAACGCGC  GCGGCGCTTT  GCCCGGTTT  TCGCTGCGTT
1251 TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNREQ  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

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647

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51 TVSLKAFFLE TFAARFAAEA FFAREMI AAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD GQFGQFSNVV FFDFVDFDVF VHFGKRNNT RAACAAGAPD
151 AVDVVFLFR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQO LFFDFALVVH AFDDDFRVF GQFARQFADR AVPSGGEQOS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQV FLDLSRQFAG
401 RRQHQRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFAREMI AAP TAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSNVV					
a284	TFAARFAAEAFFAREMI AAP TAGFTIAPAAFAFRLAACGFAGRFHAFDQFGQFSNVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVVFRLFRQVVVDNVNGRYVDTACGNI					
a284	FFDFVDFDVFVHFGKRNNTRAACAAGAPDAVDVVFRLFRQVVVDNVNGRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	GGNQNFAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDDDFRVFGQFARQFADRAVPSGGEQOS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDDDFRVFGQFARQFADRAVPSGGEQOS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQVFLDLSRQFAGRGQHQSSTRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQVFLDLSRQFAGRRQHQRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

g285.seq

```

1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

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151  tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201  gtaccaaatc cgttcctggt tcggcgtaaa ctttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactggte gatagaaacc
301  gagggggagc accttaaaat cagccgcttc cgcttcgctg gaaaccgctc
351  cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451  ggccctgccg acagcataga cctgcccgcc gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaacctgct
551  atctcgaacg cctcaacggc gcataccggt acgaccgtaa agggcacggc
601  ctcgacctga aggcgcgga cagccgtgg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaagcgaa accatacaca gtacggcgcg gctgagcggc
751  agcctgaagg atgtgcgagc cgaactgacg atcgacggcg gcaatatccg
801  ccttcggga aaatccgtca tccaccggt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgcccgatgc cgggctgaat ttcgacctga ccgccatccc
951  gtcgttttca gacggcatcg cgctggaagg ctgcctcgat ttgaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tccccgtccg tcaggttttg
1051 ggcggccttg tcatccggca ggacggcacg gtgcatacgc gcaatacgtc
1101 cgccgccctg ctcgacggg gcggcatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaatcc cgtcggcgcg
1201 gaagacgtgc tgcaaacgc gttcaaggc aggttggagc gcagcatcgg
1251 catcgcgcc acgaccgcct cgcccaaat ctcttggcaa ctcgccaccg
1301 gcaaggcacg cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtggt cgacacggtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct alctcgagct gtttaagac cgctgtctca
1451 agctggacat ccgttcccgc gcattcgacc ctccgcgcat cgatccgcaa
1501 tttccggcag gcaatatcaa cggttcgatt catcttgcg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt ttgcccgtt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcgcgc ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggtctt ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttacc ccgtttcggt ttcggaactc cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgatgt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggaacagcg cgagacatcc
1901 gttcgctcga ttttaccctc aaaggctcac ccggcacaa gcccgcgatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcgggcg gcgcgcggtt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggagc gcaaacggt caaactcgat
2101 ttggacgctt caggcgcat caacagggaa cttaccgat ggaaggcag
2151 catcggcac ctcgacatcg gcggcgcat caacctcaag ctgcaaaccc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaagc tgcggcaaat
2251 tggcaggcaa tgggcggcag cctcaacctg caacactttt cttgggacag
2301 gaaaaccggc atatcggcaa aaggcggcgc acgcgcgctt cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgccca cgggcacaa cgcgcgggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgctttt aaaaacgacc catcggaatc
2551 ctgcttgacg gcggcgcgcg ttteggacgg attaacgcg atttgggcat
2601 cggcaacgcc ttcggcggca atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ccttcccgcg ttgggcgcat tgaagccctt tctgcccgcc
2701 gccgcgcaaa acattaccg cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaaacggt ctcttcgat
2851 accgcacctt tgggcggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccg tcggacaaac cgtcaaaagg agcctgaatg
2951 ccgccgtaac cctcggcggc agcatcgccg acccgcaact gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctcggtt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaaggagcg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcgcgcgcg tgttcgacaa
3201 ataccgcatc ctgtcccgcc ccaaccgcg cctgacggtt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgac aggggctggt cggttcgcaa aaatcctcga tgcggtccgt
3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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649

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3451 ttctccggct acggcgcgga cgttaccata ggcggaacac tgacctgac
3501 cgcgcaaccg ggcggaatg tgcgtgggt gggcacggc cgcgcatca
3551 aagggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcctt tccccgcgct gtgcgggctt ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcactct caaccgtgcc ggcagcgga gcagcgcgga
3801 caatgcccgc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacag tgctgacctg
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgct aaactgattt accgctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacgcaaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MDTTPTPTD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSLEL RRLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSGSASVG LKPPALDPA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGINRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGS LD LENTKAGFAD RINGIPVRQVL
351 GGFVIRQDGT VHIGNTSAA L GRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFCG RLDGSIGIG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSPRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPC TFNGVPIACS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLLNL ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFTDLSG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAHVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSIGI LDIGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSLLN QHFSWDRKTG ISAKGGARGL HIAELHNF EK PPFEHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNITGSLN ASAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSD
951 TAPLGRLNL TVADAEAFRN FLPVQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDN SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVDPDV IGAVFDKYRI LSRPNRRLTV SGNTRLRYS P OKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGGD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GKKLTLTAAQ GGNVRGVGT V RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVAGAVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA L SAAAGALLA QINDRIGLV BDLGFTSKRS
1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGY YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1 ATGACCGATA CCGCACCGAC AGATACCGAT CCGACCGAAA ACGGCACGGC
51 CAAATGCCC TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCG3CG GCACTGCTGT CTGTCCTGAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGGCGTAAA CATTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAAAT CAGCCGCTTC CGTTCGCGT GGAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAAGC CCCGCCGCTC
451 AGCCTTCCC ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCGTGG AGCAGTTCTG CGGGGGCGGC
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG CTTGACGGC
751 AGCCTGAAGG ATGTGCGCGC GAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTC ACGCGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA
1051 GCGCGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGCGCGC
1201 GAAGACGTAC TGCAAAACGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACSACCGCCT CGCCCAAAAT CTCTTGGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACC CTTGCGCAT CGATCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAAGTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGCGAGT GCGGACATTG TTTACGAGTC CCGCCACCTT
1651 CACCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAACAGAA
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCAGCA
1751 CCGATTATC CCGTTTCGGT TTCGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CTTTCCGGC GCGGCGCGCA ACCTGCACAT CCGCAAGGCG GCAGACATCC
1901 TTGCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
1951 CCGCGCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGCGGT
2001 TGTGATACCG GCGGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTTCAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCAT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TGCGGCAAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGCGAG GCTTTGGGTT
2501 TGAACGCAAT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGGCGG TTTGCGGCGG ATTAACGCGC ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GGCGGCAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 TCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGG AGCCTGAATG
2951 CCGCGCTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGTAATCG
3101 ACAGCCTGAA ATTCGGGCAC GAAGGGACGG CCGAACTCTC CGGTACGGTC
3151 GGTATGGAAG ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCGACGGTT TCCGGCAACA
3251 CCGGCTGCG CTATTCGCGC CAAAAGGCA TATCCGTTAC CCGCATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTGCGAA AATCCTCGA TGCCGTCGCT
3351 GCGGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGCGGCGAC
3401 CGCTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TACGGGGCGT GGGCAGGTC CCGTCATCA
3551 AAGGCGTTA TAAGCATAAC GGGCAGGATT TGACATTAC CAAAGGCAG
3601 GTCTCCTTTG TCGGCGCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GCGAGCCTCA
3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGC GGCAGCGCA GCAGCGGCA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAATCA
3851 ACGACCGCAT CCGGCTG3TG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CCGCAAAACA CTGACCG3CA AACTCTACAT CGGCTACGAC TACAGCATCT
4001 CCAGCGCGGA ACAGTCC3TC AACTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTG TCGGGCGGCG AGCTGACATA

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m285.pep

1	NTDTAPTDTD	PTENGTRKMP	SEHRPTPPAK	KRRPLLKLSA	ALLSVLILAV
51	CFLGWLAGEF	AGLRFLGLYQI	PSWFGVNISS	QNLKGTLLDG	FDGDNWSJET
101	EGADLKISRF	RFAWKPSLME	KRSLHITEIS	AGDAIAVTKP	TPPKEERPEL
151	SLPDSIDLPA	AVYLDRFETG	RISMKGAFDK	QTVYLERLDA	SPPYDRKGHR
201	LDLKAADTPW	SSSSGAASVG	LKKPFALDTA	IYTKGGLEGK	TIHSTARLSL
251	SLKDVRAELA	IDGGNIRLSG	KSVIHPEFAES	LDKTLEEVLV	KGFENINPAAF
301	VPSLPDAGLN	FDLTAIPSF5	DGIALEGSLD	LENTKAGFAD	RNGIPVQRVL
351	GGFVIRQDGT	VHGTNTSAAL	LGRGGIRLSG	KIDTEKDOLD	LNGINSVGA
401	EDVLQTAFCG	RLDGSIGIGG	TTASPKISWQ	LGIGTARTDG	SLAIASDPAN
451	GQRKLVLVDTP	NIAGQGSFLT	AQGYLELFKD	RLLGLDIRSR	AFDPSRIDPQ
501	LPAGNINGSI	NLAGELAKEK	FTKGMRFLPG	TFNGVPIAGS	ADIVYESRHL
551	PRAAVDLRLG	RNI1KTDGGF	GKKGDRNLNL	ITAPDLSREF	FLAGLSLNVH
601	GHLSGDLDGG	IRTFETDLSG	AARNLHIGKA	ADIRSLDFTL	KGSPDTSRPI
651	RAD1KGSRLS	LSGGAAVVDT	ADLMLDGTGV	QHRTIATHAM	TLDGKPFKFD
701	LDASGGINRE	LTRWKGSGIGI	LDIGGAFFNLK	LQNRMTLEAG	AERVAASAAAN
751	WQAMGGSXLN	QHF5WDKKTG	ISAKAGGAHGL	HIAELHNFVK	PPEFHNLVLN
801	GDWDVAYGRN	ARGYLNISRQ	SGDAVLPGGQ	ALGLNAFSLK	TRFQNDRIGI
851	LLDGGATGRG	INADLGTANA	FGGNMANAPL	GGRIITASLPD	_GALKPFLPA
901	AAQNGITGSL	AAAQIGGRVG	SPSVNAAVNG	SSNYGKINGN	ITVQGSRSGS
951	TAPLGGRLNL	TVDAAEVERN	FLPVGQTVKG	SLNAAVTLGG	SIADPHLFGD
1001	INGDKLYYRN	QTQGIILDNG	SLRSHIAGRK	WVIDSLKFRH	EGTAELSGTV
1051	GMENSGPLVD	IGAVFDKYRI	LSRPNRRLTV	SGNTRLRYSF	QKGISVTMGI
1101	KTDQGLFGDS	KSSMPSVLGD	VSVLGEVKKE	AAAPLPVNMI	LTLDLNDGIR
1151	FAGYGADVTI	GKMLTLTAQS	GGSVRGVGTV	RVIKGRYKAY	QDQLDITKGT
1201	VSVVGPLNDP	NLNIRAERRL	SPVGAGVEIL	GSLNSPRITL	TANEFMSEKD
1251	KL5WLILNRA	GSGSGDGNAA	LSAAAGALLA	GQINDRIGLV	DDLGFTSKRS
1301	RNAQTGELNP	AEQVLTVGKQ	LTGKLYIGYE	YSISAAEQSV	KLIYRLTRA1
1351	QAVARIIGRS	SGEGLTYTIR	FDRFSGSDKK	DSAGNGKGK*	

Homology with a predicted ORF from *N. gonorrhoeae*

m285/q285 96.5% identity in 1389 aa overlap

m285.pep	10	20	30	40	50	60
	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRRPLKLKLSAALLSVLILAVCFLGWLAGTE					
g285	: : :					
	MTDTTPTDTPDPTENGTRKMPSEHRPAPPKRRRPLKLKLSAALLSVLILAVCFLGWIAGTE					
	10	20	30	40	50	60
m285.pep	70	80	90	100	110	120
	AGLRFGLYQIPSWFGVNISSQNKGTLDDGFDGDNWSIETEGADLKISRFRFAWKPSSELM					
g285						
	AGLRFGLYQIPSWFGVNISSQNKGTLDDGFDGDNWSIETEGADLKISRFRFAWKPSSELM					
	70	80	90	100	110	120
m285.pep	130	140	150	160	170	180
	RRSLHITEISAGDIAIVTKPTPPKEERPPPLSLPDSIDLPAAVYLDRFETGKISMGKAFDK					
g285	: : :					
	RRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAVYLDRFETGKISMGTFFDK					
	130	140	150	160	170	180
m285.pep	190	200	210	220	230	240
	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
g285	: : : : : : : : :					
	QTVYLERLNAAYRYDRKGHRDLKAADTPWSSSSGASVGLKKPFALDTAIYTKGGFGE					
	190	200	210	220	230	240
m285.pep	250	260	270	280	290	300
	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHHPAESLDKTTLEEVLVKGFNINPAA					

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g285						
	TIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF					
	250	260	270	280	290	300
m285.pep	310	320	330	340	350	360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT					
g285						
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT					
	310	320	330	340	350	360
m285.pep	370	380	390	400	410	420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG					
g285						
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGINSVGAEDVLQTAFKGRLDGSIGIGG					
	370	380	390	400	410	420
m285.pep	430	440	450	460	470	480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD					
g285						
	TTASPKISWQLGTGTARTDGS LPIASDPANEQRKLVFDTVNISAGEGSLTAQGYLELFKD					
	430	440	450	460	470	480
m285.pep	490	500	510	520	530	540
	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS					
g285						
	RLKLDIRSRAFDPSRIDPQFPAGNINGSIHLAGELAKEKFTGKMRFLPGTFNGVPIAGS					
	490	500	510	520	530	540
m285.pep	550	560	570	580	590	600
	ADIVYESRHLPRAAVDLR LGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR					
g285						
	ADIVYESRHLPRAAVDLR LGRNIVKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR					
	550	560	570	580	590	600
m285.pep	610	620	630	640	650	660
	GHLSGDLGGIRTFFETDL SGAARNLHIGKAADIRSLDFTLKGS PDTSRPIRADIKGSRLS					
g285						
	GHLSGDLGGIRTFFETDL SGTARNLHIGKAADIRSLDFTLKGS PGTSRPMRADIKGGRLS					
	610	620	630	640	650	660
m285.pep	670	680	690	700	710	720
	LSGGAAVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFLDASGGINRELTRWKSGSIGI					
g285						
	LSGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGKPFKFLDASGGINRELTRWKSGSIGI					
	670	680	690	700	710	720
m285.pep	730	740	750	760	770	780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSINLQHF SWDKKTGISAKGGAHGL					
g285						
	LDIGGAFNLKLQNRMTLEAGAEHVAASAANWQAMGGSINLQHF SWDRKTGISAKGGARGL					
	730	740	750	760	770	780
m285.pep	790	800	810	820	830	840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLP GGQALGLNAFSLK					
g285						
	HIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYLNISRQSGDAVLP GGQALGLNAFSLK					
	790	800	810	820	830	840
m285.pep	850	860	870	880	890	900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFPLPA					
g285						
	TRFQNDRIGILLDGGARFGRINADLGIGNAFGGNMANTPLGGRITASLPDLGALKPFPLPA					
	850	860	870	880	890	900
m285.pep	910	920	930	940	950	960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLN					

	910	920	930	940	950	960
g285	AAQNITGSLNASAQIGGRVGS	SPSVNA	AVNGSSNYGKINGNITV	GQSR	SFDTAPLGGRLNL	
m285.pep	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AAVT
g285	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AAVT
m285.pep	SLRSH	IAGRK	WVIDSL	KFRHE	GTAEL	SGTV
g285	SLRSH	IAGRK	WVIDSL	KFRHE	GTAEL	SGTV
m285.pep	SGNTR	LRYS	PQKGI	SVTGM	IKTDQ	GLFG
g285	SGNTR	LRYS	PQKGI	SVTGM	IKTDQ	GLFG
m285.pep	LTLDL	NDGIR	FAGY	GADV	TIGG	KLTL
g285	LTLDL	NDGIR	FAGY	GADV	TIGG	KLTL
m285.pep	VSFVG	PLNDP	NLNIRA	ERRLS	VPVG	AGVE
g285	VSFVG	PLNDP	NLNIRA	ERRLS	VPVG	AGVE
m285.pep	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDR	IGLV
g285	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDR	IGLV
m285.pep	LTGKL	YIGVE	YSISSA	EQSV	KLIY	RLTR
g285	LTGKL	YIGVE	YSISSA	EQSV	KLIY	RLTR
m285.pep	DSAGN	GK	GKX			
g285	DSAGN	GK	GKX			

a285.seq

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1 ATGACCAGATA CCGCACCGAC AGATAACCGAT CCGACCCGAA ACGGCCACGG
51 CAAATGCGCG TCTGAACACC GCCCTACCCC CCGGGCAAAA AAACGCCGCC
101 CCAATGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCTGAT TTTGGCAGTA
151 TGTTTTCTCG GCTGGCTCGC CGGACCGGAA CGCGGTTTGC GCTTCGGGCT
201 GTACCAAAATC CCGTCTTGTT TCGGCGTAAA CATTCTCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGGT GGAACCGTCC
351 CGAATGATG CGCCGCGAGC TGCACATTAC CGAAATTTCC GCCCGCGACA
401 TCGCCATCGT TACCAAAACG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCGCTCGGCC CGCGTCTATC TCGACCGGTT
501 CGAGACGGCG AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACC GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTCGACTCGA AGGCTGCCGA CACGCCGTGG AGCAGTTCTG CGGGGTGACG
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651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGECTTC
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCG GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGGAANAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGTCGGCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAATC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTGAGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCGCGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTCGACC CTTGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTCCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCAACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACACAGA
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC
1751 CCGATTATAT CCGTTTCGGT TTCGGAATCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CTTTCCGGCG GCGGCGCGCA ACCTGCACAT CCGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGEGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCGBA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGACGCTT CAGGCGGCAT CAACAGGGA CTTACCCGAT GGAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCGGCT GCGGAACGCG TGGCGGCAAG TGCGGCAAAAT
2251 TGGCAGGCAA TGGGCGGCG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGCG ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTTGACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGCGCA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTGCGGCGG ATTAACGCGG ATTTGGACAT
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCGTCCG TCAATGCCGC CGTCAACGCG AGCAGCAACT
2801 ACGGGAAAAT CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCGC ATCCGCACTT GGGCGGCGAG
3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CCGAACTCTC CCGTACGGTC
3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCGC CTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAGGCA TATCGGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTCGCAA AAATCCTCGA TGCCGTCCGT
3351 CCGGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCGC
3451 TTCGCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAC TGACCCTGAC
3501 CGCCCAATCG GCGGAAGCG TGCGGGGCGT GGGCAGGTC CGCGTCATCA
3551 AAGGCGGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCTTTG TCGGCGCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCGCTCG GTGCGGGCGT GGAATATTG GGCAGCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAANAAGAC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATGCGGCC CTGTCCGCG CCGCGGCGC GCTGCTTGCC GGGCAAAATCA
3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT

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3951 CCGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTG CCCGTATCGG CAGCCGTTCG TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
1 MTDAPTDTPT PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWLAGE AGLRFGLYQI PSWFGVNIS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRLHTEIS AGDIAIVTKP TPKKEERPPL
151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTFW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGLD LENTKAGFAD RNGIPVRQVL
351 GSEFVRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSIT AQGYLELEFD RLLKLDIRSR AFDPSRIDFQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIKTDDGGF GKKGDRNLN ITAPDLRSFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDTL KGSPDTSRPI
651 RADIKGSRLS LSGGAEVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
801 GDWDVAYGRN ARGYLNSRQ SGDAVLPQGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLA
901 AAQNTIGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQSRSD
951 TAPLGGRNL TVADAIEVERN FLPGQTVKG SLNAAVTLGG SIADPHLGG
1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGLTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTPTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDTAPTDTPTPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
a285	AGLRFGLYQIPSWFGVNISQNLKGTLLDGFDDGDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
m285.pep	RRLHTEISAGDIAIVTKPTPKKEERPPLSLPDSIDLPAAYVLDREFETGKISMKGAFDK					
a285	RRLHTEISAGDIAIVTKPTPKKEERPPLSLPDSIDLPAAYVLDREFETGKISMKGAFDK					
	130	140	150	160	170	180
m285.pep	RRLHTEISAGDIAIVTKPTPKKEERPPLSLPDSIDLPAAYVLDREFETGKISMKGAFDK					
a285	RRLHTEISAGDIAIVTKPTPKKEERPPLSLPDSIDLPAAYVLDREFETGKISMKGAFDK					
	130	140	150	160	170	180
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	190	200	210	220	230	240
m285.pep	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLTKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLTKTLEEVLVKGFNINPAAF					
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLTKTLEEVLVKGFNINPAAF					
a285	TIHSTARLSGSLKDVRAELADGGNIRLSGKSVIHPFAESLTKTLEEVLVKGFNINPAAF					

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a285	TIHSTARLSGSLKDVRAELAI	DGGNIRLSGKSVIH	PF	AE	SLDKTLEEVLVKGF	NINPSAF
	250	260	270	280	290	300
	310	320	330	340	350	360
m285.pep	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAGFADR	NGIPVRQVLGGF	VIRQDGT	
a285	VPSLPDAGLNFDLTAIP	SFSDGIALEGS	LDLENTKAGFADR	NGIPVRQVLGSF	VIRQDGT	
	310	320	330	340	350	360
	370	380	390	400	410	420
m285.pep	VHIGNTSAALLGRG	GIRLSGKIDTEKD	ILDNLNIGINSV	GAEVDVLTAFKGR	LDGSIGIGG	
a285	VHIGNTSAALLGRG	GIRLSGKIDTEKD	ILDNLNIGINSV	GAEVDVLTAFKGR	LDGSIGIGG	
	370	380	390	400	410	420
	430	440	450	460	470	480
m285.pep	TTASPKISWQLG	IGTARTDGLAI	ASDPANGQRKL	VLDTVN	AAGQGS	SLTAQGYLEFKD
a285	TTASPKISWQLG	IGTARTDGLAI	ASDPANGQRKL	VLDTVN	AAGQGS	SLTAQGYLEFKD
	430	440	450	460	470	480
	490	500	510	520	530	540
m285.pep	RLKLDIRSRAFD	PSRIDPQLPAG	NINGSINLAGEL	AKEKETGKMR	FLPGTFNGV	PIAGS
a285	RLKLDIRSRAFD	PSRIDPQLPAG	NINGSINLAGEL	AKEKETGKMR	FLPGTFNGV	PIAGS
	490	500	510	520	530	540
	550	560	570	580	590	600
m285.pep	ADIVYESRHLPR	AAVDLRLGRNI	IKTDGGFGKKG	DRNLNITAPDL	SRFGGLAGSL	NVR
a285	ADIVYESRHLPR	AAVDLRLGRNI	IKTDGGFGKKG	DRNLNITAPDL	SRFGGLAGSL	NVR
	550	560	570	580	590	600
	610	620	630	640	650	660
m285.pep	GHLSGDLGGIRT	FETDLGAARNL	HIGKAADIRSL	DFTLKGSPDTS	SRPIRADIKG	SRLS
a285	GHLSGDLGGIRT	FETDLGAARNL	HIGKAADIRSL	DFTLKGSPDTS	SRPIRADIKG	SRLS
	610	620	630	640	650	660
	670	680	690	700	710	720
m285.pep	LSGGAHVDTADL	MDGTGVQHRIR	THAAMTLDGK	PFKFDLDASG	GINRELTRWK	GSIGI
a285	LSGGAHVDTADL	MDGTGVQHRIR	THAAMTLDGK	PFKFDLDASG	GINRELTRWK	GSIGI
	670	680	690	700	710	720
	730	740	750	760	770	780
m285.pep	LDIGGAFLNKLQ	NRMTEAGAER	VAAASAAWQAM	GGSNLQHFSW	DKKTGISAKG	GAHGL
a285	LDIGGAFLNKLQ	NRMTEAGAER	VAAASAAWQAM	GGSNLQHFSW	DKKTGISAKG	GAHGL
	730	740	750	760	770	780
	790	800	810	820	830	840
m285.pep	HIAELHNFFKPP	FEHNLVLNGD	WDVAYGRNARG	YLNISRQSGDA	VLPGGQALGL	NAFSLK
a285	HIAELHNFFKPP	FEHNLVLNGD	WDVAYGRNARG	YLNISRQSGDA	VLPGGQALGL	NAFSLK
	790	800	810	820	830	840
	850	860	870	880	890	900
m285.pep	TRFQNDRIGILL	DGGARFGRINAD	LGIANAFGGN	MANAPLGGRIT	ASLPDLGALK	PKFLPA
a285	TRFQNDRIGILL	DGGARFGRINAD	LGIANAFGGN	MANAPLGGRIT	ASLPDLGALK	PKFLPA
	850	860	870	880	890	900
	910	920	930	940	950	960
m285.pep	AAQNITGSLNAAQ	IGRVGSPVNA	AVNGSSNYGK	INGNITVGQSR	SFDTAPLGGR	LNL

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a285	AAQNITGSLNAAQIGGRVGS	PSVNA	AVNGSS	NYGKING	NITVGQ	SRSFDTAP	LGGRLNL
	910	920	930	940	950	960	
m285.pep	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	IADPHL	GGSINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGS	IADPHL	GGSINGDKLYYRNQTQGIILDNG
	970	980	990	1000	1010	1020	
m285.pep	SLRSHIAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD	DIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD	DIGAVFDKYRILSRPNRRLTV
	1030	1040	1050	1060	1070	1080	
m285.pep	SGNTRLRYSP	QKGISV	TGMIKT	DQGLFG	SQKSSM	PSVGD	DDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYSP	QKGISV	TGMIKT	DQGLFG	SQKSSM	PSVGD	DDVVVLGEVKKEAAAPLPVNMN
	1090	1100	1110	1120	1130	1140	
m285.pep	LTLDLNDG	IRFAGY	GADVT	IGGKLT	LTAQSG	SVRGV	GTVRVIKGRYKAYGQDLDITKGT
a285	LTLDLNDG	IRFAGY	GADVT	IGGKLT	LTAQSG	SVRGV	GTVRVIKGRYKAYGQDLDITKGT
	1150	1160	1170	1180	1190	1200	
m285.pep	VSFVGPLND	PNLNIRA	ERRLS	SPVGAG	VEILGS	LNSPRIT	LTANEPMSEKDKLSWLIILNRA
a285	VSFVGPLND	PNLNIRA	ERRLS	SPVGAG	VEILGS	LNSPRIT	LTANEPMSEKDKLSWLIILNRA
	1210	1220	1230	1240	1250	1260	
m285.pep	GSGSSGDNA	ALSAAAG	ALLAGQ	INDRIG	LVDLGF	TSKRSR	NAQTGELNPAEQVLTVGKQ
a285	GSGSSGDNA	ALSAAAG	ALLAGQ	INDRIG	LVDLGF	TSKRSR	NAQTGELNPAEQVLTVGKQ
	1270	1280	1290	1300	1310	1320	
m285.pep	LTGKLYIG	EYSSIS	SAEQSV	KLIYRL	TRAIQA	VARIGS	RSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYIG	EYSSIS	SAEQSV	KLIYRL	TRAIQA	VARIGS	RSSGGELTYTIRFDRFSGSDKK
	1330	1340	1350	1360	1370	1380	
m285.pep	DSAGNGK	GKX					
a285	DSAGNSK	GKX					
	1390						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAACATTT CCTCCCAAA CTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAAAATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCTTGCCC GATGCCGGGC TGAATTTTGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CCGCATCCCC GTCCGTCAGG TTTGGGCGG
951 CTTTGTATCA CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCGTGCTCGG ACGGGCGGGC ATCAGGCTGT CCGGCAAAA' CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCTG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 GCGGAAACTG GTGTTTGACA CCGTCAACAT CTCGCGCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATT CGACCTTCG CGCATCGATC CGCAATTTC
1401 GGCAGGcgat atCAACGGTT CGATTATCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTCG CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCCGG
1551 CCGCGCGGTC GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCITCGGCAA AAAAGGCGAC CCGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGG GATTGAGCG GCGGCATCCG AACCTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCCGTTTCG
1801 CTCGATTTTA CCTCAAAGG CTCACCCGGC ACAAGCGGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCTGTG GCGCGGCGCG GCGGTGTCTG
1901 ATACCGCGCG CCGTACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGACGGCAAA CCGTTCAAAC TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACCCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAA
2201 CCGCATATAT GGGAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CCGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCAGCG GGCAGGCTTT GGGTTTGAC
2401 GCATTTTCTT TGAACGCGC CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACCGCTTCGG CCGCAATATG GCAATACAC CGCTCGCGCG CAGGATTACA
2551 GCCTCCCTCT CCGACTTGGG CGCATTTGAG CUCCTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCCT CCGGCAAAAT GCGGACGGG
2651 TAGGCTCTCG GTCCGTCAAT GCCGCGCTCA ACGGTAGCAG CAACTACGGG
2701 AAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGG
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTC CCGGCAGCAT CGCGACCCG CACTTGGGCG CAGTATCAA
2901 CGCGGACAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGGACA
2951 ACCGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAACACAGC GTGCCGATG TCGATATCGG CCGGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CCGCGCTGA CCGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAA
3201 TGATCAGGGG CTGTTTCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACCATGTCGT CGTATTGGG GAAGTCAAGA AAGAGCGGCG GGCATCGCTC
3301 CCCGTCRATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CCGCTACGGC GCGGACGTTA CCATAGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AATGTGCGT GGGGTGGGCA CCGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTCCGG CCGCTCAACG ACCCAAACCT GAACATCCGC GCCGAACGCC
3551 CCCTTTCCCC CGTCGTGCGG GCGGTGAAA TATTGGGCG CTTCAACAGC
3601 CCGCGCATTA CGTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTGCGCTC ATCTCAACC GTGCGGCGAG CCGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCA GCGCGCTGCG TTGCGGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGGAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CCGCAAATC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAAC TATTACCGG CTGACCCGCG CCATACAGCG
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCCTCTTC GGTTCGGACA AAAAGACTC GCGAGGAAAC
4051 GGCAAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

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1  LKLSAALLSV LILAVCFGLW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLIDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERINAAYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGDN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLNIGI NSVGAEDVLQ TAFKGRDLGS IGIGGTTASP KISWQLGTGT
401 ARTDGLAIA SDPANEQRKL VFDTVNISAG EGSILTAQYL ELFKDRLLKL
451 DIRSRAFDPG RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLGGGIRTFE TDLSTGARNL HIIGKAADIRS
601 LDFTLKSGSPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDSK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAAWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 NHFFKPPFEH NLVLNGDWDV AYGHNARGYL NISROSGDVA LPGAQHLGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNASHAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVSO SRSFDTAPLG GRNLNTVADA EAFRNLFPVG QTVKGSINAA
951 VTLCGSIADP HLGGSINGDK LYYRNQTQGI ILDNGLSRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDVVVLG EVKKEAASL
1101 PVNMNLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR VGTVRVIRK
1151 RYKAYQBLD ITKGTVSFVG PLNDPNLNR AERRLSPVA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDLGEF TSKRSRQAOT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AECQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLE GSKKDSAGN
1351 GKGA*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTC TTGTTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAG CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCGCT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG CGGCGCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCGAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGGCG AATCATTGGA TAAACATTG
751 GAAGAAATAC TGGTCAAAGG GTTCAACATC AATCCGCGCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGAC TGAATTTGCA CCTGACCCCG ATCCCGTCGT
851 TTTACAGACG CATCGCGCTG GAAGGTTCCG TCGATTGGA AAACACCAA
901 CGCGGCTTTG CCGACCGCAA CGGCATCCCC GTCGCTCAGG TTTTAGGCGG
951 CTTTGTCATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCG
1001 CCTGTCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAAT TATAGGCATC AACTCCGTCG CGCGGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAC CGCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 CGCGCACGCG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 CGGAAACTG GTGCTCGACA CCGTCAACAT CGCGCCGCGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CGGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCCGCGCT GATTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGT GATTGGACG CGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGCGC CGGCAACCTG CACATCGGCA AGGCGGCGAG CATCCGTTCC
1801 CTGATTTCAC CGCTCAAAGG TTCGCCGAC ACAAGCGGCC CGATACCGCG
1851 CGACATCAAA GGCAGCGGCC TTTGCTGTC GGGCGGAGCG CGCGTTGTCG
1901 ATACCGCGCA CTTGATGCTG GACGGCACGG GCGTGACGCA CCGCATCCCG
1951 ACACACCGCG CATGACGCT SGATGGCAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGCGCGC SCATTCAACC TCAAGTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTCCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGGAACAC AATCTGGTTT TAAACCGCGA
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2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAAAT GCGGACGCGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCGTCA ACGGCAGCAG CAACTACGGG
2701 AAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGACGCTT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CCGCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACCGCTCGCT GCGTTCGCAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGTA CGGTCGGTAT
3051 GGPAAACAGC GGACCCGATG TCATATCCG CGCGGTGTTT GACAAATACC
3101 GCATCCTCTC CCGCCCAAC CGCGCCTGA CGGTTTCCGG CAACACCGCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAACAA
3201 GGTATCAGGG CTGTTCGTT CGCAAAATC CTGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGCG GGCACCGCTC
3301 CCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGCGCG AAGCGTACGG GCGGTGGGCA CGGTCCGCT CATCAAAGG
3451 CGTTATAAGG CATACGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGG GCGGTGAAA TATTGGCAG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGCTC ATCCTCAACC GCGCCGCGAG CGGCAGCAGC GGCAGCAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GGCAGAACTC ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CCGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CCGGAACAGT CCGTCAAACT GATTACCGG CTGACCGCGC CCATACAGGC
3951 GGTGCGCGT ATCGGCGGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1  LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFCDGN WSIETEGADL KISRFRPAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAEALIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPAAFPVSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP RVQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 UHSKAFDPS KIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLG DLDGGIRTFE TDLGGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRN
701 TLEAGAERVA ASANWQAMG GSNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVQ SRFDTPALG GRNLTVADA EVFRNPLPVG QTVKGSLNAA
951 VTLGGSIADP HLGGISINGDK LYRNTQTQGI ILDNGLSLSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTQDQ LFGSQXSMP SVGDVVVLG EVKKEAAAPL
1101 PVNMNLTIDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAQIND
1251 RIGLVDDLGF TSKRSRNAOT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRFS GSKDKDSAGN
1351 GKCK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

661

g285-1.pep	LKLSAALLSVLILAVCF LGWIAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN
m285-1	LKLSAALLSVLILAVCF LGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS
	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
	IDLPAAVYLDRFETGKISMGKTFDKQTVYLERLNAAARYDRKGHRDLKAADTPWSSSSG
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
	PFAESLDKLTLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
m285-1	PFAESLDKLTLEEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLDLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
	AGFADRNGIPVRQVLGGFVIRQDGTVHIGNTSAAALLGRGGIRLSGKIDTEKDILDNLIGI
m285-1	AGFADRNGIEVRQVLGGFVIRQDGTVHIGNTSAAALLGRGGIRLSGKIDTEKDILDNLIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
	NSVGAEDVLQTAFAKGRLDGSIGIGGTTASPKISWQLGTGTARTDGS LAIASDPANEQRKL
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGGTTASPKISWQLGIGTARTDGS LAIASDPANGQRKL
	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSPRIDPQFPAGDINGSIHLAGE
m285-1	VLDTVNIAAGQGS LTAQGYLELFKDRLLKLDIRSRAFDPSPRIDPOLPAGNINGSINLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRRAVDLRLGRNIVKTDGGFGKKGD
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRRAVDLRLGRNIIKTDGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRT FETDLSGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRT FETDLSGAARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
	LDFTLKGSPGTSRPMRADIKGGRLSLSGGA AVVDTAGLTLEGTGAQHRI RTHAAMTLDGK
m285-1	LDFTLKGSPGTSRPIRADIKGSRLSLSGGA AVVDTADLMLDGTGVQHRI RTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
	PFKLDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRM TLEAGAEHVAASAANWQAMG
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRM TLEAGAEHVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
	GSLNLQHFSWDRKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
m285-1	GSLNLQHFSWDRKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSLNAAVTLGSSIADP					
m285-1	KINGNITVQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSLNAAVTLGSSIADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVVKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVVKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANPEMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1 CTGAAGCTGT CGGCGGCACT SCTGTCTGTT CTGATTTTGG CAGTATGTTT
51 CCTCGGCTGG CTCGCCGGCA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATCGCGCG CAGCCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCAGACAG ATAGACCTGC CTGCCGCGGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTC ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGCGGCAAT ATCCGCTCT
701 CGGGAAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTCGA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CGCTGTCTCG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG CGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 CGGGAACATG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGGA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATRAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTCAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTTCGGCA AAAAGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CTTTTCCGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGCGCGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGCGGAGCGG GAGGTTGTCG
1901 ATACCGCCGA CCTGATGCTC CACGGCACCG CCGTGCACCA CCCATCCGCC
1951 ACACACGGCG CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGCGG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGCAC CGCTCGGCGG CAGGATTACC
2551 CGCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAT GCGGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAAGC GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG CCGGAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAC CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAATTTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCGGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCCTGA CGGTTTCCGG CAACACCGCG
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CGCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTCCG
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CACACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGC CCGCTCAACG ACCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAT TATTGGGAG CCTCAACAGT
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAT AAGACAAGCT
3651 CTCCTGGCTT ATCCTCAACC GCGCCGGCAG TGCGAGCAGC GGCACAAATG
3701 CCGCCCTGTG CGCAGCCGCC GCGCGCTGCT TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCCGCGCA ACAGGTGCTG ACCGTGCGCA
3851 AACAACGTAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACCT GATTACCAGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGTCTCTCC GGTTCGGACA AAAAAGACTC CGCGGAAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

664

a285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAEALIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLRGG IRLSGKIDTE
351 KDILDNLIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLSLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLSC DLDGGIRTFE TDLSCAARNL HIGKAADIRS
601 LDFTLKGSFD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHFIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRN
701 TLEAGAERVA ASANWQAMG GSLNLQHFWS DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGFRT
851 ASLPDLGLTK PFLPAAQNI TGSNLAAQI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLITVADA EVFRNPLPVG QTVKGSNLAA
951 VTLGGSIAADP HLGGSSINGDK LYRNTQTOGI LDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDDVVVLG EVKKEAAPL
1101 PVMNMLTDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIK
1151 RYKAYQDDLD ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGOIND
1251 RIGLVDDLCF TSKRSRNAQT GELNPAEQVL TVGQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELADGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELADGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
m285-1	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGCCIRLSCKIDTEKDILDNLIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLRGCCIRLSCKIDTEKDILDNLIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGLSLAASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGLSLAASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTACGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE			
m285-1	VLDTVNIAAGQGS	LTACGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE			
	430	440	450	460	470
					480
a285-1.pep	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNI	IKTDGGFGKKGD			
m285-1	LAKEKFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNI	IKTDGGFGKKGD			
	490	500	510	520	530
					540
a285-1.pep	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLDGGI	RTFETDLSGAARNLHIGKAADIRS			
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLDGGI	RTFETDLSGAARNLHIGKAADIRS			
	550	560	570	580	590
					600
a285-1.pep	LDFTLKGS	PDTSRPIRADIKGSRLSLSGGAEVVD	TADLMDGTGVQHRIRTHAAMTLDGK		
m285-1	LDFTLKGS	PDTSRPIRADIKGSRLSLSGGA	AVVD	TADLMDGTGVQHRIRTHAAMTLDGK	
	610	620	630	640	650
					660
a285-1.pep	PFKFDLDASGGINRELTRWKSGIGILDIGGAFNLKLQNRMTLEAGA	ERVAASAANWQAMG			
m285-1	PFKFDLDASGGINRELTRWKSGIGILDIGGAFNLKLQNRMTLEAGA	ERVAASAANWQAMG			
	670	680	690	700	710
					720
a285-1.pep	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770
					780
a285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM				
	790	800	810	820	830
					840
a285-1.pep	ANAPLGGGRITASLPDLGTLKPF	LPAQAQNTIGSLNAAQIGGRVGS	PSVNAAVNGSSNYG		
m285-1	ANAPLGGGRITASLPDLGTLKPF	LPAQAQNTIGSLNAAQIGGRVGS	PSVNAAVNGSSNYG		
	850	860	870	880	890
					900
a285-1.pep	KINGNITVGQSR	SFDTAPLGGRLNLTVA	DAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADP
m285-1	KINGNITVGQSR	SFDTAPLGGRLNLTVA	DAEVFRNFLPVGQTVKGS	LNAAVTLGGS	IADP
	910	920	930	940	950
					960
a285-1.pep	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHIAGRKWVIDSLKFRHEGTAELS	SGTVGMENS		
m285-1	HLGGSINGDKLYYRNQTQGI	ILDNGSLRSHIAGRKWVIDSLKFRHEGTAELS	SGTVGMENS		
	970	980	990	1000	1010
					1020
a285-1.pep	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISV	TGMIKTDQSLFGSQKSSMP			
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISV	TGMIKTDQSLFGSQKSSMP			
	1030	1040	1050	1060	1070
					1080
a285-1.pep	SVGDDVVVLGEVKKAAAPLPVNMNLTLDLNDGIRFAGY	GADVITIGGKLT	LTASGGSVR		
m285-1	SVGDDVVVLGEVKKAAAPLPVNMNLTLDLNDGIRFAGY	GADVITIGGKLT	LTASGGSVR		
	1090	1100	1110	1120	1130
					1140
a285-1.pep	GVGTVRVIKGRYKAYQDLDITKGT	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
m285-1	GVGTVRVIKGRYKAYQDLDITKGT	VSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
	1150	1160	1170	1180	1190
					1200

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSGDNAALSAAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNSKKGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

```

g286.seq
1  atgcagaaca ccggtaccat gatgatcaaa cgcaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgcgcgc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaaacc caaattcccc gtccgcacgc acacgcagga
201 cagtgaaatc aaagatatgg tcgaagaaca cctgcgcgtc atcacgcagc
251 agcaggaaga ggttttgat aggaacaga cgggattcct tgccgaagaa
301 qcaccggaca acgttaaaac aatgtccgc agcaaaaggc atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggt cacatcacac
401 cgggcccgcg caccaaaatc gccacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tyggaaaaca
551 gcaaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601 aagctcggca acacccgggc ggccgtcaac cccgataacc ccaccgccga
651 ttgaaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacccg cacacagcgt taccccaac aaaccgtctc cggcctggcg
751 cgettccaac cgggcacgcc ctacgacctc gacctgtgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattattc cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901 cgaggtaaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcgtcgt ctgggatatg gacaaatacg aaaccacgct
1051 tgccgcggcg atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaaacgcgc
1151 ttctccggcg gcattctgga tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaaatccc cgctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgcaggt tattttctca cgcccgaaaa caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cacgcgacaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc cgctcttccg
1551 tgccgcgtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

```

g286.pep
1  MONTGTMMIK PTALLLPALF EFPAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTKDGAYTV HITPGPRTKI ANVGVAIIGD
151 ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLDQQAAL EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRFGIRFG RQNRLLRLQ LQRLYRLGR LGYQIIRNHA
351 GRRHQPAQL SGQLLDKQRF LQPFDEHKPR KTRLLRRILV CARPRGHRCQ
401 AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDEFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRQ
501 CRCLGADV P QRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq
1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTTATT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCAGACACC
151 GAATCAGTCA AATTAAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCACGCAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACGACG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTTCA CCGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAACTTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGTCGGCA ATACGCAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GGCGACTTTG
701 AAATCACCAG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CCGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAACT CGAAACGGC ATCCGCGCTC ATTGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCGCAACTAT CCGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCA AAACCTCGAA AAACGCGCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGCGG AATTCTCTGC AGAAGGCCGG AAAATCCCCG GCTCGGCTGT
1251 CGATTGGGC AACAGCCACG CCACGATGCT GACCGCTCTT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTCA CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCCGACGTTT CTTACGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCTTTCCGG CGCGGTGTTC CACGATATGG GCGATGCGCG
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTTGC CCGTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep
1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAIGD
151 ILSGNI AEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPIA
201 KLGNTQAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDR LQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIA YDYNNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGN YWTSNVS YNRSTQNL E KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAAGR KIPGSAVDLG NSHATMLTAS WKRL LNNVL HPENGHYLDG
451 KIGTTLGTFL SSTALIRTS A RAGYFFTPEN KKLGT FFIIRG QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRLSGAVF HDMGDAAANE KRMKLKHGSG LGVRWF S PLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

668

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKCLKPKFP					
g286	MONTGTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKCLKPKFP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFALAEAPDNVKTMLRSKGYFSSKVS					
g286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFALAEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m286.pep	LTEKDGAYTVHITPGPRTKIANVGVAIILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
g286	LTEKDGAYTVHITPGPRTKIANVGVAIILGDILSDGNLAEYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m286.pep	WENSKTSVLGAVTRKAYPLAKLGNTOAAVNPDATADLNWVVDVSGRPIAFGDFEITGTQR					
g286	WENSKTSVLGAVTRKGYPLAKLGNTRAAVNPDATADLNWVVDVSGRPIAFGDFEITGTQR					
	190	200	210	220	230	240
	250	260	270	280	290	299
m286.pep	YPEQIVSGLARFQPGMPYDLDDLDFQQALEQNGHYSYGASVQADFRL-QGDRVPVKVSV					
g286	YPEQTVSGLARFQPGTPYDLDDLDFQQALEQNGHYSYGASVQADFRLPRGFRPRQSQRN					
	250	260	270	280	290	300
	300	310	320	330	340	359
m286.pep	TEVKRHKLETGIRLDSEYGLGGKIAYDYNFLNKGYIGSVVWMDMKYETTLAAGISQPRN					
g286	RGQTPQTRNRHPPRFGRFGRQNRRLRLQLQRLYRLGRLGYQIRNHACRRHQPAAL					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1197>:

```

a286.seq
1  ATGCACGACA CCCGTACCAT GATGATTAAA CCGACCGCCC TGCTCCTGCC
51  GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACAC
151 GAATCAGTTA AATTAAAACC CAAATTCCTC GTCCGCATCG ACACGCAGGA
201 TAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCGAGC
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCACCGGACA ACGTTAAAAC AATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCGCGC CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GTGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ACACCCGGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGGACTTTG
701 AAATTACCGG CACGCAGCGT TACCCGAAC AAATCGTCTC CGGCTTGGCG
751 CGCTTCCAAC CGGGCACGCC CTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCCTC GAACAAAACG GGCATTATTC CCGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAGCT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCGGCCGGCA TCAGCCAGCC GCGCAACTAT CCGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGCGCG CATCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCCAGG
1201 CTGGGGGCGG AGTTTCTCGC AGAAGGCCGG AAAATCCCCG GCTCGGATAT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCTCTT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC

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669

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGCGCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCGGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTTCGGG CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

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This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

```

a286.pep
1  MHDTRTMMIK PTALLLPALF FFFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAYTV HITPGPRTKI ANVGVAIGD
151 ILSGDLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLN VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGTPYDL DLLDFQQA EQNGHYS GASVQADFRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG KIAIDYNNL FNKGYSVSV WMDKYETTL
351 AAGISQPRNY RGNWYTNVS YNRSTQNL KRAFGGIWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSDIDLG NSHATMLTAS WKRLNNNL HPENGHYIDG
451 KIGTTLGAFL SSTALIRTS RAGYFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLGAVF HDMGDAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

m286/a286 98.7% identity in 615 aa overlap

      10      20      30      40      50      60
m286.pep MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
a286      MHDTRTMMIKPTALLLPALFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLPKFP
      10      20      30      40      50      60

      70      80      90     100     110     120
m286.pep VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
a286      VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS
      70      80      90     100     110     120

      130     140     150     160     170     180
m286.pep LTEKDGAYTVHITPGPRTKIANVGVAIGDILSDGNLAEYRNALENWQQPVGSDFDQDS
a286      LTEKDGAYTVHITPGPRTKIANVGVAIGDILSDGNLAEYRNALENWQQPVGSDFDQDS
      130     140     150     160     170     180

      190     200     210     220     230     240
m286.pep WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
a286      WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLNVVDSGRPIAFGDFEITGTQR
      190     200     210     220     230     240

      250     260     270     280     290     300
m286.pep YPEQIVSGLARFQPGMPYDLDLLDFQQA EQNGHYS GASVQADFRLQGDRVPVKVSVT
a286      YPEQIVSGLARFQPGTPYDLDLLDFQQA EQNGHYS GASVQADFRLQGDRVPVKVSVT
      250     260     270     280     290     300

      310     320     330     340     350     360
m286.pep EVKRHKLETGIRLDSEYGLGGKIAIDYNNL FNKGYSVSVWMDKYETTLAAGISQPRNY
a286      EVKRHKLETGIRLDSEYGLGGKIAIDYNNL FNKGYSVSVWMDKYETTLAAGISQPRNY
      310     320     330     340     350     360

      370     380     390     400     410     420

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670

m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWIYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKLKHGSGLGVRWFSPAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTREX
a286	SDKKIRWHISLGTREX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID.1199>:

g287.seq

1	atgtttaaac	gcagtgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcgggtggc	gatcgcccga	tgtcaagtcg	gcggacacgc
101	cgtaaaacc	ggccgcccc	gttggtgcty	aaaatgccg	ggaaggggtg
151	ctgccgaaag	aaaagaaaga	tgaggaggca	gcgggcggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcggcag
251	tttcggcaga	aaatacagcg	aatggcggtg	cggaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgcgca
351	atccgcaaat	caaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	ccccgcgtc	aaacctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaatataac
501	gttgaccac	tgtaaaggcg	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaaagta	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacagg	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaaac	acctactcgt	tctgcacggt	cgaggaggtc	gcttccggcc
751	gagattccgc	tgattcccgt	caatcaggcc	gatacgctga	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccgaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cggcggatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttggttg
951	cacggcgtg	tacaacggcg	aagtgtcgca	ttccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aaatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaattc	aaagccgcca	tcgatggaaa	cggttttaag	gggacttgga
1151	cggaaaatgg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gagggaagtgg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaagg
1251	cggattccgc	gtgtttgccc	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQN	MPQNAAESAN	QTGNNQFAGS	SDSAPASNPA	PANGGSDFGF

671

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151  TNVGNSSVID  GPSQNTLTH  CKGDSCNGDN  LLDEEAPSKS  EFEKLSDEEK
201  IKRYKKDEQR  ENFVGLVADR  VKKDGNTKYI  IFYTDKP?TR  SARSRRLPA
251  EIPLIPVNOA  DTLIVDGEAV  SLTGHSGNIF  APEGNYRYLT  YGAEKLPGGG
301  YALRVQGEPA  KGEMLVGTAV  YNGEVLHFHM  ENGRPYPSGG  RFAAKVDFGS
351  KSVDDGIIDSG  DDLHMGTOKF  KAAIDGNFGK  GTWTENGSGD  VSGRFYGPAG
401  EEVAGKYSYR  PTDAEKGGFG  VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1  ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTGT  CCCTTTCAGC
51  CTGCGGGGGC  GGCGGTGGCG  GATCGCCCGA  TGTCAGTTCG  GCGGACACGC
101  TGTCAAAACC  TGCCGCCCTT  GTTGTTCCTG  AAAAAGAGAC  AGAGGCAAAG
151  GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201  AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAAATACA  GGCAATGGCG
251  GTGCGGTAAC  AGCGGATAAT  CCCAAAATG  AAGACGAGGT  GGCACAAAAT
301  GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGAATCACAC
351  CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAATCAA  GCAACGGATG
401  CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451  GACGGAATGC  AGGGGGACGA  TCCGTCCGCA  GGCGGGCAAA  ATGCCGGCAA
501  TACGGCTGCC  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCGCCGGTT
551  CTTCAGATCC  CATCCCCGCG  TCAAACCTTG  CACCTGCGAA  TGGCGGTAGC
601  AATTTTGGAA  GGGTTGATTT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651  GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701  ATTTCTTGGA  TGAAGAAGTA  CAGCTAAAT  CAGAATTGA  AAAATTAAGT
751  GATGCAGACA  AAATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801  TGTGCGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851  TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901  GCACGGTCGA  GGCGGTCGCT  TCCGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951  TCAGGCGGAT  ACGCTGATTG  TCGATGGGGA  AGCGGTCAGC  CTGACGGGGC
1001  ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051  GGGCGGGA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101  ACCGGCAAAA  GCGAATAAGC  TTGCGGGCGC  GGCCGTGTAC  AACGGCGAAG
1151  TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCGAG
1201  TTTGCCGCAA  AAGTCGATTT  CGGCAGCAA  TCTGTGGACG  GCATTATCGA
1251  CAGCGCGCAT  GATTTCGATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301  ATGGAACG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351  TCCGGAAGT  TTTACGGCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401  CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGCGA
1451  AAAAAGAGCA  GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1  MFKRSVIAMA  CIFALSACGG  GGGGSPDVKS  ADTLSPKPAAP  VVSEKETEA
51  EDAPQAGSQ  QGAPSAQGSQ  DMAAVSEENT  GNGGAVTADN  PKNEDEVAQN
101  DMPQNAAGTD  SSTPNHTPDP  NMLAGNMENQ  ATDAGESSQP  ANQPDMAANA
151  DGMQGDPSA  GGQNAAGTAA  QGANQAGNNQ  AAGSSDPIPA  SNPAPANGGS
201  NFGRVDLANG  VLIDGPSQNI  TLTHCKGDSC  SGNNFLDEEV  QLKSEFEKLS
251  DADKISNYKK  DGKNDKFVGL  VADSVQMKGI  NQYIIIFYKPK  PTSFARFRRS
301  ARSRRLPAE  MPLIPVNOAD  TLIVDGEAVS  LTGHSGNIFA  PEGNYRYLTY
351  GAELPGGSY  ALRVQGEPAK  GEMLAGAAVY  NGEVLHFHTE  NGRPYPTRGR
401  FAAKVDFGSK  SVDGIIDSGD  DLHMGTOKF  AADGNFGFK  TWTENGSGDV
451  SGKFYGPAGE  EVAGKYSYRP  TDAEKGGFV  FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

          10      20      30      40      49
m287.pep  MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g287      MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTSPKPAAPVVAENAGEVLPKEKKDEEA
          10      20      30      40      50      60

```


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m287.pep	50	60	70	80	90	100	109
	KEDAPQAGSCGQGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT						
g287	AGGAPQADTQD--ATAGEGSDMAAVSAENTGNGGAATTDNPKNECAGAQNMPQNAA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLAGNMENQATDAGESSQPANQPDMAAADGMQGDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNIITLTHCKGDS						
g287	-ESANQTGNNQPAGSSDSA PASNPAPANGGSDFGRTNVGNVVIDGPSQNIITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADADKISNYKKDGNKDFVGLVADSVQMKGINQYIIFYKP						
g287	CNGDNLLDEEAPSKSEFEKLSDEEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
g287	KPPT-----RSARSRSLPAEIPVNPQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVLDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYR						
g287	KSVLDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGSGDVSGRIFYGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGGFGVFAGKKEQDX						
g287	PTDAEKGGFGVFAGKKDRDX						
	420	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1203>:

```

a287.seq
1  ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51  CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA
451 AACCAACCGG ATATGGCAAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAATGCGG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACTGTT ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTG AAAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA

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```
801 AGACGAGCAA CGAGAGAATT TTGTCGTTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTCAG GCGTTCTGCA CGGTCGAGGC GGTCGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTGCGGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGGCGG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGTACAAC GCGGAAGTGC TGCATTTCCA TATGAAAAAC
1201 GGCCGTCCGT CCCCGTCCGG AGGCAGGTTT GCGGCAAAAG TCGATTTCGG
1251 CAGCAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGAA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGCGGATT CGGCGTTTT GCCGCAAAA AAGAGCAGGA TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:

```
a287.pep
1 MFKRSVIAMA CIVALSCGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMAAAD GMQDDPSAG ENAGNTADQA ANQAENNVQV GSQNPASSTN
201 PNATNGGSD FGRINANGIK LDGSGENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRLPAEM FLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGDD LHMGTQKFKA VIDGNGFKGT
451 WTENGGDVVS GRFYGPAGEE VAGKYSYRPT DAEKGGFVGF AGKKEQD*

m287/a287 77.2% identity in 501 aa overlap

10 20 30 40 50 60
m287.pep MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSKPAAPVSE-----KETE
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 MFKRSVIAMACIVALSCGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGQAPSAGSQDMAAVSEENTGNGGAVTADNPKNEDVAQNMPQNAAGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNKDEGPQNDMPQNAADT
70 80 90 100 110

110 120 130 140 150 160 169
m287.pep DSSTPNHTPDENMLAGNMENQATDAGESSQPANQPDMAAADGMQDDPSAGGQNAAGNTA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAAADGMQDDPSAG-FNAGNTA
120 130 140 150 160 170

170 180 190 200 210 220 229
m287.pep AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 DQAANQAENNVGGSQNPASSTNPNATNGGSDFGFRINANGIKLDGSGENVTLTHCKDKV
180 190 200 210 220 230

230 240 250 260 270 280 289
m287.pep CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDKNDKFVGLVADSVQMKGINQYIIFYKP
||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
a287 CD-RDFLDEEAPPKSEFEKLSDEEKINKYKDEQRENFVGLVADRVEKNGTNKYVIIYKD
240 250 260 270 280 290

290 300 310 320 330 340
m287.pep KP--TSFARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
| :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a287 KSASSSARFRRSARSRRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNRY
300 310 320 330 340 350
```

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	350	360	370	380	390	400
m287 . pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFTENGREYPTRGRFAAKVDF					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFMENGRPSPSCGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287 . pep	GSKSVVDGIIDSGDDLHMGTKQKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVVDGIIDSGDDLHMGTKQKKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287 . pep	YRPTDAEKGGFGVFAGKKEQDX					
a287	YRPTDAEKGGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcggtg cgcccttacc gcaccttttc
201 acccttgccct gtgctgccaa agcagccatc ggcggttttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccggt actttcctcc ccgtatgcct tacgcgatac gcgcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtcgccg tccaatacgg
501 ctttgggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGCC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTIACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GCGCGTTTTC CTTTCTGTTC
251 CACTTTCCGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	I:I					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CCGTTGCCGG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCTTGCCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTTCTGTTC
251	CACTTTCCTG	CGCGTTACCG	CGCCCGGCCG	TTAACCAGCA	TTCTACCCTG
301	CGGAGCCCGG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACACGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	REAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
		:		:		:

676

a288	PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADVFVACAQVF
	130 140 150 160 170 180
m288.pep	DTX
	::
a288	NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1   atggcaaaaa tgatgaaatg ggcggctgtt ggcggcggtcg cggcgggcagc
51  gggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt cgcgcgtccaa cctggtatcg gtcggcgcgcg aggccttcggg
201 gcagattaaa aagctttatg tcaactcgg gcaacaggtc aaaaaggggcg
251 atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc agcgcggaaa aaaaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 cgcgcgcgcca aagccaatgt tgcgagttg aaggctttta tcagacagag
501 caaaatttcc atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat ggacggcacg gtggtggcga ttcccggtga agaggggcag
601 actgtgaacg cggcgcgatc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggatacg
751 ccgattaagg cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcggc tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc agaatacggg tgaaatcgac ggtgtgaaaa atgtgttgct
951 tattccgctc ctgaccgtga aaaatcgcgg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc ggacggcaag gcagtggaa cgcgaatccg gaccggtatg
1051 aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa
1101 agtgggtcatc tccgaaataa ccgcgcgcga gcagcaggaa agcggcgaaac
1151 gcgcccctagg cggcccgcgc gcgcgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1   MAKMMKWAAY AAVAAAAYWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STTQNTIDM
101 EKSLETYQA KLVSQAIALG SAEKKYKROA ALWKDDATSK EDLESAQDAL
151 AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTMSGGG YNSSTDASN AVYYYARFV PNPDGKLTATG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1   ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTGCA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GAAAACGTAT
151 CAGGCGAAGC TGGTGTCCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GCGCATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCTG
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCTTCG TTTGTGCCGA

```

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGA AAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGTGTG GGTGCGGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC C TAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
  1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDIAE INSTSQNTNL NTEKSKLETY
 51 QAKLVSAQIA LGSAEKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTD TA SNAVYYARS FVNPDKGLA TGMTTQNTVE
251 IDGVKNVLII PSLTVKNRGG KAFVRVLGAD GAAEREIRT GMRDSMNTVE
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                         VSVGAQASGQIKILYVKLGQVKKGDIAE
                                         |||
g290      PQAAYTEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKILYVKLGQVKKGDIAE
          30      40      50      60      70      80

m290.pep          40      50      60      70      80      90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKYKRQAALWKENATSKEDLESAQD
|||:||||: |||
g290      INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAEKYKRQAALWKDDATSKEDLESAQD
          90     100     110     120     130     140

m290.pep          100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPVEEGQTVNAAQST
          150     160     170     180     190     200

m290.pep          160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
          210     220     230     240     250     260

m290.pep          220     230     240     250     260     270
GGYNSSTDASNAVYYARSFVNPDKGLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
|||
g290      GGYNSSTDASNAVYYARSFVNPDKGLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
          270     280     290     300     310     320

m290.pep          280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTVEKSGLKEGDKV VISEITAAEQQESGERALGG
|||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTVEKSGLKEGDKV VISEITAAEQQESGERALGG
          330     340     350     360     370     380

m290.pep      PPRRX
              ||||
g290          PPRRX
              390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GGCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGA AAC GGT CAGGCGC GGCGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACCTCG GCAACAGGTT AAAAAGGCGC
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGA AAC GTATCAGGCG AAGCTGGTGT CCGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTCTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAATTTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCGAG
601 ACTGTGAACG CGGCGCAGT TACGCGGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTGTCCGA ACCGGATACG
751 CCATTAAAG CGAAGCTCGA CAGCGTCGAC CCGGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCC TTCTGTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CGGCAGGGCG TTTGTGCGCG
1001 TGTTGGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCCGCGG CGCGGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWA AVAVAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTMMSSGG YNSSTDASN AVYYYARFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

```

                                     10      20      30
m290.pep                               VSVGAQASGQIKILYVKLGQOVKKGDLIAE
a290      PQAAAYITETVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQOVKKGDLIAE
          30      40      50      60      70      80

          40      50      60      70      80      90
m290.pep  INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
a290      INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD
          90     100     110     120     130     140

          100     110     120     130     140     150
m290.pep  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
a290      ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
          150     160     170     180     190     200

          160     170     180     190     200     210
m290.pep  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTMMSS
a290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPLTMMSS
          210     220     230     240     250     260

          220     230     240     250     260     270
```

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```

m290.pep    GGYNSSTDASNAVYYYYARSEFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
            |||||
a290        GGYNSSTDASNAVYYYYARSEFVPNPDGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
            270      280      290      300      310      320

            280      290      300      310      320      330
m290.pep    KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
            :|||
a290        KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
            330      340      350      360      370      380

m290.pep    PPRRX
            ||||
a290        PPRRX
            390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgccgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaatctt atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaa gcaaatcccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaaaac acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAASLKR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRNGNKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTYVSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFFVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHFPQK AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTG ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCATTG CCGGCTGCA CCCCAGATGC GCGCGCAAGG
551 CGCAATCTT ATGGTGTGAG CCCGACCGCG CCAAGCGGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCT GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG GCGAGCCAAA GCGGTACAG CCCGATGCC

```


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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAAALKAR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238.aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP	PAVKAESAGKSVAAALKARLEKTYSAQDL				
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAES	AVKAESAGKSVAAALKARLEKTYSAQDL				
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGY	MFVGELINIDTRKNLTEERAADLNKIDF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
g292	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKR	LEHEFEKMTDVTVYSFMMPIAGLHPDA				
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFN	GTPTLVFPNG			
g292	ARKAQILWCQPDRAKAWTDWMRKGKFPVGG	SICDNPVAETTSLGEQFGFN	GTPTLRLPQR			
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPQX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTT GAAAGCGCGT
151 TTGGAAGAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCGCC
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAACCGCT TGGAAACCGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCATTG CCGGCTGCA CCCCATGCC GCGCGCAAGG
551 CGCAAACTCT ATGGTGTGAG CCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCAACGGG GCGAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

681

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
 51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101  IDTRKNLTEE RAADLNKIDF ASPLDKAIK EVRGNGKLKV AVFSDPDCPF
151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251  QLEEIIRKNQ *

m292/a292  100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292.pep  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR LEKTYSAQDL
a292      MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR LEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292.pep  KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
a292      KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN IDTRKNLTEE RAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292.pep  ASPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
a292      ASPLDKAIK EVRGNGKLKV AVFSDPDCPF CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292.pep  ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
a292      ARKAQILWCQ PDRAKAWTDW MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292.pep  RSQSGYSMP QLEEIIRKNQX
a292      RSQSGYSMP QLEEIIRKNQX
      250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atcgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtcctggtc
 51  gggttcgggct gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151  tgcgcacggg tgcggcggtt caagtcgaat cggcggaacg gtggcggtgaa
201  gccgttgaaa aaaccttatac tggcgagggg ggcggaatgc agatgcaggc
251  gcccggtggc ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301  ccgaggcggt gcgggaagcg gtatgcggac atcgggggag atagtgtatc
351  aatccgtatc cgagctttcc ggttgagca tcgtatgagt atttatgccg
401  tcgcgcacat catccacctg tattgcgcca cgcctttgt cggcggcgtg
451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgtcgcg
501  cgaggcgcgg gcggaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggaac tctagagtcg
601  actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVWSVRA VRTSSNRFPA ALRRYSAFRP TIFPKPAGTP
 51  WRRVRRFKSN RRTRGVPLK KPYLARGAEC RCRRAWTALS HNIAERARES
101  PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVCGV
151  FFEVLVLSVL HTGRVSRER REVEKAMS YRVRMPFAVG LLFARGTLES
201  TAAACP...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGGAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGAAGCG GTATGCGGAT ATCGGGGCGC ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC GGTCCGTTGG
 751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
 51 WHRVRRFKN RMRGGKPLK KPYRPRGGC RCRRWTALS HNIAERARES
 101 PRRCGKRYAD IGGSDTIRI RVERLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEFVVG LLEFASGIVMA
 201 ANRYLSILGE PFATSGTML TLKILLAFSV LAHFAIAVVK MARSTLTGVW
 251 SKYIHAVVET HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSA	AVWSVRAVRTSS	NRFFAALRRYSA	FRPTIFPKPAGT	PWHRVRRFKN	
m294	MRITCAPMSLLSA	AVWSIRVVRTSS	NRFFAALRRYSA	FRPTIFPKPADT	PWHRVRRFKN	
	10	20	30	40	50	60
g294.pep	RRTRGVKKPKPY	LARGAECRCRRA	WTALSHNIAERA	RESPRRCGKRYA	DIGGSDTIRI	
m294	RRMRGGKPLKKP	YRPRGGCRRRA	WTALSHNIAERA	RESPRRCGKRYA	DIGGSDTIRI	
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIY	AVAHIIHLYCAT	AFVGGVFFEVLS	VLHTGRVSREAR	REVEKAMSYR	
m294	RVFRLEHRMSIY	AVAHIVHLYCAI	AFVGGVFFEVLS	VLHTGRVSREAR	REVEKAMSYR	
	130	140	150	160	170	180
g294.pep	AVRVMPEFVGLL	EFARGTLESTAA	ACP			
m294	AVRVMPEFVGLL	EFASGIVMAANR	YLSILGEPFATS	SGTMLTLKILLAF	SVLAHFAIAVVK	
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTTCGGGT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCGGAC
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
 151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGAG GCGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
 451 TTTTGTGAAG TGCTGGTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

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701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPRP TIFPKPAGTP
 51 WHRVRRFKSN RRTGGKPLK KTYRPRRAEC RCRRTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRV	RTSSNRFPAAFRRYSAFQPT	IFPKPADT	PWHRVRRFKSN		
a294	MRITCAPMSLLSAAVWSIRV	RTSSNRFPAAFRRYSAFRPT	IFPKPAGT	PWHRVRRFKSN		
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGG	CRRAWTALSHNIAERARES	PRRCGKRYADIGDSDTIRI			
a294	RRTGGKPLKKTYRPRRAEC	RCRRARTALSHNIAERARES	PRRYGKRYADIGDSDTIRI			
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSVL	LHTGRVSREARREVEKAMSYR			
a294	RVFRLEYRMSIYAVAHIVH	LYCAIAFVGGVFEVLVLSVL	LHTGRVSCEARREVEKAMSYR			
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGLLFASGIVMA	ANRYLSILGEPFATSGTML	TLKILLAFSVLAHFAIAVVK			
a294	AVRVMFVVGLLFASGIVMA	ANRYLSILGEPFATSGTML	TLKILLAFSVLAHFAIAVVK			
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVF	THMLLIVFLAKAMFYISWX				
a294	MARSTLTVGWSKYIHTVVF	THMLLIVFLAKAMFYISWX				
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcacgc ccgcgatatt
 51 gttgccacgc cgcacagcgt tttccgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cactgcacg gatgcgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggggc
 451 gtgttcgcgc aaaaactgcc gtaccacagt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgcgggttc ccgtcccgtc
 551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcgcgtatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgcgggta acgggattcg gatgcggcct gccgaaacgc
 701 tcgtccctat cgcgccggtg tgccggggca cttccggagc gtttgtccaa
 751 ataacgccgt atccatatcg gcgcaagcag ccacaataca tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

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g295.pep

```

1  MLGMAHDDQ  QGIAAILLFR  RQOFFRLVFA  PINARAAAHG  NRPASDAFFK
51  LPRQRHFLFR  RHQVVFGLAA  HLHGCRAQFR  QPRRIRLRLR  QTPRQRSGCG
101 TDQAADFQIT  VQRFFRQPRI  RQKQRHTRSP  AFLHQIGPDF  GFHQNAEHRH
151 VFAQKLPYPR  FFVIRKIAAL  RIGKQNLRGF  PSRRGHLRHQ  QRRIGKTPPQ
201 LAYQGLGGTR  FSDRNGVYPN  RAGNGIRMRL  AETLVPMRPV  CRGTSAGFVQ
251 ITPYPYRRKQ  PQYIIPLEH  LSISCKTNAV  RTVRTAFRQR  NQIS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

```

1  ATGCTCGGGA  TGGCGCGGCA  CGACGACCAG  CAGCGCATCG  CCGCGATATT
51  GTTGCCACGC  CGCCAGCAGT  TTTTCCGCCT  CGTCTTCACC  CCGATAAACG
101 CGCGTGCTCC  CGCACACGGC  AACCGGCGGG  CCTCCGATGC  GTTTTCAAAA
151 CTGCCCCGCC  AGCGTTTTC  TCTGTTCGGA  CGGTATGATG  TCGTATT7GG
201 TATTGCCGCA  CACCTGCACG  GATGCCGCGC  CCAATTTTCG  CAACCGCGCC
251 GCATCCGCCT  CTGTCTGCGC  CAGACACCCC  GTCAGCGAAG  CGCGCGCAGG
301 ACGGATCAGG  CGCGGACTT  TCAGATAACC  GTTCAACGAT  TTTTCCGACA
351 GCCCGGCATT  CGCCAAAAC  AGCGGCACAC  CCGCGCGCCG  GCATTCCCTC
401 ATCAGGTGG  GCCAGATTTC  GGTTCATC  AAAATGCCGA  ACATCGGGCG
451 GTGTTCGGCG  AAAAAGTCC  GTACCCACGT  TTTTGTGTC  TACGGAAGAT
501 AGCGCAATG  CGCATCGGGA  AACAGAACTT  GCGCGGTTT  CCGCCCGTTC
551 GGGGTATCT  GCGTCATCAG  CAGCGGCGCA  TCGGGAAC  GCCGCCGCAA
601 CTCGCGTATC  AAGGACTGG  CGGCACGCGT  TTCTCCGACC  GAAACGGCGT
651 GTATCCAAAC  CGCGCCGTA  ACGGGATTTC  GATACGGCTT  GCCGAAACGC
701 TCGTCCCGAT  GCGCCCGATA  TCGCGGGGCA  CTTCCGAGC  GTTTGTCCAA
751 ATAACGCGT  ATCCATATCG  GCGCAAGCAG  CCACAATACA  TCATAAGGCC
801 ATTGGAACAT  CTTTCTATT  CCTGCAAAAC  AAATGCCGTC  TGAACGGTTC
851 AGACGGCATT  TCGCAACCG  AATCAATAT  CGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep

```

1  MLGMAHDDQ  QRIIAAILLFR  RQOFFRLVFT  PINARAAAHG  NRPASDAFFK
51  LPRQRHFLFR  RYDVVFGLAA  HLHGCRAQFR  QPRRIRLCLR  QTPRQRSGGR
101 TDQAADFQIT  VQRFFRQPRI  RQKQRHTRAP  AFPHQVGPFD  GFHQNAEHRH
151 VFAQKLPYPR  FFVIRKIAAL  RIGKQNLRGF  PPRRGLRHQ  QRRIGKTPPQ
201 LAYQGLGGTR  FSDRNGVYPN  RAGNGIRIRL  AETLVPMRPI  CRGTSAGFVQ
251 ITPYPYRRKQ  PQYIIPLEH  LSISCKTNAV  XTVQTAFRQR  NQIS*

```

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMAHDDQ	QRIIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRHFLFR
g295	MLGMAHDDQ	QGIAAILLPR	RQOFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRHFLFR
	70	80	90	100	110	120
m295.pep	RYDVVFGLAA	HLHGCRAQFR	QPRRIRLCLR	QTPRQRSGGR	TDQAADFQIT	VQRFFRQPRI
g295	RHQVVFGLAA	HLHGCRAQFR	QPRRIRLRLR	QTPRQRSGGT	TDQAADFQIT	VQRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQKQRHTRAP	AFPHQVGPFD	GFHQNAEHRH	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
g295	RQKQRHTRSP	AFLHQIGPDF	GFHQNAEHRH	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRIRL	AETLVPMRPI
g295	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
	250	260	270	280	290	
m295.pep	CRGTSAGFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
g295	CRGTSAGFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACS
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTC TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCGCGCC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCCGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTGCGCCG GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCG ACATCGGGCG
451 GTGTTCCGCG AAAAAGTGG GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGCGCGA TCGGGAAC GCTGCCGCAA
601 CTCGCGTATC AAAGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTTCCGGAGC GTTGTGTCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAGCC
801 ATTGGAACAT CTTTCTATT CTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMAHDDQ QGIAAILLPR RQQFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQREHLFR RHQVVGIAA HLHGCRAQFR QPRRIRLRLC QTARQSGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQAETHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLFQ
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMAHDDQQRIAAILLPRRQFFRLVFTPINARAAAHGNRPASDAFFKLPRQREHLFR					
a295	MLGMAHDDQOGIAAILLPRRQFFRLVFTPINARAAAHGNLPVSDAFFKLPRQREHLFR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m295.pep	RYDVVGIAAHLHGCRAQFRQPRRIRLCLRQTPRQRSGGRDQAADFQITVQRFFRQPRI					
a295	RHQVVGIAAHLHGCRAQFRQPRRIRLRLCQTARQSGGRDQAADFQITVXRFFRQPRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m295.pep	RQQRHTRAPAFPHQVGPDFGFHQAETHRAVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
a295	RQQRHTRAPAFPHQVGPDFGFHQAETHRAVFAQKLPYPRFFVIRKIAALCIRKQNLRGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDNRGVYPNRAGNGIRIRLAETLVPMRPI					
a295	PSRRGHLRHQRRIGKTPPQLAYQGLGGTRFSDNRGVYPNRAGNGIRIRLAETLAPMRPI					
	190	200	210	220	230	240
	250	260	270	280	290	
m295.pep	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
a295	CRGTSGAFVQITPYPYRRKQPQYIIKPLEHLSISCKTNAVXTVQTAFRQRNQISX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT GcTtcgacag
101 aggggaccga gcgcgtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTtGGg gcggcaacg9 CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301 TTGCGgcatt tGCCTGCCGA CCAGTCGGTT CATGTTTtGG TCGGCGGCGA
351 CGGcAGTGCG CGCGAAGTGC AGTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTcGC TTTGGAaaaa AAAGGCGGCA TATGGCGGCG GTCCGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCGCCT GCTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGCGGCGA
701 CAACCCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACCGCGACT TGAGCGCGTT TTCGAGGGCA
1051 CAAGGCATG TCGCGGCGCG CGAGGTATC GGTTTTGTcG GTTCGACAGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCGGAATT GACGAGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGGCG GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PQRVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSA REVQFFDDED GERNLVALEK KGGIWRRSAS
151 DADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQQVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDDEGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTfVRA SADGVITfKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAFAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAARACAT CGGAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GcTTCGACAG
101 AGAGGACGGA CGCGCTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTtGG TCGGCGGCGA
351 CGCGCGGCGC CGCGAAGTGC AGTTTtTtAC CGACGAAGAC GGCAGCGCA
401 ATCTGGTcGC TTTGGAaaaA AAAGGCGGCA TATGGCGGCG GTCCGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCATG CCGTGCCCTT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGCGGCGA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACCGCGACT TGAGCGCGTT TTCGAGGGCA
1051 GAAGGCATG TCGCGGCGCG CGAGGTATC GGTTTTGTcG GTTCGACCGG
1101 GCGTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCGGAATT GACGAGGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGGCG GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERVV PQRVEQNLP
51  LSWGGSGVQT AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFFDDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

```

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201 EGDVRLMYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
 301 AAPQGTTPVRA SADGVITFKG RKGGYGNAVMI RHANGVETL YAHLSAFSQA
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEAR NGQPVNPVSV ALPTPELTQA
 401 DKAFAAQAQK KADALLARLR GIPVTVSQSD *

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKRYALRALAVSII	LVSAAYIASTERTERV	RPQRVEQNLP	PLSWGSGVQT		
g297	MAVFPLSAKHKRYALRALAVSII	LVSAAYIASTEGT	ERVPRQVEQKL	PPLSWGNGVQT		
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEA	VPQPGDSLADVLARSGMARDEI	ARITEKYGG	EADLRHLRADQSVHVLVGGDGGA		
g297	AYWVQEA	VPQPGDSLADVLARSGMARDEI	ARITEKYGG	EADLRHLRADQSVHVLVGGDGSA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTDE	DGERNLVALEKKGGIWR	RSASEADMKVLP	TLRSVVVKT	SARGSLARAEVPV	
g297	REVQFFTDE	DGERNLVALEKKGGIWR	SASDADMKVLP	TLRSVVVKT	SARGSLARAEVPV	
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIF	AGRFSLDGLKEGDAVRLMYD	SLYFHGQQAAGDILAAEVV	KGGTRHQAFY		
g297	EIRESLSGIF	AGRFSLDGLKEGDAVRLLYD	SLYFHGQQAAGDILAAEVV	KGGTTHQAFY		
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGG	NYDEDEGKVLQEKGGFNIE	PLVYTRISSP	FGYRMHPILHTWRLHTGIDY		
g297	YRSDKEGGGG	NYDEDEGKVLQEKGGFNIE	PLVYTRISSP	FGYRMHPILHTWRLHTGIDY		
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGT	PVRASADGVITFKGRKGGYGNAVMI	RHANGVETLYAHLSAFSQA	EGNVRGGEVI		
g297	AAPQGT	PVRASADGVITFKGRKGGYGNAVMI	RHANGVETLYAHLSAFSQA	QGNVRGGEVI		
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRST	GPHLHYEARINGQPVNPVSV	ALPTPELTQADKAFAAQAQK	KADALLARLR		
g297	GFVGSTGRST	GPHLHYEARINGQPVNPVSV	ALPTPELTQADKAFAAQAQK	KADALLARLR		
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1	ATGGCTGTCT	TCCCACTTTC	GGCAAAACAT	CGGAAATACG	CGCTGCGCGC
51	GCTTGCCGTT	TCGATTATTT	TGGTGTCCGC	GGCATACATT	GCTTCGACAG
101	AGAGGACGGA	GCGCGTCAGA	CCGCAGCGCG	TGGAACAAAA	ACTGCCGCCG
151	CTGTCTTGGG	GCGGCAGCGG	TGTTCAAGACG	GCATATTGGG	TGCAGGAGGC
201	GGTGCAGCCA	GGCGACTCGC	TGGCGGACGT	GCTGGCGCGT	TCGGGTATGG
251	CGCGGGACGA	AATTGCCCGA	ATAACGGAAA	AATATGGCGG	CGAAGCCGAT
301	TTGCGGCATT	TGCGTGCCGA	CCAGTCGGTT	CATGTTTGG	TCGGCGGCGA
351	CGGCGGCGCG	CGCGAAGTGC	AGTTTTTTAC	CGACGAAGAC	GGCGAGCGCA
401	ATCTGGTCGC	TTTGGAAGAAA	AAAGGCGGCA	TATGGCGGCG	GTCGGCTTCT
451	GAGGCGGATA	TGAAGGTTT	GCCGACGCTG	CGTTCGGTCG	TGGTCAAAAC
501	GTCGGCGCGC	GGTTCGCTGG	CGCGGGCGGA	AGTGCCCGTC	GAAATTCGCG

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCCCTT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTCTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGCTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 CTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGSAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCATT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGC CGCGCGCG CGAGGTCATC GGT TTTGTCG GTTCGACCGG
1101 GCGTTCGACG GGCCCGCACC TGCATTACGA GCGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGT TTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 CACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

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This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1 MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTERV PQRVEQKLPE
51 LSWGGSGVQT AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGGAD
101 LRHLRADQSV HVLVGGDGGG REVQFTDED GERNLVALEK KGGIWRRSAS
151 EADMKVLPFL RSVVVKTSAR GSLARAEVPV EIRELSLGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQQA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTTPVRA SADGVITFKG RGGYGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGTGRST GPHLHYEAR NGQPVNPSV ALPTPELTQA
401 EKAAFAAQKQ KADALLARLR GIPVTVSQSD *

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m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKH	RYALRALAV	SIILVSAAYI	ASTERTERV	PQRVEQKLPE	LSWGGSGVQT
a297	MAVFPLSAKH	RYALRALAV	SIILVSAAYI	ASTERTERV	PQRVEQKLPE	LSWGGSGVQT
	70	80	90	100	110	120
m297.pep	AYWVQEAQVP	GDSDLADVLAR	SGMARDEIAR	ITEKYGGGAD	LRHLRADQSV	HVLVGGDGGG
a297	AYWVQEAQVP	GDSDLADVLAR	SGMARDEIAR	ITEKYGGGAD	LRHLRADQSV	HVLVGGDGGG
	130	140	150	160	170	180
m297.pep	REVQFTDED	GERNLVALEK	KGGIWRRSAS	EADMKVLPFL	RSVVVKTSAR	GSLARAEVPV
a297	REVQFTDED	GERNLVALEK	KGGIWRRSAS	EADMKVLPFL	RSVVVKTSAR	GSLARAEVPV
	190	200	210	220	230	240
m297.pep	EIRELSLGIF	AGRFSLDGLK	EGDAVRLMYD	SLYFHGQQA	AGDILAAEVV	KGGTRHQAFY
a297	EIRELSLGIF	AGRFSLDGLK	EGDAVRLIYD	SLYFHGQQA	AGDILAAEVV	KGGTRHQAFY
	250	260	270	280	290	300
m297.pep	YRSDKEGGGG	NYDEDEGRV	LQEKGGFNIE	PLVYTRISSP	FGyRMHPILH	TWRLHTGIDY
a297	YRSDKEGGGG	NYDEDEGRV	LQEKGGFNIE	PLVYTRISSP	FGyRMHPILH	TWRLHTGIDY
	310	320	330	340	350	360
m297.pep	AAPQGTTPVRA	SADGVITFKG	RGGYGNVAVM	IRHANGVETL	YAHLSAFSQA	EGNVRGGEVI
a297	AAPQGTTPVRA	SADGVITFKG	RGGYGNVAVM	IRHANGVETL	YAHLSAFSQA	EGNVRGGEVI

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	370	380	390	400	410	420
m297. pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297. pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298. seq

1	ATGAAAACT	TTCTTTCCCT	TTTCGCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACCGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	ACCGGAGCGG	CGTTGCAAGA	AAACGCTAC	GCCCTTTCAG	ACGGCATCAA
201	AACCTTCCTG	TCCGGCGAAA	cgccccccac	ggCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GCCTGAAGCC	GCCGCATCCG	AAGCCGCCCC	GCCGGCCGGC
301	GGACAGAAT	GGAAACAAGG	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTCGCCGGAG	ATTGCTGAT	GCAGGGCGTT	GCGCTTTTCG
401	TGCAAAAAG	CCTGAAACAG	CAATACGGCA	TGCAATCCGC	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTTTC	CTATCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCTTGAAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCCTCGGCCC	GAACGACCCG	TGGGATTTC	CCGTCCGCAA	ACGTACCTC
601	AAATTGCTTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GCGTCGACCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCTACAT	GAAAAAAGTC	AAGCTCGACG	GTCAGATGCG	CTACCTCGAC
751	AACTGCTTT	CGGAACACTT	GAAAGGCAAA	ATCATCCTGA	TTCCCAACCGC
801	GCAAACTCTG	AGCGGCGGGA	AAGgcGCTA	CACCGATTCC	GTCACAGTCA
851	ACGGCAAAAC	CGTCCGCTAC	CGCAGTAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGAAAAATA	ATGAAAAAAA	TCGTTTTTGA
951	ACCGAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298. pep

1	MKNFLSLFAS	ILMSALIAVW	FSQNPINAYW	QOTYHRNSPL	EPLAAYGWR
51	SGAALQENAY	ALSDGIKTFI	SGETPPTAQD	GGSadMPPEA	AASEAAPPAG
101	GTEWKQSTEA	AAVRSGDKVF	FAGDSLMOGV	APFVQKSLKQ	QYGIENSLNLS
151	KQSTGLSYPS	FFDWPKTIEE	TLKKHPEISV	LAVFLGPNDP	WDFPVGKRYL
201	KFASDEWAQE	YLKRVDRILE	AAHTRVQVW	WLGIPIYMKV	KLDGQMRVLD
251	KILSEHLKKG	ILIPTAQTL	SGGKGRYTD	VNVNGKPVRY	RSKDGIFHTA
301	EGQKLAEKI	MEKIVFEPST	QPSSTQP*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298. seq

1	ATGAAAACT	TTCTTTCCCT	TTTCTCCTCC	ATACTGATGT	CTGCCCTGAT
51	TGCCGTGTGG	TTCAGCCAAA	ACCCCATCAA	CGCCTACTGG	CAGCAGACCT
101	ACCACCGCAA	CAGCCCGCTC	GAACCGCTTG	CCGCCTACGG	ATGGTGGCGG
151	ACCGGTGCGG	CGTTGCAAGA	AAACGCTAC	GCCCTTTCAG	ACGGCATCAA
201	AGCCTTCCTG	TCCGGCGAAA	CGCCGCGGAC	GGCTCAAGAC	GGCGGTTCCG
251	CAGATATGCC	GTCTGAAGCC	GCCGCATCCG	AAGCCGTCCT	TCAAAACGGT
301	GAACAGAAT	GGAAACAAGA	CACCGAAGCC	GCCGCCGTCC	GCAGCGGCGA
351	CAAAGTCTTT	TTTGTGCGCG	ACTCGCTGAT	GCAGGGCGTT	GCCCCCTTCG
401	TGCAAAAAG	CCTGAAACAG	CAATACGGCA	TGCAATCCGT	CAACCTCAGC
451	AAACAAAGCA	CGGGGCTGTC	CTACCCCTCA	TTCTTCGACT	GGCCGAAAAC
501	GATTGAAGAA	ACCTTGCAAA	AACATCCCGA	AATCAGCGTA	CTCGCCGTCT
551	TCTTCGGACC	GAACGACCCG	TGGGATTTC	CCGTCCGCAA	ACTCTATCTC
601	AAATTGCTTT	CCGACGAATG	GGCGCAAGAA	TACCTGAAAC	GTGTGACCCG
651	CATCCTTGAA	GCCGCACACA	CGCACCGCGT	CCAAGTCGTC	TGGCTCGGCA
701	TCCCTACAT	GAAAAAAGCC	AAGCTCGACG	GACAGATGCG	CTACCTAGAC
751	AACTGCTTT	CGGAACATTT	GAAAGGCAAA	ATCATCCTGA	TTCCCAACAC
801	GCAACACCTG	AGCGGCGGGA	AAGACCGCTA	CACCGACTCC	GTCACAGTCA
851	ACGGCAAAAC	CGTCCGCTAC	CGCAGCAAGG	ACGGCATACA	CTTTACCGCC
901	GAAGGACAAA	AACTGCTGGC	GGCAAAAATA	ATGAAAAAAA	TCGTTTTTGA
951	ACCAAGTACG	CAACCATCAA	GTACACAGCC	ATGA	

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This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep

```

1  MKNFLSLFSS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAPL SGETPPTAOD GGSADMPSEA AASEAVPQTG
101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNL
151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGIPLYMKA KLDGQMRYLD
251 KLLSEHLKGK IILIPTTHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFSLSGETPPTAQDGGSDMPSEAAASEAVPQTGETENKQDTEAAAVRSGDKVF					
g298	ALSDGIKFTLSGETPPTAQDGGSDMPPEAAASEAPPAGGTENKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIRSVNLKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQQYGIBANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFADEWAQYELKRVDRIEAAHTRVQVVWLGIPLYMKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFADEWAQYELKRVDRIEAAHTRVQVVWLGIPLYMKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRYLDKLLSEHLKGKIILIPTTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
g298	KLDGQMRYLDKLLSEHLKGKIILIPTAQTLGGKGRYTDVNVNGKPVRYRSKDGIFHTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq

```

1  ATGAAAAACT TTCTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACTGGC
301 GAAACAGAAT GGAAACAAAA CACCGAAGCC GCCCGCTCC GAACAGGGGA
351 CAAAGTCTTT TTCGCCGGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG
401 TGCAAAAAAG CTTGAAACAG CAATACGGCA TCGAATCCG' CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551 TCCTCGGTCC GAACGACCCG TGGGATTTCC CCGTTGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCTCTGA TTCCCACCGC
801  GCACACCTTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAA TCGTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1   MKNFLSLFAS IIMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTA AAVRTGDKVF FAGDSLMQGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDF WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AAHTHYVQVV WLGIPYMKKA KLDGQMRYL
251 KLLSEYLGK IILIPHTL SGGKDRYTD VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWF	SQNPNAYWQQTYHRNSPLE	EPLAAYGWWRSGAALQENAY			
a298	MKNFLSLFASILMSALIAVWF	SQNPNAYWQQTYHRNSPLE	EPLAAYGWWRSGAALQENAY			
	10	20	30	40	50	60
m298.pep	ALSDGIKAFISGETPPTAQD	GGSADMPSEAAASEAVPQT	GETEWKQDTEAAAVRSGDKVF			
a298	ALSDGIKAFISGETPPTAQD	GGSADMPSEAAAPETAPQT	GETEWKQNTAATAVRTGDKVF			
	70	80	90	100	110	120
m298.pep	FVGDSLMQGVAPFVQKSLKQ	QYGIESVNLSKQSTGLSYPS	FFDWPKTIEETLQKHPEISV			
a298	FAGDSLMQGVAPFVQKSLKQ	QYGIESVNLSKQSTGLSYPS	FFDWPKTIEETLKKHPEISV			
	130	140	150	160	170	180
m298.pep	LAVFLGPNDFWDFPVGKLYL	KFASDEWAQEYLKRVDRIE	AAHTHYVQVVWLGIPYMKKA			
a298	LAVFLGPNDFWDFPVGKRYL	KFASDEWAQEYLKRVDRIE	AAHTHYVQVVWLGIPYMKKA			
	190	200	210	220	230	240
m298.pep	KLDGQMRYLKLLSEHLKGI	IILIPHTLSSGGKDRYTD	VNVNGKPVRYRSKDGIFHTA			
a298	KLDGQMRYLKLLSEYLGKI	IILIPHTLSSGGKDRYTD	VNVNGKPVRYRSKDGIFHTA			
	250	260	270	280	290	300
m298.pep	EGQKLLAAKIMEKIVFEP	STQPSSTQPX				
a298	EGQKLLAAKIMEKIVFEP	STQPSSTQPX				
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1   ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
51  GGCAGAAGCC CTGCCCGTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCGCCCG CCTCGCCTTG GATGAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGGCGAG GCCTTCGCGA TCCTGCAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACGCC CTGCGCAAC GCCTGCAAAA AACATGGGGC
301 GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGCGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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501 TTCCCTGTTT GCCAAACCGC TGCTCGCCGA ACAAACCTG ACCGTCAAACG
551 GCAACACCGT CTCGCCAAC GCGGCGGCT GGCAGTACT GGATACGGGC
601 GCGGCACTGC CCTGGCCAT ACAGACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTGACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCC TTCAACAACA ACATCGACAT TGCCGATACC GAACAAAAAT
851 GGTGGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCCGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACGCGCCCC GTCTCTCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCGTCAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC AATGGGCGGC
1051 ATATGCAGCA TGA AAAA ACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGCGGAA ATGCTTGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCGCGCGC CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1248; ORF 299.ng>:

g299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSPDT VTVSPSAPYT DTNGLLTDYG
51 NAAASPMWKK LRSVAQSGSE AFRILQIGDS HTAGDFFTDA LKRRLQKTWG
101 DGGIGWYYP NVKGQRMMAV RHSGNWQSFT SRNNTGDFPL GGILAQTGSG
151 GGMILTASDG KTGKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLAIQTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VLLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKWNWLNQ GWAADGVHVF SAQGYRRAAE MLADSLEELV RAAAIRQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1249>:

m299.seq

```

1 ATGAACCCCA AACACCTCAT CGCATTITTC GCCCTATTTC CCGCCACGCA
51 GGCGAAGGCC CTACCTGTGC CCTCCGTGAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCCTCCG CCGCGCTTG GATGAAAAAA CTCCAATCCG TCGCAACAGG
201 CAGCGCGGAG ACCTTCCGTA TCCTGCAAAT CGCGGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTGCAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCGCGC AACGTCAAAG GGCAGCGCAT
351 GCGCGCGGTC CGGCACAACG GTAACCTGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCCGCTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCTG ACCGTCAAACG
551 GCAACACCGT CTCGCCAAC GCGGCGGCT GGCAGTACT GGATACGGGC
601 GCGGCACTGC CCTGACCAT ACACACGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTCG CCCAAACCGG CGCCGATTG GTTATCCTTT CCTACGGCAC
801 CAACGAAGCT TTCAACAACA ACATCGACAT TGCCGACACC GAACAAAAAT
851 GGTGGGATAC CGTCCGCCAA ATCCGCGACA GCCTGCCTGC CGCCGGCATC
901 CTCATCATCG GCGCACCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCGTCG
1001 CCGTCTAGGG GCAGACGATG TTTTGGTCTT GGCAAAACGC CATGGGCGGC
1051 ATATGCAGCA TGA AAAA ACTG GCTCAACCAA GGATGGGCGC CCAAAGACGG
1101 CGTACACTTC TCCGCCAAG GCTACCGCGC CGCGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGTCCGCTG CAATCAGGCA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1250; ORF 299>:

m299.pep

```

1 MNPKEHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51 NASASPMWKK LQSVQSGSE TFRILQIGDS HTAGDFFTDS LKRRLQKTWG
101 DGGIGWYYP NVKGQRMMAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILSYGTNEA FNNNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGTRP VRLTEVQQMQ RRVARQGQTM FWSWQNAMGG
351 ICSMKWNWLNQ GWAADGVHVF SAKGYRRAAE MLADSLEELV RSAAIRQ*

```

m299/g299 95.5% identity in 397 aa overlap

```

10 20 30 40 50 60
m299.pep MNPKEHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPMWKK
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDVTVTSPSAPYTDNGLLLTDYGNAAASFWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQRMMAV
	70 80 90 100 110 120
g299	LRSAVQSGGEAFRILQIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQRMMAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNNTGDFPLGGILAHTSGSGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNNNTGDFPLGGILAHTSGSGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGLVCGTRPVRLTEVQQMQRVARQQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGLVCGTRPVLLTEVQQMQRVARQQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAGYRRAEMLADSLLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAGYRRAEMLADSLLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

```

1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTCC CCGCCACGCA
51  GGCAGAAAGCC CTACCTGTCTG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAGG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCAGGCGTC CGGCACAAAC GTAACCTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTCCTCGTC GCGGCGATCC TCGCCACAC CGGCAGCGGC
451 GGCAGCATGA CCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAAACCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGGCT GGCAGGTACT GGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC CGCATGGGCA
701 TCAACGGCGC ACAATTAAAC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGTAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCAGCA TGA AAAA ACTG GCTCAACCAC GGATGGGCGC CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGAACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

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This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSV AQSGE TFRILQIGDS HTAGDFFTDS LRKRLQKTWG
101  DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151  GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIADIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRP VRLTEVQOMQ RRIARQGQTM FWSWQNAMGG
351  VCSMKNLNLH GWAAKDGVHF SAKGYQSAE MLADSLEELV RAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

```

      10      20      30      40      50      60
m299.pep  MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
a299      MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK
      10      20      30      40      50      60

      70      80      90     100     110     120
m299.pep  LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKGQMAAV
a299      LQSV AQSGE TFRILQIGDSHTAGDFFTDSLRLKRLQKTWGDGGIGWVYPANVKGQMAAV
      70      80      90     100     110     120

      130     140     150     160     170     180
m299.pep  RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
a299      RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
      130     140     150     160     170     180

      190     200     210     220     230     240
m299.pep  TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
a299      TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
      190     200     210     220     230     240

      250     260     270     280     290     300
m299.pep  QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
a299      QWSKWRADRMNDLAQTGADLVILAYGTNEAFGDNIADIADTEQKWLDTVRQIRDSLPAAGI
      250     260     270     280     290     300

      310     320     330     340     350     360
m299.pep  LIIGAPESLKNTLGVCGRPVRLETVQOMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ
a299      LIIGAPESLKNTLGVCGRPVRLETVQOMQRRRIARQGQTMFWSWQNAMGGVCSMKNLNLH
      310     320     330     340     350     360

      370     380     390
m299.pep  GWAAKDGVHFSAGYRRAAEMLADSLEELVRSAAIRQX
a299      GWAAKDGVHFSAGYQSAEMLADSLEELVRSAAIRQX
      370     380     390
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGGGGCG AAAGGACGTG CC3ATGACGG TTTGATTCAC GTTGTACGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GG3AACGGTG TTGTTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCGCTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTTTATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTTGT CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTTC CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTTGT
1001 TTGCGCTGCC GGGCATTGTT TATGGCCGGA TAACCCGAAG TTGCGCGGCC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTTTAAAT
1151 GGACGAATAT TGGCAATAT ATTGCGGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 CTCATTCAAG CCGCTTACCG CATCGGTGAT TCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GCGCAGGTA ATCAAATACA
1451 AAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGGTATTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDRPVGK KGRADDGLIH VVSLLDADGL IKILTHTVKV
101 FTGFAPLGTV LVSLLGVGIA EKSGSLISALM RLLLTKSPRK LTTFMVVFTEG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIYPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVLGGSVLF IGFIICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPO
451 VIQAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTGGTGC AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGT ACTGAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GGCAATCCAA
801 TGAATACACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTGCTCTT ATCCGCCCTA TTGGCTTGA GCATCGTCCC TGCCGACGGT
901 ATTTGCGTTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTTATTT TCTGTTGTT TGCATGyCG GGCmTTGTTT
1001 ATGGMCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

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1051 ATGGCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kcATCTTTT
1101 TGCCGCACAG TTTGTCGCAT TTTTAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTAA AGGGGCGACG TTCTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCGCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTTGTT TTGGGCCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MESIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLILTKSPRK LTFMVVFTG
151 ILSNTASELG YVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVLSAL LAWSIYPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAAQ FVAFFNWTNI GQYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMMLAGY APEVIQAAYR
451 IGDVNTNIIT PMMSYFGLIM ATVIKYKDA VGTLISMML PYSAFFLIAW
501 IALFCIWVVFV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng) from *N. gonorrhoeae*:

m302/g302

m302.pep	10	20	30	40	50	60
	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
m302.pep	70	80	90	100	110	120
	SVPDRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
g302	SVPDRPVGAKGRADDGLIHVVSLLDADGLIKILTHTVKNFTGFAPLGTVLVSLLGVGIA					
	70	80	90	100	110	120
m302.pep	130	140	150	160	170	180
	EKSLISALMRLILTKSPRKLTTFMVVFTGILSNTASELGYYVLIPLSAIIFHSLGRHPL					
g302	EKSLISALMRLILTKSPRKLTTFMVVFTGILSNTASELGYYVLIPLSAVIFHSLGRHPL					
	130	140	150	160	170	180
m302.pep	190	200	210	220	230	
	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQI IHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
m302.pep	240	250	260	270	280	290
	ALIGYFVTEKIVEPQLGYPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVLSALLAW					
g302	ALIGYFVTEKIVEPQLGYPYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVFVLSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep  SIVPADGILRHPETGLVSGSPFLKSIVVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
          |||||:|||||:|||||:|||||:|||||:
g302      SIVPADGILRHPETGLVAGSPFLKSIVVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
          310      320      330      340      350      360

          360      370      380      390      400      410
m302.pep  SMSTLXLXLLXI FFAAQFVAFNWTNIGQYIAVKGATFLKEVGLGGSVLFIGFILICAFI
          |||||:|||||:|||||:|||||:|||||:
g302      SMSTLGLYLVII FFAAQFVAFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIGFILICAFI
          370      380      390      400      410      420

          420      430      440      450      460      470
m302.pep  NLMIGSASQAQWAVTAPIFVPNLMLAGYAPEVIQAAYRIGDSVTNIIITPMMSYFGLIMATV
          |||||:|||||:|||||:|||||:|||||:
g302      NLMIGSASQAQWAVTAPIFVPNLMLAGYAPQVIQAAYRIGDSVTNIIITPMMSYFGLIMATV
          430      440      450      460      470      480

          480      490      500      510      520
m302.pep  IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGAPTFFYPAPX
          |||||:|||||:|||||:|||||:|||||:
g302      IKYKKDAGVGTLSMMLPYSAFFLIAWIALFCIWVFLGLPVGPGTPTFFYPVPX
          490      500      510      520      530

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTGATTACAC GTTGTCAGCC
251 TGCTCGATGC TGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCAACCGGT TCGCGCCGTT GGAACCGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 TGCCGCCATC ATCTTTCATT CCTCGGCGG CCATCCGCTT GCCGCTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGCGGCTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACCTG TTTTATATGG
701 TAGCCAGTAC GTTGTGATT GCTTGATTG GTTATTGTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGCGC TGCGGTGGTG TTGTTGCCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTCG CCGTTTTTAA AATCAATTGT TGTTTTTATT TTCTTGTTGT
1001 TTGCACTGCC GGCATTGTT TATGGCCGGG TAACCCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTGGTTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATTT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATTT GGGTATTGTT
1551 TTGGGCGCTG CCCGTCGGTC CCGGCGGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQDTQRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL FVGPGAPTFY PAP*

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m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QTDGRFLRTV	EWLGNMLPH	PVTLFII	FIVLLLLIAS	AVGAYFGL
a302	MHSIYFFKEKQMSQTD	QTDGRFLRTV	EWLGNMLPH	PVTLFII	FIVLLLLIAS	AAGAYFGL
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLN	ADGFIKILTHT	VKNFTGFAP	LGTVLVLSLL	GVGIA
a302	SVPDPRPVGAKGRADD	GLIHVVSLLD	ADGLIKILTHT	VKNFTGFAP	LGTVLVLSLL	GVGIA
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	KSPRKLTTFM	VVFTGILSNT	ASELG YVVLIP	LSAII FHSLGR	HPL
a302	EKSGLISALMRLLLT	KSPRKLTTFM	VVFTGILSNT	ASELG YVVLIP	LSAII FHSLGR	HPL
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSAN	LFLSTIDPELLAC	ITHQAA-----	VVGPEANW	FFMVASTFVI	
a302	AGLAAAFAGVSGGYSAN	LFLGTIDPELLAG	ITQQAQIIHP	DYVVGPEANW	FFMVASTFVI	
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQL	GPYQSDLSQEEK	DIRHSNEITPLE	YKGLIWAGVV	FVALSALLAW	
a302	ALIGYFVTEKIVEPQL	GPYQSDLSQEEK	DIRHSNEITPLE	YKGLIWAGVV	FVALSALLAW	
	250	260	270	280	290	300
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPETG	LVSGSPFLKSIV	VFI FLLFALXG	VYGRVTRSLR	GEQEVVNAMAE	
a302	SIVPADGILRHPETG	LVSGSPFLKSIV	VFI FLLFALPG	IVYGRVTRSLR	GEQEVVNAMAE	
	310	320	330	340	350	360
	360	370	380	390	400	410
m302.pep	SMSTLXLXLIFFAAQ	FVAFNNWTNIGQY	IAVKGATFLKEV	GLGGSVLF	IGFILICAFI	
a302	SMSTLGLYLVIIFFAAQ	FVAFNNWTNIGQY	IAVKGATFLKEV	GLGGSVLF	IGFILICAFI	
	370	380	390	400	410	420
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAVTAP	IFVPMMLAGYA	PEVIQAAYRIGD	SVTNIITPMM	SYFGLIMATV	
a302	NLMIGSASAQWAVTAP	IFVPMMLAGYA	PEVIQAAYRIGD	SVTNIITPMM	SYFGLIMATV	
	430	440	450	460	470	480
	480	490	500	510	520	
m302.pep	IKYKKDAGVGT	TLISMMLPYS	SAFFLIAWIAL	FCIWVFLGL	PVPGAPTFY	PAPX
a302	IKYKKDAGVGT	TLISMMLPYS	SAFFLIAWIAL	FCIWVFLGL	PVPGAPTFY	PAPX
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq
 1 ATGGATTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
 101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CCGTTTTTGGC GGTAGTGT TTGAATACCGGC AGCGTTTCAG
 201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
 251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
 301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTTTG GCGCGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GTGTTGCCCA AGTGTTCGCA CTGGTTCGG GTACGTCCCG
 501 TTCGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
 551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTCAGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCG GGTTCGTTAG
 701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
 751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTTC
 801 GGGCTGGATA AGTTGGGAAT GA

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
 101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMVAA
 201 TAYDVLKHYR FFLHVDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
 251 AYYRIVFGLV IILLWLSGWI SWE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)
 1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
 51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
 101 GCAATCTGAT TGGTTTTTAC AGCAATCACA AGGTTTTTGA AATTGCCATC
 151 CAGCTCGGTG CAGTTTTTGGC GGTAGTGT TTGAATACCGGC AACGTTTCAG
 201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
 251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
 301 TGCACAAACA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
 351 GCTGGTTyTG GCGGTTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
 401 GAGCAGAGCC TAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
 451 TTGATGATCG GCGTTGCCCA AGTGTTCGCA CTGGTTCGG GTACGTCCCG
 501 TTCGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
 551 TTGCGACAGA ATTCTCGTTT TTCTTGGCTG TGCCGATGAT GGTTCGCGCA
 601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
 651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTC A GGCTTGGTAG
 701 CGGTAAAAGC GTTGTGAGG TTGTTTCGG GTAC...

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)
 1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
 51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLAI AF IPAAVMGLLF
 101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
 151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMVAA
 201 TAYDVLKHYR FFLHVDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKQRSRAEPKIADV DALRPIDALMIGVAQVFALVPGTSRSGSTVMGMLWGI					
	:					
m305	XGFXILWVEKQRSRAEPKIADV DALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCC
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGT TTGAATACCGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTGTTC
301 GGCAACAATA TCAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGTTTTTG GCGGTTTTT TTATTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTGTC GATGTTGAT CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTGGCCCA AGTGTGTCGA CTGGTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTGGCCG TTCGATGAT GGTGTCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTGTTTCA GGCTTGGTG
701 CGGTCAAAGC GTTGCTGAGG TTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AFIPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK QRSRAEPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSN HKVFEIAIQLGAVLAVVF					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSN HKVFEITIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPKIADVLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
a305	GGFFILWVEKRSRAEPKIVDLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCAATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCCAGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 ACAAACCGT  CAGGGAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAACCG  ACCCGGAAC
551 AAATCCTCAA  CAGCCGAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCA  AAATGAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAATGG  GCGCGTATGC  CGAACCCCG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1  MFMNKFSQSG  KLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKALT  EEREQTVREK  AQKDAETVK
151 KKAVKPSKET  EKKASKEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1  ..GGTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCmAwAA  CCAGCyTAAG
151 GAAGACATCC  AACCTGAWCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAWGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGACCG  ACAGGCAGTG  CGTAAGAAAG  CGTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTAAAAAw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGAACAA  ATCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCAAAGA  AGTCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

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702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
 701 GGC GGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)

1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPNQXK
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
 101 EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
 151 SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
 201 IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
 251 MR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

		10	20	30	40		
m306.pep		GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX					
		: : : : :					
g306		MFMNKSQSGKGLSGFFGLILATVIIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK					
		10	20	30	40	50	60
	50	60	70	80	90	100	
m306.pep	NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED						
	:						
g306	NQPKEDIQPEPADQNALSEPDAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED						
	70	80	90	100	110	120	
	110	120	130	140	150	160	
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP						
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKAAKEKVAPKP						
	130	140	150	160	170	180	
	170	180	190	200	210	220	
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KORIICKWARMPTVRARKGSVPNWSWA						
	:						
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGGGSQRIICKWARMPTNPGARKGSVPNWSWA						
	190	200	210	220	230	240	
	230	240	250				
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX						
	: : :						
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX						
	250	260					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq

1 ATGTTTATGA ACAAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTT
 51 CTTCGGTTTG ATACTGGCGA CGGTCATAT TCGCGGTATT TTGTTTTATC
 101 TGAACCAGAG CGGTCAAAT SCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAAGCTA AGGAAGACAT
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
 251 AAGAGGCAGA GCACTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA
 351 AAAGTCGGAC GGACAGGCAG TCGCAAGAA AGCACTGACG SAAGAGCGTG
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAACCG ACCCGGAAC
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

703

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601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTTCGGTAT CAGGCGGGAC
751 ATAAAACGCT TTACCGGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
1 MFMNKFSQSG KGLSGFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD QAVRKKALT EEREQTVGEK AQKKAETVK
151 KQAVKPSKET EKKASKEKK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

          10      20      30      40
m306.pep      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
               |:|||||||||||||||||||||||||:|||||||||
a306          MFMNKFSQSGKGLSGFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
               10      20      30      40      50      60

          50      60      70      80      90      100
m306.pep      NOXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          NQPKEDIQPEPADQNALSEPDAAKEAEQSDAEKAADKQPVADKADEVEEKADEPEREKSD
               70      80      90      100      110      120

          110     120     130     140     150     160
m306.pep      QAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          QAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
               130     140     150     160     170     180

          170     180     190     200     210     220
m306.pep      TPEQILNSGSIEKARSAAAEVQKMKTPTTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
               ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a306          TPEQILNSGSIEKARSAAAEVQKMKTPTTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
               190     200     210     220     230     240

          230     240     250
m306.pep      LPRWSVIRRDIKRFTGCKAAICLPMRX
               ||||||| ||||||| |||||||
a306          LPRWSVIRRDIKRFTGCKAAICLPMRX
               250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
1 atgaaaacct tcttcaaaac ctttcgacc gcgtaactcg cgctcatcct
51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgceg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcattggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccgggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgcccaac
451 gaccgtcca acttcgcacg cgccttggtg atgctgaacg aactgggttg
501 gatcaaaactc aaagacggca tcaatccgct gaccgatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaaatcg tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcaga agctgaccga agccctgttc caagagccga

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704

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
 751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
 801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
 851 aaggcgcagc caataaa

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

g307.pep

1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSADNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFQ
 101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLSLEEV KDGSTVSAPN
 151 DPSNFARALV MLNELGWIKL KDGINPLTAS KADIAENLKN IKIVELEAAQ
 201 LPRSRAVDVF AVVNGNYAIS SGMKLTEALF OEPSFAYVNW SAVKTADKDS
 251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYPA AWNEGAAX*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

m307.seq (partial)

1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
 101 AAGGCGCAGC CAAATAA

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

m307.pep (partial)

1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAX*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

m307/g307

				10	20	30
m307.pep				QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA		
g307	SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYPA					
	230	240	250	260	270	280

	39
m307.pep	AWNEGAAXX
g307	AWNEGAAXX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

a307.seq

1 ATGAAACCT TCTTCAAAAC CCTTCCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCTGCG GGCGGTCAAA AAGATAGCGC GCCCGCGCA TCCGCTTCTG
 101 CCGCCGCCGA CAACGGCGCG GCGAAAAAG NAATCGTCTT CGGCACGACC
 151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
 201 GAAAAAAGGC TACACCGTCA AACTGGTCGA GTTTACCGAC TATGTGCGCC
 251 CGAATCTGGC ATTGGCTGAG GGCGAGTNGG ACATCAACGT CTTCACACAC
 301 AAACCCATATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
 351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GCAAGCTGA
 401 AATCGCTGGA AGAAGTCAAA EACGGCAGCA CCGTATCCGC GCCCAACGAC
 451 CCGTCCAAC TCGCCCGCGT CTTGGTGATG CTCGACGAAC TGGGTTGGAT
 501 CAAACTCAAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
 551 CCGAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
 601 CCGCGTAGCC GCGCCGACGT GGATTGTGNC GTCGTCAACG GCAANTACGC
 651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
 701 TTGCCTATGT CAACCTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
 751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
 801 CGCGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
 851 GCGCAGCCAA ATAA

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

a307.pep

1 MKTFFKTLISA AALALILAAC GGQKDSAPAA SASAAAADNGA AKKXIVFGTT

705

```

51  VGDGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKNI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEQYKSPAA  WNEGAAX+

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                                OWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
          220      230      240      250      260      270

          39
m307.pep      AWNEGAAXX
          |||||
a307      AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTCCTG
101  TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151  GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201  TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251  AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301  TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGCGGT  GCATTGCCAG
351  CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401  CGCTTGCTTC  TGTGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451  GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501  AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551  TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAGCCGCG
601  ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTGCTGTT
651  CGGAATCGAT  ACSCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYFIRL  GVADNLYPCL  SDFCFETIIA  GLPLQAVLWE  RMMVRLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101  LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151  ADVVLKERRR  LVLMVRETP  LAHLNLMKR  VTEMGGVVP  PVPAMYRKPO
201  TADDIVAHSI  AHTLSLFGID  TPDLAEQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTCT  GTTTTTCAC  TATAATAGCC  GGTGTCCTG
101  TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151  GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201  TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251  AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301  TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGCGGT  GCATTGCCAG
351  CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401  CGCTTGCTTC  TGTGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451  GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501  AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAA
551  TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTTG  CGATGTACCG  CAAACCGCAG
601  ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTGCTGTT
651  CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPVAMYRKPTADDIVAHSAHLSFLGIDTPDSAEWQGMA					
g308	VTEMGGVVFPVPVAMYRKPTADDIVAHSAHTLSFLGIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCCGA
401 CGCTTGCTTC  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCTG  CGATGTACCG  CAAACCGCAG
601 ACGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RMMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSAEWQGM  AD*

```

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m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRV	FYRIL	GVADN	LYPRL	SDFCF	FTIIAGL
a308	MLNRIF	YRILGV	ADNLYP	RLSDFC	FFFTII	AGLPLQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALE	LLRAQD	VETHLV	VSKGAEM	ARASET	AYARDEV
a308	GVKALX	LLRAQD	ETHLVV	SKGAEM	ARASET	XYARDXV
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KT	DGMLV	APCSM	RTLAS	VAHGF	GDNLLT
a308	KT	DGMLV	APCSM	RTLAS	VHVGFD	NLLTRA
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XT	ENG	GVVFP	VPV	PAMYR	EPQTAD
a308	VT	ENG	GVVFP	VPV	PAMYR	EPQTAD
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCTGTTA TCGGATTCTT GTTTTTCAC  TATAATAGCC GGTTCGCCGT
101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGAACT
201 TTTGCCGCGC CAAGATGTCG AAACGCACCT TGTGATATCG AAAGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCCGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGGCGGA
501 AACCGCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAAGCCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGVVFP VPVAMYRKPKQ
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA
51  TCCGCTGTTA TCGGATTCTT GTTTTTCAC  TATAATAGCC GGTTCGCCGT
101 TGCAGCGCGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGAACT
201 TTTGCCGCGC CAAGATGTCG AAACGCACCT TGTGATATCG AAAGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
401 CGCTTGCCCT TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGGCGGA
501 AACCGCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTCG CGATGTACCG CAAAGCCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTIIA GLPLQAVLWE RMMVRRLLI

```

708

51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA
 101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSAEWQGM AD*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVYFIRILGVADNLYPRLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRVYFIRILGVADNLYPCLSDFCFFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASEDYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFSDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					
g308-1	KTDGMLVAPCSMRTLASVAHGFSDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKQPTADDIVAHSAHLSFGIDTPDSAEWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKQPTADDIVAHSLHTLSFGIDTPDLAEWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA
 51 TCCGTATTTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTITGCCGT
 101 TGCAGCGCGT TTTATGGGAA AGCGGATGA TGGTACGGCG TTTGATAATC
 151 GGCATCAGTG GGGCGAGCGG TTCCAATAC GCGGTGAAGG CTTTGGANCT
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC
 301 TTGCGGACT TNGTGCATCC GATCGGCAAT ATCGGGCGGT GCATTGCCAG
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCCGA
 401 CGCTTGCTTC GGTCTGCAC GGCTTCGGCG ACAACCTCTT GACCGGTGCG
 451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTCTGA TGGTGC CGGA
 501 AACGCCGCTG AACCTGCCC ATTTGGACAA TATGAANCGG GTAACGGAAA
 551 TGGGCGGCGT GGTGTTTCCC CTTGTTCTG CGATGTACCG CAAACCGCAG
 601 ACGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTGCTGTT
 651 CGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

1 MLNRIFYRIL GVADNLYPYL SDFCFFTIIA GLPLOAVLWE RMMVRRLLI
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVH GFGDNLTRA
 151 ADVVLKERRR LVLVRETPL NLAHLNMMKR VTEMGGVVFP PVPAMYRKPO
 201 TADDIVAHSV AHALSFGID TPDSAEWQGM AD*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRVYFIRILGVADNLYPRLSDFCFFTIIAGLPLOAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVHGFSDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMMKR					

m308-1	RTDGNLVAPCSMRTLASVAHGFQDNLNLTAAADVVLKERRRLVLMVRETPLNLAHLDNMKRR										
	130		140		150		160		170		180
a308-1	VTEMGGVVFPVPVPMYRKPQTADDVAHSVAAHLSLFGIDTFDSAEWGGMADX										
	190		200		210		220		230		
m308-1	VTEMGGVVFPVPVPMYRKPQTADDVAHSVAAHLSLFGIDTFDSAEWGGMADX										
	190		200		210		220		230		

g311.seq

g311.pap

m311.seq (partial)

1	ATGTTTCAGT	TTGGCTGGGT	GTTTGACCGG	CCGCAGTATG	AGTTGGGGTTC
51	GCTGTCGCCT	GTTGCGCGCA	TGGCGTGTGC	GCGCGCCTTG	TCGCGTTTAG
101	GTTTGGATGT	GCArATTAA	TGGCCCAATG	ATTTGGTTGT	CGGACGCGAC
151	AAATTGGGGC	GCAITTCGAT	TGAACACGT	AGGACGCGCA	GCAAAACCGT
201	TGCCGTGGTC	GGTATCGGCA	TCAATTTTGT	CCTGCCCAAn	GAAGTAGAAA
251	ATGCCGCTTC	CGTGAATCG	CTGTTTTCAGA	CGGCATCGCG	CGCGGGCAAT
301	GCCGATGCCG	CCGTGCTGT	nnnnnnnnnn	nnnnnnnnnn	nnnnGGAAT
351	CACGTCGCGG	TCGGAACACA	GGCGGGTTTC	CGTgnCGAAG	CGCGGGGATT

710

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401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTCGCCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TGGGAGAAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACCC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTTC GCGGAAAATA CCGTGCGCGT
1101 GCGGACAAC CTCGTCAATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
51 KLGILITV RTGGKTAVV GIGINFLPX EVENAASVOS LFQTASRRGN
101 ADAAVLLXXX XXXXEISLR SDXRPVSXK RRDSEFLLL DGGNSRLKWA
151 WVENGTFAV GSAPYRDLSP LGAEWAEKAD GNVRIVCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMMDAVCG SVMMHGRLK EKTGAGKPDV VIITGGGAAK
351 VAEALPPAFL AENTVRVADN LVIYGLNMI AEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

          10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGILITV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETOIKWPNDLVVGRDKLGILITV
          10      20      30      40      50      60

          70      80      90      100     110
m311.pep RTGGKTAVVVGIGINFLPXEVENAASVQSLFQTASRRGNADAADVLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVVVGIGINFLPKEVENAASVQSLFQTASRRGNADAADVLLLETLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXX
          :
g311      YAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVDRGVLHLETAEGEQTIVVS
          130     140     150     160     170     180

          120     130     140     150     160     170
m311.pep XEISLRSDXRPVSXKRRDSEFLLLDGGNSRLKWAVVNGTFAVGSAPYRDLSPGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      GEISLRPDNRSVSPKRPDSEFLLEGGNSRLKWAVVNGTFAVGSAPYRDLSPGAE
          190     200     210     220     230     240

          180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLFSSAQALFGIRNHYRHPEEHGSDR
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLFSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```

711

	240	250	260	270	280	290
m311.pep	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRRFSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTGNASGMMDAVCGSVMMHGRLEKKTGAGKPVVDVIITGGGAAKVAEA					
g311	PAGKRYFPFPTTGNASGMMDAVCGSIMMHGRLEKKNAGKPVVDVIITGGGAAKVAEA					
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1  ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CCGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTGTC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGAA ACGGCAGAGG GCAAACAGAC GGTCTGCAGC GGCGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTCT
601 GAACGTTTTC TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAGAC GGCACGTTCT CAACCGTCGG TAGCGGCGCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCGCG
751 ATCGTCGGT GCGCCGIGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCAGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGETAA CGGTTGACGC GCTCACCAGT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCSATGTCAT CATTACCGGC GCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1  MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTAVAV GIGINEVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETL LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLHE TAEGKQTVVS GEISLRSDDR PVSVPKRRDS
201 ERFLLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPGLAE WAEKVDGNVR
251 IVGCAVCGEF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYPFPTT TGNASGMM DAVCGSVMMH HGRLEKKTGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIIETV					
a311	MFSFGWVFDRPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLXXXXXXXX-----					
a311	RTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGQGVHLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVSVXKRRDSEFLLLDGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
a311	GEISLRSDDRPVSVPKRRDSEFLLLDGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKV DGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGNASVSGMMDAVCGSVMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA					
a311	HAGKRYPFPTTTGNASVSGMMDAVCGSVMMHGRLEKKTGAGKPVVDVITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLNIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLNIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTGATGCC GAAGGTTTGC GCGATCTGGG GGAAGGTCG GGTTCAGAA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCG GATGTTCACT TTCGCTGCGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTGCGTGCC GCGCGCCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAATCAA GTGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAAACCGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGAGTGC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTATTGC TGGAAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TCGGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACCTTGA AACGCGAGaa ggcGAACAGa cggtcGtcag
951 cggcGaaATC AGcctTGGGc CGGacaacag gtcggtttcc GTgcccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgtttg aagcggggaa cagccggctc
1051 aAGTGGGcgt gGgTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcGCC
1101 gtaCCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGCGCGATG
1151 GAAATGTCCG CATCGTCGGT TGCGCCGTGT GCGGAGAATC CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAAATCGCT CGCCGTCCGA ACCGCCAAC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCTTT TCCCGACCAC AACGGGCAAC GCCGTCGCAA GCGGCATGAT
1551 GGACCGCGAT TCGCGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CCGCGCGCGG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGCGCG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

```

g311-1.pep
1  MTVLKPISHWR VLAELADGLF QHVSQALREA DMKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLOSK GRGRGGRKWS HRLGECMF SFGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVODG
301 RGVLLHLETAE GEQTVVSGEI SLRPNRSVS VPKRPDSERF LLEGGNSRL
351 KWAWVENGTF ATVGSAFYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHEP EHGSDRWENA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRPAKG
501 RYFFPTTTGN AVASGMMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

```

m311-1.seq
1  ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGGCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA CATACCGGGG
151 CTGTTGGCGC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTCGAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCACACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAGAA GGCAGGGGGC GGCAGGGGCG GAAAGTGGTC CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTGACCG GCCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCGA GTGGCGGTGC GCGCGGCTT
501 GTCGCGTTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGTTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CGGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTACG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGACGCGCG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACCTTGA AACGCGAGAG GGCAAAACAG CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG CCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGCGGTA ACGGTTGACG CGCTCACCAG
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAAATCCCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGG GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGCGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQARMAD MKPQQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GGRQGRKWS HRLGECLMFS FGWVDRPQY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGDRKLG GILLETVRTG
201 GKTVAVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVHLLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRNA
451 CVVSCGTAV TVDALDDGH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

m311-1.pep	10	20	30	40	50	60
	MTVLKLSHWRVLAELADGLPQHVSQARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
m311-1.pep	70	80	90	100	110	120
	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
m311-1.pep	130	140	150	160	170	180
	GGRQGRKWSHRLGECLMFSFGWVDRPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
m311-1.pep	190	200	210	220	230	240
	DLVVGDRKLGILLETVRTGGKTVAVVIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGDRKLGILLETVRAGGKTVAVVIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
m311-1.pep	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	250	260	270	280	290	300
m311-1.pep	310	320	330	340	350	360
	QGVHLLETAEKGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAVVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVFKRPDSERFLLLEGGNSRLKWAVVENGTF					
	310	320	330	340	350	360
m311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLAEWAEEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL					
	370	380	390	400	410	420
m311-1.pep	430	440	450	460	470	480
	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
g311-1	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALDDGHYLGGTIMPGF					
	430	440	450	460	470	480
m311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPFTTGNASGMMDAVCGSVMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFTTGNASGMMDAVCGSVMHGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

715

```

m311-1.pep  VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
              |||||
g311-1      VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLNLI AEGGESEHAX
              550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGCTC CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTTCGATGC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTCACAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGTCTG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTCGACCG GCCGCGATAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA GTGGCGTGCC GGC CGCCTT
501 GTCGCGTTTG GGTTTGAAAA CGCAAATCAA GTGCCAAAC GATTGCTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGC AAAACGG TTGCGGTGGT CGGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTCGAA AACCCCGCTT CCCTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGCGGAAAA TGCCGATGCC GCCGTGTTGC TGGAAACGCT GTTGGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGCGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGCGCTTC TGCACCTGGA AACGCGAGAG GGCAACAGA CGGTCGTCAG
951 CCGCGAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTT CTGCTGTTGG ACGCGGCGAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGA AAA CCGCACGTT CCAACCGTCG GTAGCCGCGC
1101 GTACCGCGAT TTGTCGCCTT TGGCGCGGGA GTGGCGGAA AAGGTGGATG
1151 GAAATGTCGG CATCGTCGGT TGCGCGGTGT GCGGAGAAAT CAAAAAGGCA
1201 CAAGTGCAAG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TGCGTCTGTC TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCGGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGSCAAT GCCGTCGCA CGGGCATGAT
1551 GGTGCGGTTT TGCGGCTCGG TTATGATGAT GCACGGCGGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTC TATTACCGG CGGCGCGCGG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACGG GCTGCTGAAC CTGATTGCGC
1751 CCGAAGCGCG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTLVKPSHWR VLAELADGLP QHVSQALRMA DMKPOQLNGF WQMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVDFRPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGDRKLG GILLETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEETVKGVDG
301 QGVHLLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAFYRD LSLPGAWEAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAAL GIRNHYRHPE EHGSDRWENA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGCH YLGGTIMGPF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVIITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

              10      20      30      40      50      60
a311-1.pep  MTLVKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              |||||
m311-1      MTLVKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQMPAHIRGLLRQHDGYWR
              10      20      30      40      50      60

              70      80      90      100     110     120
a311-1.pep  LVRPLAVFDAEGLRELTERS GFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              |||||
m311-1      LVRPLAVFDAEGLRELTERS GFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
              70      80      90      100     110     120

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVDRPQYELGSLSPVAACRRALSRLGLKTQIKWPN					
m311-1	GRGRQGRKWSHRLGECIMFSFGWVDRPQYELGSLSPVAACRRALSRLGLDVQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIEVTRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	DLVVGRDKLGGILIEVTRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
m311-1	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
a311-1.pep	310	320	330	340	350	360
	QGVLEHLETAEGKQTVVSGEISLRSDRPVSVPKRRDSERFLLLDGGNSRLKWAWEVNGTF					
m311-1	QGVLEHLETAEGKQTVVSGEISLRSDRPVSVPKRRDSERFLLLDGGNSRLKWAWEVNGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
m311-1	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHRYRHEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
m311-1	GIRNHRYRHEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGTTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAGGEGSEHTX					
m311-1	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLLNMIAGGEGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTaccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggctcg gcaaagactT GGTGGCAacy Gcgaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt cgcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAGGTA TGTCGCCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCTCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCCGCTGCG
551 CCAAATCGT CGTGTTCTGC AACGCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTTC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GCGGTGGTCA AAGCCGCGT GGAAAAATCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTTGT CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CGGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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717

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCGG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTTG GTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCGCGGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMM SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDNIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGCGCA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACTACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATCTT ACGTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTCGCCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTG3CGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAAATTGT CGTGTTCTGC AACGCGGTGG AAGACAACCC GTTTwTGGCG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACTG CTTTCAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTCCGCGA CCCCCGCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCCGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCat GATCAACAGC AAAACCACTG CCGTGCCCAT TATTCGGTA
1201 ACCGGTAAAA CCGTCGCGCA CAcGGTCGAG TTCGGCGGCT TGTGGgCTA
1251 CGCGCCTGTG ATGCCGCTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQ
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCXSIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHSGSDAV INVGVSGPGV VKAALENSDA TTLTEVAEVV EKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA BAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRIPA PVQSMKN*

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